

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2006, 05:46:37 ; Search time 851.046 Seconds
(without alignments)
2103.915 Million cell updates/sec

Title: US-10-601-913-1
Perfect score: 28
Sequence: 1 GACATTATGTTATGTTGATGAGAC 28

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 1000 summaries

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_strs:*
8: gb_sy:*
9: gb_un:*
10: gb_vl:*
11: gb_ov:*
12: gb_hcg:*
13: gb_in:*
14: gb_cm:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Match length	ID	Description
1	28	100.0	28 2 AR349061	AR349061 Sequence
2	28	100.0	28 2 AR349062	AR349062 Sequence
3	28	100.0	28 2 AR349063	AR349063 Sequence
4	28	100.0	28 2 AR349064	AR349064 Sequence
5	28	100.0	87 2 AR577462	AR577462 Sequence
6	28	100.0	87 2 AX057044	AX057044 Sequence
7	28	100.0	272 10 HPUI4512	HPUI4512 Human papil
8	28	100.0	272 10 HPUI4513	HPUI4513 Human papil
9	28	100.0	370 10 AF404692	AF404692 Human pap
10	28	100.0	421 10 SS1110	SS1110 orf B6 [hum
11	28	100.0	451 10 AF404695	AF404695 Human pap
12	28	100.0	451 10 AF404703	AF404703 Human pap
13	28	100.0	456 10 HPUI34111	HPUI34111 Human papil
14	28	100.0	456 10 HPUI34115	HPUI34115 Human papil
15	28	100.0	456 10 HPUI34120	HPUI34120 Human papil
16	28	100.0	456 10 HPUI34121	HPUI34121 Human papil
17	28	100.0	456 10 HPUI34123	HPUI34123 Human papil
18	28	100.0	456 10 HPUI34124	HPUI34124 Human papil

19	28	100.0	456 10 HPUI34126	HPUI34126 Human papil
20	28	100.0	456 10 HPUI34129	HPUI34129 Human papil
21	28	100.0	458 10 AF003016	AF003016 Human pap
22	28	100.0	477 2 AR577459	AR577459 Sequence
23	28	100.0	477 2 AX057038	AX057038 Sequence
24	28	100.0	477 2 AX766063	AX766063 Sequence
25	28	100.0	477 10 AF486529	AF486529 Human pap
26	28	100.0	477 10 AF486530	AF486530 Human pap
27	28	100.0	477 10 AF486531	AF486531 Human pap
28	28	100.0	477 10 AF486532	AF486532 Human pap
29	28	100.0	477 10 AF486533	AF486533 Human pap
30	28	100.0	477 10 AF486534	AF486534 Human pap
31	28	100.0	477 10 AF486535	AF486535 Human pap
32	28	100.0	477 10 AF486536	AF486536 Human pap
33	28	100.0	477 10 AF486537	AF486537 Human pap
34	28	100.0	477 10 AF486538	AF486538 Human pap
35	28	100.0	477 10 AF486539	AF486539 Human pap
36	28	100.0	477 10 AF486540	AF486540 Human pap
37	28	100.0	477 10 AF486541	AF486541 Human pap
38	28	100.0	477 10 AF486542	AF486542 Human pap
39	28	100.0	477 10 AF486543	AF486543 Human pap
40	28	100.0	477 10 AF486544	AF486544 Human pap
41	28	100.0	477 10 AF486545	AF486545 Human pap
42	28	100.0	477 10 AF486546	AF486546 Human pap
43	28	100.0	477 10 AF486547	AF486547 Human pap
44	28	100.0	477 10 AF486548	AF486548 Human pap
45	28	100.0	477 10 AF486549	AF486549 Human pap
46	28	100.0	477 10 AF486550	AF486550 Human pap
47	28	100.0	477 10 AF486551	AF486551 Human pap
48	28	100.0	477 10 AF486552	AF486552 Human pap
49	28	100.0	519 2 AR095319	AR095319 Sequence
50	28	100.0	519 2 AR095320	AR095320 Sequence
51	28	100.0	519 2 AR173472	AR173472 Sequence
52	28	100.0	519 2 AR173473	AR173473 Sequence
53	28	100.0	540 10 AF404705	AF404705 Human pap
54	28	100.0	543 10 AF404693	AF404693 Human pap
55	28	100.0	543 10 AF404697	AF404697 Human pap
56	28	100.0	556 10 AY098919	AY098919 Human pap
57	28	100.0	596 10 AF548023	AF548023 Human pap
58	28	100.0	654 10 AF469198	AF469198 Human pap
59	28	100.0	776 2 I19491	I19491 Sequence 1
60	28	100.0	779 2 AR199235	AR199235 Sequence
61	28	100.0	780 10 AF187866	AF187866 Human pap
62	28	100.0	780 10 AF187867	AF187867 Human pap
63	28	100.0	780 10 AF187868	AF187868 Human pap
64	28	100.0	780 10 AF187869	AF187869 Human pap
65	28	100.0	790 2 I88813	I88813 Sequence 7
66	28	100.0	801 2 AR095318	AR095318 Sequence
67	28	100.0	801 2 AR173471	AR173471 Sequence
68	28	100.0	822 2 A98742	A98742 Sequence 3
69	28	100.0	822 2 BD080312	BD080312 Vaccine.
70	28	100.0	822 2 BD103161	BD103161 Vaccine.
71	28	100.0	822 2 AR183573	AR183573 Sequence
72	28	100.0	822 2 AX020926	AX020926 Sequence
73	28	100.0	879 2 A98748	A98748 Sequence 9
74	28	100.0	879 2 BD080315	BD080315 Vaccine.
75	28	100.0	879 2 BD103164	BD103164 Vaccine.
76	28	100.0	879 2 AR183576	AR183576 Sequence
77	28	100.0	879 2 AX020932	AX020932 Sequence
78	28	100.0	939 2 AX403959	AX403959 Sequence
79	28	100.0	939 2 AX460903	AX460903 Sequence
80	28	100.0	1000 2 A07622	A07622 Amplified s
81	28	100.0	1000 2 I18920	I18920 Sequence 3
82	28	100.0	1116 2 A98744	A98744 Sequence 5
83	28	100.0	1116 2 BD080313	BD080313 Vaccine.
84	28	100.0	1116 2 BD103162	BD103162 Vaccine.
85	28	100.0	1116 2 AR183574	AR183574 Sequence
86	28	100.0	1116 2 AX020928	AX020928 Sequence
87	28	100.0	1173 2 A98752	A98752 Sequence 13
88	28	100.0	1173 2 BD080317	BD080317 Vaccine.
89	28	100.0	1173 2 BD103166	BD103166 Vaccine.
90	28	100.0	1173 2 AR183578	AR183578 Sequence
91	28	100.0	1173 2 AX020936	AX020936 Sequence

92	28	100.0	1267	10	HPA388056	AJ388056 Human pap	165	26.4	94.3	3531	10	AF001599	AF001599 Human pap
93	28	100.0	1267	10	HPA388058	AJ388058 Human pap	166	26.4	94.3	7904	2	I70143	AF125673 Sequence 2
94	28	100.0	1267	10	HPA388059	AJ388059 Human pap	167	26.4	94.3	7904	10	AF125673	AF125673 Human pap
95	28	100.0	1267	10	HPA388060	AJ388060 Human pap	168	26.4	94.3	7904	10	AF472509	AF472509 Human pap
96	28	100.0	1267	10	HPA388061	AJ388061 Human pap	169	26.4	94.3	7904	10	AF536179	AF536179 Human pap
97	28	100.0	1267	10	HPA388066	AJ388066 Human pap	170	26.4	94.3	7905	10	HPB089348	HPB089348 Human pap
98	28	100.0	7902	2	AX800450	AX800450 Sequence	171	26.4	94.3	7906	10	AF536180	AF536180 Human pap
99	28	100.0	7904	2	BD070940	BD070940 Tissue sp	172	26.4	94.3	7906	10	AF686580	AF686580 Human pap
100	28	100.0	7904	2	BD225188	BD225188 Human pap	173	26.4	94.3	7907	10	AF686583	AF686583 Human pap
101	28	100.0	7904	2	CS073238	CS073238 Sequence	174	26.4	94.3	7908	10	AF472508	AF472508 Human pap
102	28	100.0	7904	2	CS195904	CS195904 Sequence	175	24.8	88.6	245	10	HPU14515	HPU14515 Human pap
103	28	100.0	7904	2	I70142	I70142 Sequence 1	176	24.8	88.6	274	10	HPU14516	HPU14516 Human pap
104	28	100.0	7904	2	I72345	I72345 Sequence 1	177	24.8	88.6	456	2	AR167393	AR167393 Sequence
105	28	100.0	7904	2	AX763489	AX763489 Sequence	178	24.8	88.6	456	10	HPU34107	HPU34107 Human pap
106	28	100.0	7904	2	PPH16	KO2718 Human pap	179	24.8	88.6	456	10	HPU34108	HPU34108 Human pap
107	28	100.0	7905	10	AF534061	AF534061 Human pap	180	24.8	88.6	456	10	HPU34112	HPU34112 Human pap
108	28	100.0	7906	10	AY686581	AY686581 Human pap	181	24.8	88.6	456	10	HPU34116	HPU34116 Human pap
109	28	100.0	7906	10	AY686584	AY686584 Human pap	182	24.8	88.6	456	10	HPU34119	HPU34119 Human pap
110	26.4	94.3	149	2	DD187314	DD187314 SPLICBOSO	183	24.8	88.6	456	10	HPU34132	HPU34132 Human pap
111	26.4	94.3	253	10	HPU14511	UI4511 Human pap	184	24.8	88.6	477	10	AF486325	AF486325 Human pap
112	26.4	94.3	273	10	HPU14514	UI4514 Human pap	185	24.8	88.6	543	10	AF404706	AF404706 Human pap
113	26.4	94.3	298	10	AF404704	AF404704 Human pap	186	24.8	88.6	592	10	AY089923	AY089923 Human pap
114	26.4	94.3	451	10	AF404696	AF404696 Human pap	187	24.8	88.6	602	10	AY112662	AY112662 Human pap
115	26.4	94.3	451	10	AF404699	AF404699 Human pap	188	24.8	88.6	755	10	AY089952	AY089952 Human pap
116	26.4	94.3	451	10	AF404700	AF404700 Human pap	189	24.8	88.6	1267	10	HPA388065	HPA388065 Human pap
117	26.4	94.3	451	10	AF404701	AF404701 Human pap	190	24.8	88.6	7906	10	AF402678	AF402678 Human pap
118	26.4	94.3	456	2	AR177943	AR177943 Sequence	191	24.8	88.6	7905	10	AY686579	AY686579 Human pap
119	26.4	94.3	456	10	AF327851	AF327851 Human pap	192	24.8	88.6	7907	10	AY686582	AY686582 Human pap
120	26.4	94.3	456	10	HPU34109	UI4109 Human pap	193	22	78.6	23	2	BD227573	BD227573 Assay uet
121	26.4	94.3	456	10	HPU34110	UI4110 Human pap	194	22	78.6	23	2	AR476279	AR476279 Sequence
122	26.4	94.3	456	10	HPU34113	UI4113 Human pap	195	21.8	77.9	268478	12	AC182158	AC182158 Bos tauru
123	26.4	94.3	456	10	HPU34114	UI4114 Human pap	196	21.8	77.9	268478	12	AC182158	AC182158 Bos tauru
124	26.4	94.3	456	10	HPU34117	UI4117 Human pap	197	21.2	75.7	146976	6	AC171199	AC171199 Mus muscu
125	26.4	94.3	456	10	HPU34118	UI4118 Human pap	198	21.2	75.7	146976	6	AC173444	AC173444 Atelerix
126	26.4	94.3	456	10	HPU34122	UI4122 Human pap	199	21.2	75.7	170087	12	AC159465	AC159465 Atelerix
127	26.4	94.3	456	10	HPU34125	UI4125 Human pap	200	21.2	75.7	185344	6	AC164163	AC164163 Mus muscu
128	26.4	94.3	456	10	HPU34128	UI4128 Human pap	201	21.2	75.7	236028	12	AC175140	AC175140 Bos tauru
129	26.4	94.3	456	10	HPU34130	UI4130 Human pap	202	21.2	75.0	92053	6	CR030235	CR030235 Mouse DNA
130	26.4	94.3	456	10	HPU34131	UI4131 Human pap	203	21	75.0	200859	13	AC010030	AC010030 Drosophill
131	26.4	94.3	456	10	HPU34133	UI4133 Human pap	204	21	75.0	200859	13	AE003546	AE003546 Drosophill
132	26.4	94.3	456	10	HPU34134	UI4134 Human pap	205	21	75.0	281589	13	AE003546	AE003546 Drosophill
133	26.4	94.3	456	10	HPU34135	UI4135 Human pap	206	20.8	74.3	149436	12	AC118970	AC118970 Rat
134	26.4	94.3	456	2	AX658022	AX658022 Sequence	207	20.8	74.3	149436	12	AC103223	AC103223 Rat
135	26.4	94.3	458	10	AF003013	AF003013 Human pap	208	20.8	74.3	227070	12	AC103223	AC103223 Rat
136	26.4	94.3	458	10	AF003014	AF003014 Human pap	209	20.8	74.3	242810	12	AC103223	AC103223 Rat
137	26.4	94.3	458	10	AF003015	AF003015 Human pap	210	20.8	74.3	242810	12	AC103223	AC103223 Rat
138	26.4	94.3	458	10	AF003017	AF003017 Human pap	211	20.8	74.3	242810	12	AC103223	AC103223 Rat
139	26.4	94.3	458	10	AF003018	AF003018 Human pap	212	20.6	73.6	118153	5	AC092829	AC092829 Homo sapi
140	26.4	94.3	458	10	AF003019	AF003019 Human pap	213	20.6	73.6	118153	5	AC092829	AC092829 Homo sapi
141	26.4	94.3	473	10	AF040694	AF040694 Human pap	214	20.6	73.6	120070	12	AC176718	AC176718 Strongylo
142	26.4	94.3	477	2	CS113240	CS113240 Sequence	215	20.6	73.6	136417	12	AC176718	AC176718 Strongylo
143	26.4	94.3	477	2	CS113240	CS113240 Sequence	216	20.6	73.6	136417	12	AC176718	AC176718 Strongylo
144	26.4	94.3	477	10	AF486322	AF486322 Human pap	217	20.6	73.6	141182	12	AC179326	AC179326 Strongylo
145	26.4	94.3	477	10	AF486322	AF486322 Human pap	218	20.6	73.6	141182	12	AC179326	AC179326 Strongylo
146	26.4	94.3	477	10	AF486322	AF486322 Human pap	219	20.6	73.6	151188	12	AC180762	AC180762 Strongylo
147	26.4	94.3	477	10	AF486322	AF486322 Human pap	220	20.6	73.6	151188	12	AC180762	AC180762 Strongylo
148	26.4	94.3	482	10	AF404698	AF404698 Human pap	221	20.6	73.6	164158	6	AC116788	AC116788 Mus muscu
149	26.4	94.3	570	10	AY098922	AY098922 Human pap	222	20.6	73.6	164158	6	AC116788	AC116788 Mus muscu
150	26.4	94.3	600	10	AY098922	AY098922 Human pap	223	20.6	73.6	169100	6	AC115803	AC115803 Mus muscu
151	26.4	94.3	601	10	AY098918	AY098918 Human pap	224	20.6	73.6	174530	12	AC176694	AC176694 Strongylo
152	26.4	94.3	601	10	AY098918	AY098918 Human pap	225	20.6	73.6	174530	12	AC176694	AC176694 Strongylo
153	26.4	94.3	755	10	AY089953	AY089953 Human pap	226	20.6	73.6	182564	12	AC091757	AC091757 Sus scrofa
154	26.4	94.3	755	10	AY089953	AY089953 Human pap	227	20.6	73.6	182564	12	AC091757	AC091757 Sus scrofa
155	26.4	94.3	755	10	AY089954	AY089954 Human pap	228	20.6	73.6	182564	12	AC091757	AC091757 Sus scrofa
156	26.4	94.3	755	10	AY089954	AY089954 Human pap	229	20.6	73.6	206805	12	AC084708	AC084708 Homo sapi
157	26.4	94.3	755	10	AY089954	AY089954 Human pap	230	20.6	73.6	206805	12	AC084708	AC084708 Homo sapi
158	26.4	94.3	1267	10	HPA388057	HPA388057 Human pap	231	20.6	73.6	216677	6	AC125643	AC125643 Rat
159	26.4	94.3	1267	10	HPA388057	HPA388057 Human pap	232	20.6	73.6	216677	6	AC125643	AC125643 Rat
160	26.4	94.3	1267	10	HPA388062	HPA388062 Human pap	233	20.6	73.6	222900	12	AC094350	AC094350 Strongylo
161	26.4	94.3	1267	10	HPA388063	HPA388063 Human pap	234	20.6	73.6	222900	12	AC094350	AC094350 Strongylo
162	26.4	94.3	1267	10	HPA388064	HPA388064 Human pap	235	20.6	73.6	253733	6	AC154393	AC154393 Mus muscu
163	26.4	94.3	1267	10	HPA388067	HPA388067 Human pap	236	20.6	73.6	253733	6	AC154393	AC154393 Mus muscu
164	26.4	94.3	1267	10	HPA388068	HPA388068 Human pap	237	20.6	73.6	336098	12	AC156054	AC156054 Bos tauru

C 238	20.4	72.9	99	2	DD187318	311	19.8	70.7	163576	6	AL807744	AL807744 Mouse DNA
C 239	20.4	72.9	104	2	DD187316	312	19.8	70.7	171142	6	AC113378	AC113378 Rattus no
C 240	20.4	72.9	112591	5	HS189814	313	19.8	70.7	182088	6	AC100734	AC100734 Mus muscu
C 241	20.4	72.9	141009	12	AC009925	314	19.8	70.7	191775	12	AC074358	AC074358 Mus muscu
C 242	20.4	72.9	158765	12	AC178280	315	19.8	70.7	191833	6	AC161347	AC161347 Mus muscu
C 243	20.4	72.9	170455	12	AC025054	316	19.8	70.7	200266	6	AL772315	AL772315 Mouse DNA
C 244	20.4	72.9	211847	12	AC176876	317	19.8	70.7	204649	4	AC120986	AC120986 Oryza sat
C 245	20.2	72.1	448	2	CG672519	318	19.8	70.7	205616	12	CNS05TDE	AL356033 Homo sapi
C 246	20.2	72.1	42328	6	AL954338	319	19.8	70.7	218519	12	AC135393	AC135393 Rattus no
C 247	20.2	72.1	110000	12	BX248101_2	320	19.8	70.7	223246	12	AC164047	AC164047 Bos tauru
C 248	20.2	72.1	110000	15	AE017197_10	321	19.8	70.7	224569	12	AC110623	AC110623 Rattus no
C 249	20.2	72.1	112303	5	AC093836	322	19.8	70.7	227385	12	AC091407	AC091407 Rattus no
C 250	20.2	72.1	124185	5	AC007560	323	19.8	70.7	229305	12	AC117925	AC117925 Rattus no
C 251	20.2	72.1	138006	12	AC068246	324	19.8	70.7	246027	12	AC097408	AC097408 Rattus no
C 252	20.2	72.1	153938	12	AC080050	325	19.8	70.7	247489	12	AC162999	AC162999 Bos tauru
C 253	20.2	72.1	157978	12	AP001444	326	19.8	70.7	249761	12	AC115089	AC115089 Rattus no
C 254	20.2	72.1	162511	5	AC009470	327	19.8	70.7	258207	12	AC175556	AC175556 Bos tauru
C 255	20.2	72.1	168738	12	AC093632	328	19.6	70.0	423	7	G51331	G51331 SHGC-82851
C 256	20.2	72.1	169470	12	AC019291	329	19.6	70.0	751	4	AJ843120	AJ843120 Plantago
C 257	20.2	72.1	170320	5	AC012486	330	19.6	70.0	1500	13	AK117096	AK117096 Homo sapi
C 258	20.2	72.1	175872	5	AP001266	331	19.6	70.0	4315	4	SBORP2	X71636 S.bicolor o
C 259	20.2	72.1	196261	5	AC100779	332	19.6	70.0	4423	2	CG57241	CG57241 Sequence
C 260	20.2	72.1	204508	5	AC103833	333	19.6	70.0	5240	2	CG607964	CG607964 Sequence
C 261	20.2	72.1	209242	5	CNS01RGM	334	19.6	70.0	7082	12	AC014876	AC014876 Homo sapi
C 262	20.2	72.1	220028	12	AC153442	335	19.6	70.0	28809	11	BX539306	BX539306 Zebrafish
C 263	20.2	72.1	232443	12	AC099251	336	19.6	70.0	39472	5	HSN7A10	Z68324 Human DNA s
C 264	20	71.4	2135	11	BC108531	337	19.6	70.0	39624	5	AC069504	AC069504 Homo sapi
C 265	20	71.4	33398	4	SPBC3B8	338	19.6	70.0	41449	6	AC167190	AC167190 Mus muscu
C 266	20	71.4	80472	4	F24J2	339	19.6	70.0	43115	12	AC162070	AC162070 Bos tauru
C 267	20	71.4	84544	4	AC007134	340	19.6	70.0	43115	12	AC160518	AC160518 Strongylo
C 268	20	71.4	87119	4	AC005897	341	19.6	70.0	49162	12	AC087594	AC087594 Homo sapi
C 269	20	71.4	88239	12	AP007978	342	19.6	70.0	66608	12	AC162237	AC162237 Bos tauru
C 270	20	71.4	97864	4	AP006093	343	19.6	70.0	72208	12	AC178420	AC178420 Strongylo
C 271	20	71.4	104684	4	AP006124	344	19.6	70.0	74129	12	AC169052	AC169052 Bos tauru
C 272	20	71.4	117945	4	AC007045	345	19.6	70.0	90971	12	AC161958	AC161958 Bos tauru
C 273	20	71.4	119419	11	BX465183	346	19.6	70.0	94348	11	AC109580	AC109580 Danio rer
C 274	20	71.4	135391	5	HS805C22	347	19.6	70.0	98558	5	AL137138	AL137138 Human DNA
C 275	20	71.4	137336	4	AC007915	348	19.6	70.0	101325	12	AC166898	AC166898 Medicago
C 276	20	71.4	147738	12	CR848712	349	19.6	70.0	103541	12	AC158508	AC158508 Pan trogl
C 277	20	71.4	148870	5	HS173A13	350	19.6	70.0	105001	2	ARE59586	ARE59586 Sequence
C 278	20	71.4	159852	5	AC097476	351	19.6	70.0	105002	2	ARE59780	ARE59780 Sequence
C 279	20	71.4	170095	5	AL356131	352	19.6	70.0	106321	12	AC148344	AC148344 Medicago
C 280	20	71.4	175908	12	AC025879	353	19.6	70.0	106951	4	AC147963	AC147963 Medicago
C 281	20	71.4	176009	11	BX465834	354	19.6	70.0	110000	4	AP008207_358	Continuation (359
C 282	20	71.4	181535	6	AC123529	355	19.6	70.0	110000	4	AP008207_322	Continuation (323)
C 283	20	71.4	183355	6	AC178035	356	19.6	70.0	110000	15	AE017321_00	Continuation (2 of
C 284	20	71.4	225738	6	AC102633	357	19.6	70.0	110000	15	AE017321_01	Continuation (2 of
C 285	20	71.4	230139	6	AC116731	358	19.6	70.0	113259	12	AC181952	AC181952 Strongylo
C 286	20	71.4	255663	6	AC091276	359	19.6	70.0	121026	6	AC146777	AC146777 Medicago
C 287	20	71.4	273739	12	CR848028	360	19.6	70.0	128574	6	BX545905	BX545905 Mouse DNA
C 288	20	71.4	278729	12	CR848028	361	19.6	70.0	129355	5	AC004080	AC004080 Homo sapi
C 289	20	71.4	300661	12	AC106916	362	19.6	70.0	129778	4	AC091123	AC091123 Oryza sat
C 290	20	71.4	300661	12	AC106916	363	19.6	70.0	134355	12	AC176911	AC176911 Strongylo
C 291	19.8	70.7	4864	15	AJ937360	364	19.6	70.0	142991	12	AC151805	AC151805 Medicago
C 292	19.8	70.7	29993	2	DD194608	365	19.6	70.0	144047	12	AC175222	AC175222 Atelerix
C 293	19.8	70.7	29993	2	DD194610	366	19.6	70.0	152113	5	AL592285	AL592285 Human DNA
C 294	19.8	70.7	29993	2	AX825168	367	19.6	70.0	154772	13	AC009214	AC009214 Drosophi
C 295	19.8	70.7	29993	2	AX825170	368	19.6	70.0	156381	11	AL954313	AL954313 Zebrafish
C 296	19.8	70.7	38342	2	AX251503	369	19.6	70.0	157544	12	AC162255	AC162255 Bos tauru
C 297	19.8	70.7	38342	2	AX344502	370	19.6	70.0	159584	12	AC150232	AC150232 Papio anu
C 298	19.8	70.7	87937	5	CNS05TDE	371	19.6	70.0	160190	12	AC158833	AC158833 Bos tauru
C 299	19.8	70.7	89995	5	AC133794	372	19.6	70.0	161134	5	AC079161	AC079161 Homo sapi
C 300	19.8	70.7	110000	4	CR382138_12	373	19.6	70.0	161654	5	AC116608	AC116608 Papio ham
C 301	19.8	70.7	110000	4	AP008211_280	374	19.6	70.0	162215	6	AL731773	AL731773 Mouse DNA
C 302	19.8	70.7	110000	13	CR548612_00	375	19.6	70.0	162996	12	AL391359	AL391359 Homo sapi
C 303	19.8	70.7	149167	12	AC158838	376	19.6	70.0	163050	12	AC020696	AC020696 Homo sapi
C 304	19.8	70.7	149358	6	AC081751	377	19.6	70.0	163640	12	AC093328	AC093328 Homo sapi
C 305	19.8	70.7	150568	12	AC168579	378	19.6	70.0	165194	12	AC176112	AC176112 Strongylo
C 306	19.8	70.7	156196	11	BX072559	379	19.6	70.0	166756	12	AC149184	AC149184 Papio anu
C 307	19.8	70.7	157916	11	BX511133	380	19.6	70.0	167794	12	AP215844	AP215844 Homo sapi
C 308	19.8	70.7	159933	12	AC170027	381	19.6	70.0	169511	13	AC007531	AC007531 Drosophi
C 309	19.8	70.7	160907	4	AC120990	382	19.6	70.0	170193	11	AL935189	AL935189 Zebrafish
C 310	19.8	70.7	161067	5	AL353638	383	19.6	70.0	170759	4	AP003271	AP003271 Oryza sat

530	19.2	68.6	202311	12	AC179831	Strongylo	603	19	67.9	1981	2	AX764575	Sequence
C 531	19.2	68.6	205873	12	AC073147	Homo sapi	C 604	19	67.9	2119	6	BC101869	AX764575 Rattus no
C 532	19.2	68.6	209293	6	AC153906	Mus muscu	C 605	19	67.9	2834	4	CP969275	BC101869 Rattus no
C 533	19.2	68.6	210643	12	AC103432	Rattus no	C 606	19	67.9	2901	6	AX591743	U69275 Cryptoelect
C 534	19.2	68.6	212426	5	AC104335	Homo sapi	C 607	19	67.9	6092	12	AX345922	AX345922 Sequence
C 535	19.2	68.6	216157	12	AF485269	Mus muscu	C 608	19	67.9	12231	15	AE002118	AE002118 Ureaplas
C 536	19.2	68.6	219254	12	AC172524	Homo sapi	C 609	19	67.9	12415	13	CEY102FS	AL032829 Caenorhab
C 537	19.2	68.6	221989	5	AY220878	Strongylo	C 610	19	67.9	17684	14	RBA811CG	M77195 Oryctolagus
C 538	19.2	68.6	226866	12	AC170217	Bos tauru	C 611	19	67.9	18008	5	AC093147	AC093147 Homo sapi
C 539	19.2	68.6	228443	13	AE003772	Drosophila	C 612	19	67.9	20112	14	AT284844	AT284844 Oryctolag
C 540	19.2	68.6	229087	12	AC181100	Strongylo	C 613	19	67.9	30082	5	AL606759	AL606759 Human DNA
C 541	19.2	68.6	230267	11	BX324146	Zebrafish	C 614	19	67.9	33745	13	U97551	U97551 Caenorhabdi
C 542	19.2	68.6	237800	12	AC171216	Bos tauru	C 615	19	67.9	34009	5	AC105447	AC105447 Homo sapi
C 543	19.2	68.6	240562	12	AC166667	Bos tauru	C 616	19	67.9	42301	5	AP000528	AP000528 Homo sapi
C 544	19.2	68.6	243188	12	AC106625	Rattus no	C 617	19	67.9	43503	12	AC150000	AC150000 Strongylo
C 545	19.2	68.6	243188	12	AC106625	Rattus no	C 618	19	67.9	43503	12	AC150000	AC150000 Strongylo
C 546	19.2	68.6	244237	6	AC136921	Mus muscu	C 619	19	67.9	55012	5	AL136976	AL136976 Human DNA
C 547	19.2	68.6	245819	12	AC172437	Bos tauru	C 620	19	67.9	55722	12	AC168987	AC168987 Bos tauru
C 548	19.2	68.6	250036	12	AC125669	Rattus no	C 621	19	67.9	55981	11	CR388122	CR388122 Zebrafish
C 549	19.2	68.6	252928	12	AC166438	Bos tauru	C 622	19	67.9	56448	13	AC006679	AC006679 Caenorhab
C 550	19.2	68.6	253434	12	AC170235	Bos tauru	C 623	19	67.9	64976	12	AC026256	AC026256 Homo sapi
C 551	19.2	68.6	253950	12	AC111282	Rattus no	C 624	19	67.9	65556	12	AC100220	AC100220 Mus muscu
C 552	19.2	68.6	254107	12	AC169777	Bos tauru	C 625	19	67.9	66252	12	AC108772	AC108772 Mus muscu
C 553	19.2	68.6	268549	12	AC136581	Rattus no	C 626	19	67.9	67644	12	AC100474	AC100474 Mus muscu
C 554	19.2	68.6	268549	12	AC136581	Rattus no	C 627	19	67.9	67644	12	AC100474	AC100474 Mus muscu
C 555	19.2	68.6	271869	13	AE003531	Drosophila	C 628	19	67.9	72371	12	AC113530	AC113530 Mus muscu
C 556	19.2	68.6	272890	12	AC016653	Homo sapi	C 629	19	67.9	72371	12	AC113530	AC113530 Mus muscu
C 557	19.2	68.6	294609	13	AE003787	Drosophila	C 630	19	67.9	79383	11	BX248110	BX248110 Zebrafish
C 558	19.2	68.6	301146	12	AC111317	Rattus no	C 631	19	67.9	79383	11	BX248110	BX248110 Zebrafish
C 559	19.2	68.6	301146	12	AC111317	Rattus no	C 632	19	67.9	86514	5	AL136117	AL136117 Human DNA
C 560	19.2	68.6	349980	2	AX344555	Sequence	C 633	19	67.9	90139	12	AC174600	AC174600 Strongylo
C 561	19.2	68.6	349980	2	AX344555	Sequence	C 634	19	67.9	90139	12	AC174600	AC174600 Strongylo
C 562	19.2	68.6	349980	2	AX344555	Sequence	C 635	19	67.9	90139	12	AC174600	AC174600 Strongylo
C 563	19.2	68.6	349980	2	AX344555	Sequence	C 636	19	67.9	90139	12	AC174600	AC174600 Strongylo
C 564	19.2	68.6	349980	2	AX344555	Sequence	C 637	19	67.9	90139	12	AC174600	AC174600 Strongylo
C 565	19.2	68.6	349980	2	AX344555	Sequence	C 638	19	67.9	90139	12	AC174600	AC174600 Strongylo
C 566	19.2	68.6	349980	2	AX344555	Sequence	C 639	19	67.9	90139	12	AC174600	AC174600 Strongylo
C 567	19.2	68.6	349980	2	AX344555	Sequence	C 640	19	67.9	90139	12	AC174600	AC174600 Strongylo
C 568	19.2	68.6	349980	2	AX344555	Sequence	C 641	19	67.9	90139	12	AC174600	AC174600 Strongylo
C 569	19.2	68.6	349980	2	AX344555	Sequence	C 642	19	67.9	90139	12	AC174600	AC174600 Strongylo
C 570	19.2	68.6	349980	2	AX344555	Sequence	C 643	19	67.9	90139	12	AC174600	AC174600 Strongylo
C 571	19.2	68.6	349980	2	AX344555	Sequence	C 644	19	67.9	90139	12	AC174600	AC174600 Strongylo
C 572	19.2	68.6	349980	2	AX344555	Sequence	C 645	19	67.9	90139	12	AC174600	AC174600 Strongylo
C 573	19.2	68.6	349980	2	AX344555	Sequence	C 646	19	67.9	90139	12	AC174600	AC174600 Strongylo
C 574	19.2	68.6	349980	2	AX344555	Sequence	C 647	19	67.9	90139	12	AC174600	AC174600 Strongylo
C 575	19.2	68.6	349980	2	AX344555	Sequence	C 648	19	67.9	90139	12	AC174600	AC174600 Strongylo
C 576	19.2	68.6	349980	2	AX344555	Sequence	C 649	19	67.9	90139	12	AC174600	AC174600 Strongylo
C 577	19.2	68.6	349980	2	AX344555	Sequence	C 650	19	67.9	90139	12	AC174600	AC174600 Strongylo
C 578	19.2	68.6	349980	2	AX344555	Sequence	C 651	19	67.9	90139	12	AC174600	AC174600 Strongylo
C 579	19.2	68.6	349980	2	AX344555	Sequence	C 652	19	67.9	90139	12	AC174600	AC174600 Strongylo
C 580	19.2	68.6	349980	2	AX344555	Sequence	C 653	19	67.9	90139	12	AC174600	AC174600 Strongylo
C 581	19.2	68.6	349980	2	AX344555	Sequence	C 654	19	67.9	90139	12	AC174600	AC174600 Strongylo
C 582	19.2	68.6	349980	2	AX344555	Sequence	C 655	19	67.9	90139	12	AC174600	AC174600 Strongylo
C 583	19.2	68.6	349980	2	AX344555	Sequence	C 656	19	67.9	90139	12	AC174600	AC174600 Strongylo
C 584	19.2	68.6	349980	2	AX344555	Sequence	C 657	19	67.9	90139	12	AC174600	AC174600 Strongylo
C 585	19.2	68.6	349980	2	AX344555	Sequence	C 658	19	67.9	90139	12	AC174600	AC174600 Strongylo
C 586	19.2	68.6	349980	2	AX344555	Sequence	C 659	19	67.9	90139	12	AC174600	AC174600 Strongylo
C 587	19.2	68.6	349980	2	AX344555	Sequence	C 660	19	67.9	90139	12	AC174600	AC174600 Strongylo
C 588	19.2	68.6	349980	2	AX344555	Sequence	C 661	19	67.9	90139	12	AC174600	AC174600 Strongylo
C 589	19.2	68.6	349980	2	AX344555	Sequence	C 662	19	67.9	90139	12	AC174600	AC174600 Strongylo
C 590	19.2	68.6	349980	2	AX344555	Sequence	C 663	19	67.9	90139	12	AC174600	AC174600 Strongylo
C 591	19.2	68.6	349980	2	AX344555	Sequence	C 664	19	67.9	90139	12	AC174600	AC174600 Strongylo
C 592	19.2	68.6	349980	2	AX344555	Sequence	C 665	19	67.9	90139	12	AC174600	AC174600 Strongylo
C 593	19.2	68.6	349980	2	AX344555	Sequence	C 666	19	67.9	90139	12	AC174600	AC174600 Strongylo
C 594	19.2	68.6	349980	2	AX344555	Sequence	C 667	19	67.9	90139	12	AC174600	AC174600 Strongylo
C 595	19.2	68.6	349980	2	AX344555	Sequence	C 668	19	67.9	90139	12	AC174600	AC174600 Strongylo
C 596	19.2	68.6	349980	2	AX344555	Sequence	C 669	19	67.9	90139	12	AC174600	AC174600 Strongylo
C 597	19.2	68.6	349980	2	AX344555	Sequence	C 670	19	67.9	90139	12	AC174600	AC174600 Strongylo
C 598	19.2	68.6	349980	2	AX344555	Sequence	C 671	19	67.9	90139	12	AC174600	AC174600 Strongylo
C 599	19.2	68.6	349980	2	AX344555	Sequence	C 672	19	67.9	90139	12	AC174600	AC174600 Strongylo
C 600	19.2	68.6	349980	2	AX344555	Sequence	C 673	19	67.9	90139	12	AC174600	AC174600 Strongylo
C 601	19.2	68.6	349980	2	AX344555	Sequence	C 674	19	67.9	90139	12	AC174600	AC174600 Strongylo
C 602	19.2	68.6	349980	2	AX344555	Sequence	C 675	19	67.9	90139	12	AC174600	AC174600 Strongylo

822	19	67.9	243489	12	AC096036	895	18.8	67.1	158004	5	AC087319	AC087319 Homo sapi
C 823	19	67.9	244971	6	AL662891	C 896	18.8	67.1	161873	4	AC090056	AC090056 Oryza sat
C 824	19	67.9	245476	12	AC098496	897	18.8	67.1	161938	4	AB006758	AB006758 Oryza sat
C 825	19	67.9	245489	12	AC170939	898	18.8	67.1	166235	6	AC138292	AC138292 Mus muscu
C 826	19	67.9	247805	12	AC131604	899	18.8	67.1	166642	5	AC018919	AC018919 Homo sapi
C 827	19	67.9	250014	12	CR938713	C 900	18.8	67.1	167067	11	BX511268	BX511268 Zebrafish
C 828	19	67.9	250701	5	CR974412	901	18.8	67.1	168062	12	AC012857	AC012857 Homo sapi
C 829	19	67.9	250701	12	CR974436	902	18.8	67.1	168062	12	AC022477	AC022477 Homo sapi
C 830	19	67.9	250804	12	AC097842	C 903	18.8	67.1	168919	12	AC019172	AC019172 Mus muscu
C 831	19	67.9	250906	12	AC123491	C 904	18.8	67.1	168979	11	BX005444	BX005444 Zebrafish
C 832	19	67.9	252271	12	AC157192	C 905	18.8	67.1	169029	5	CNS0067R	AL390800 Human chr
C 833	19	67.9	257078	12	AC118300	906	18.8	67.1	169884	11	CR848728	CR848728 Zebrafish
C 834	19	67.9	261065	12	AC128913	C 907	18.8	67.1	170813	12	AC181012	AC181012 Strongylo
C 835	19	67.9	263874	12	AC167337	908	18.8	67.1	170908	5	HSB828009	AL121582 Human DNA
C 836	19	67.9	267058	12	AC134185	C 909	18.8	67.1	172479	13	AC008559	AC008559 Drosophi
C 837	19	67.9	270080	12	AC113644	C 910	18.8	67.1	173688	4	AP005705	AP005705 Oryza sat
C 838	19	67.9	275507	12	AC099381	C 911	18.8	67.1	177660	11	BX276188	BX276188 Zebrafish
C 839	19	67.9	281092	12	AC098047	C 912	18.8	67.1	177770	5	AC110027	AC110027 Homo sapi
C 840	19	67.9	282066	12	AC166668	C 913	18.8	67.1	180916	6	AL844195	AL844195 Mouse DNA
C 841	19	67.9	285689	12	AC160355	914	18.8	67.1	181413	5	AC080032	AC080032 Homo sapi
C 842	19	67.9	287635	12	AC174454	C 915	18.8	67.1	187783	12	AC137462	AC137462 Rattus no
C 843	19	67.9	289818	12	AC108322	C 916	18.8	67.1	188482	12	AC144467	AC144467 Papio anu
C 844	19	67.9	313631	12	AC129821	C 917	18.8	67.1	188876	12	AC162312	AC162312 Mus muscu
C 845	19	67.9	319109	12	AC091368	918	18.8	67.1	189355	11	BX649503	BX649503 Zebrafish
C 846	19	67.9	320208	12	AC157391	C 919	18.8	67.1	194086	6	AC134382	AC134382 Mus muscu
C 847	19	67.9	340000	5	HS21C004	920	18.8	67.1	196129	12	AC167617	AC167617 Bos tauru
C 848	19	67.9	347145	12	AC173518	921	18.8	67.1	196408	12	AC130420	AC130420 Homo sapi
C 849	19	67.9	348540	12	AC132503	922	18.8	67.1	196661	6	AC119667	AC119667 Mus muscu
C 850	19	67.9	349402	15	BX842644	923	18.8	67.1	196758	12	AC009653	AC009653 Homo sapi
C 851	19	67.9	349980	2	AX344566	924	18.8	67.1	199447	11	BX510918	BX510918 Zebrafish
C 852	18.8	67.1	572	13	AY254855S2	925	18.8	67.1	199612	5	AC021582	AC021582 Homo sapi
C 853	18.8	67.1	572	15	NMU93902	C 926	18.8	67.1	201310	6	AC109222	AC109222 Mus muscu
C 854	18.8	67.1	618	15	NMU93903	927	18.8	67.1	204653	6	AC005302	AC005302 Mus muscu
C 855	18.8	67.1	2014	11	BC059513	C 928	18.8	67.1	204720	12	AC008052	AC008052 Homo sapi
C 856	18.8	67.1	2387	13	AY817736	929	18.8	67.1	208170	12	BX901911	BX901911 Danto rer
C 857	18.8	67.1	3780	2	CQ806947	930	18.8	67.1	210130	6	CT009723	CT009723 Mouse DNA
C 858	18.8	67.1	3780	2	CQ807221	931	18.8	67.1	210145	12	AC114314	AC114314 Homo sapi
C 859	18.8	67.1	17758	13	U56959	C 932	18.8	67.1	210950	6	AC129317	AC129317 Mus muscu
C 860	18.8	67.1	29756	13	U70858	933	18.8	67.1	211817	11	BX649401	BX649401 Zebrafish
C 861	18.8	67.1	55858	6	AL929080	C 934	18.8	67.1	215455	12	AC132224	AC132224 Rattus no
C 862	18.8	67.1	59372	4	AB023039	C 935	18.8	67.1	220008	6	AC165235	AC165235 Mus muscu
C 863	18.8	67.1	71127	12	AC131278	936	18.8	67.1	223812	6	AC131716	AC131716 Mus muscu
C 864	18.8	67.1	74671	5	AL449106	937	18.8	67.1	224213	6	AC147051	AC147051 Mus muscu
C 865	18.8	67.1	75485	11	CR381654	C 938	18.8	67.1	227600	12	CR956432	CR956432 Homo sapi
C 866	18.8	67.1	87489	12	AC166745	C 939	18.8	67.1	228177	11	BX547928	BX547928 Zebrafish
C 867	18.8	67.1	94773	12	AC144930	940	18.8	67.1	234740	12	AC158693	AC158693 Bos tauru
C 868	18.8	67.1	110000	4	BD061520_3	C 941	18.8	67.1	240675	12	AC106325	AC106325 Rattus no
C 869	18.8	67.1	110000	2	AR409405_3	C 942	18.8	67.1	251681	12	CR788226	CR788226 Danto rer
C 870	18.8	67.1	110000	4	AP008215_063	C 943	18.8	67.1	252440	11	BX005425	BX005425 Zebrafish
C 871	18.8	67.1	110000	4	AP008215_096	C 944	18.8	67.1	256833	12	AC109530	AC109530 Rattus no
C 872	18.8	67.1	110000	4	AE016859_096	C 945	18.8	67.1	260027	13	AE003659	AE003659 Drosophi
C 873	18.8	67.1	110000	12	CR848710_0	946	18.8	67.1	267375	12	AC095339	AC095339 Rattus no
C 874	18.8	67.1	110000	12	TANN4_12	947	18.8	67.1	285218	12	AC112982	AC112982 Bos tauru
C 875	18.8	67.1	110000	15	AE014133_18	948	18.8	67.1	295117	12	AC118895	AC118895 Rattus no
C 876	18.8	67.1	110000	15	BA000003_3	949	18.8	67.1	305666	12	AC166698	AC166698 Bos tauru
C 877	18.8	67.1	114231	5	HS3900C10	950	18.8	67.1	330580	12	AC101959	AC101959 Mus muscu
C 878	18.8	67.1	119811	5	AL161787	951	18.8	67.1	348885	12	AC151274	AC151274 Mus muscu
C 879	18.8	67.1	120709	12	AC034185	C 952	18.8	66.4	664	7	BV051539	BV051539 S212P6792
C 880	18.8	67.1	123159	4	AC135798	953	18.8	66.4	664	15	AF062845	AF062845 Escherich
C 881	18.8	67.1	136162	6	AL645994	C 954	18.8	66.4	711	2	AR507851	AR507851 Sequence
C 882	18.8	67.1	138335	4	AC119148	955	18.8	66.4	715	7	AR507851	AR507851 Sequence
C 883	18.8	67.1	141705	11	BX571715	956	18.8	66.4	725	7	BV477275	BV477275 G591P6421
C 884	18.8	67.1	143299	5	AL353519	957	18.8	66.4	759	13	AM040168	AM040168 Drosophi
C 885	18.8	67.1	144723	5	AC008818	C 958	18.8	66.4	1222	11	AY144593	AY144593 Delima mol
C 886	18.8	67.1	144951	12	AC171445	C 959	18.8	66.4	1495	4	BC077273	BC077273 Danto rer
C 887	18.8	67.1	148648	12	AC171445	960	18.8	66.4	1524	11	AF483211	AF483211 Alonboa m
C 888	18.8	67.1	148673	6	AC123048	C 961	18.8	66.4	1574	11	BC095064	BC095064 Danto rer
C 889	18.8	67.1	151365	6	AC127304	C 962	18.8	66.4	1600	11	AY583695	AY583695 Trioroxy a
C 890	18.8	67.1	153307	6	AL845441	C 963	18.8	66.4	2402	2	CO574074	CO574074 Sequence
C 891	18.8	67.1	154730	13	AC008184	C 964	18.8	66.4	2543	3	AY069621	AY069621 Drosophi
C 892	18.8	67.1	155637	6	AC111012	C 965	18.8	66.4	2624	13	BT053715	BT053715 Drosophi
C 893	18.8	67.1	155992	12	AC083854	C 966	18.8	66.4	2630	13	AY119523	AY119523 Drosophi
C 894	18.8	67.1	155992	12	AC034184	C 967	18.8	66.4	3090	2	AR528057	AR528057 Sequence

ACCESSION AR349062 GI:33749767
VERSION AR349062.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Carter,N.M.
TITLE Nucleic acid probes complementary to human papilloma virus nucleic acid
JOURNAL Patent: US 6583278-A 2 24-JUN-2003;
Gen-Probe Incorporated; San Diego, CA
FEATURES
source location/Qualifiers
1..28
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 28; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACATTATGTTATAGTTGTATGGAAC 28
|||||
1 GACATTATGTTATAGTTGTATGGAAC 28

Db 1 GACATTATGTTATAGTTGTATGGAAC 28

RESULT 2
AR349062/c 28 bp DNA linear PAT 17-AUG-2003
LOCUS AR349062
DEFINITION Sequence 2 from patent US 6583278.

ALIGNMENTS

RESULT 1
AR349061 28 bp DNA linear PAT 17-AUG-2003
LOCUS AR349061
DEFINITION Sequence 1 from patent US 6583278.
ACCESSION AR349061
VERSION AR349061.1 GI:33749766
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Carter,N.M.
TITLE Nucleic acid probes complementary to human papilloma virus nucleic acid
JOURNAL Patent: US 6583278-A 1 24-JUN-2003;
Gen-Probe Incorporated; San Diego, CA
FEATURES
source location/Qualifiers
1..28
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 28; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACATTATGTTATAGTTGTATGGAAC 28
|||||
1 GACATTATGTTATAGTTGTATGGAAC 28

Db 1 GACATTATGTTATAGTTGTATGGAAC 28

RESULT 2
AR349062/c 28 bp DNA linear PAT 17-AUG-2003
LOCUS AR349062
DEFINITION Sequence 2 from patent US 6583278.

ACCESSION AR349062 GI:33749767
VERSION AR349062.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Carter,N.M.
TITLE Nucleic acid probes complementary to human papilloma virus nucleic acid
JOURNAL Patent: US 6583278-A 2 24-JUN-2003;
Gen-Probe Incorporated; San Diego, CA
FEATURES
source location/Qualifiers
1..28
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 28; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACATTATGTTATAGTTGTATGGAAC 28
|||||
28 GACATTATGTTATAGTTGTATGGAAC 1

Db 28 GACATTATGTTATAGTTGTATGGAAC 1

RESULT 3
AR349063 28 bp DNA linear PAT 17-AUG-2003
LOCUS AR349063
DEFINITION Sequence 3 from patent US 6583278.
ACCESSION AR349063
VERSION AR349063.1 GI:33749768
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Carter,N.M.
TITLE Nucleic acid probes complementary to human papilloma virus nucleic acid
JOURNAL Patent: US 6583278-A 3 24-JUN-2003;
Gen-Probe Incorporated; San Diego, CA
FEATURES
source location/Qualifiers
1..28
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 28; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACATTATGTTATAGTTGTATGGAAC 28
|||||
28 GACATTATGTTATAGTTGTATGGAAC 1

Db 28 GACATTATGTTATAGTTGTATGGAAC 1

RESULT 4
AR349064 28 bp DNA linear PAT 17-AUG-2003
LOCUS AR349064
DEFINITION Sequence 4 from patent US 6583278.
ACCESSION AR349064
VERSION AR349064.1 GI:33749769
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Carter,N.M.
TITLE Nucleic acid probes complementary to human papilloma virus nucleic acid
JOURNAL Patent: US 6583278-A 4 24-JUN-2003;

Gen-Probe Incorporated; San Diego, CA

FEATURES
source
1.28
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match
Best Local Similarity 100.0%; Score 28; DB 2; Length 28;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
1 GACATTATTGTTATAGTTGTATGGAAC 28
|||||
28 GACATTATTGTTATAGTTGTATGGAAC 1

RESULT 5
AR577462 87 bp DNA linear PAT 14-DEC-2004
LOCUS
DEFINITION Sequence 7 from patent US 6783763.
ACCESSION AR577462
VERSION AR577462.1 GI:56580067
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 87)
Choppin,J., Villada,I.B., Guillet,J.-G., Connan,F. and Ferries,E.
Polyepitopic proceinlc fragments of the E6 and E7 HPV proteins,
production and use thereof in vaccines
Patent: US 6783763-A 7 31-AUG-2004;
Peptide Immune ligands and Institut National de la Sante et de la
Recherche Medicale (INSERM); Labège, Cedex;
FR;

FEATURES
source
1.87
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/mol_type="genomic DNA"

ORIGIN

Query Match
Best Local Similarity 100.0%; Score 28; DB 2; Length 87;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
1 GACATTATTGTTATAGTTGTATGGAAC 28
|||||
14 GACATTATTGTTATAGTTGTATGGAAC 41

RESULT 6
AX057044 87 bp DNA linear PAT 17-JAN-2001
LOCUS
DEFINITION Sequence 7 from Patent WO0075336.
ACCESSION AX057044
VERSION AX057044.1 GI:12309885
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
1
Choppin,J., bourgault Villada,I., Guillet,J.-G., Connan,F. and
Ferries,E.
Proteinfiragmente die verschiedene epitope der hpv proteine e6 und
e7 umfassen, ihre herstellung und verwendungen insbesondere zur
impfung
Patent: WO 0075336-A 7 14-DEC-2000;
Biovector Therapeutics S.A. (FR) ; Institut National de la Sante et
de la Recherche Medicale (INSERM) (FR)
Location/Qualifiers
1.87
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

FEATURES
source

/note="fragment de la sequence codant pour E6 de HPV et
sequence peptidique correspondante"
1..>87
/note="unnamed protein product"
/codon_start=1
/transl_table=11
/protein_id="CAC22413.1"
/db_xref="GI:12309886"
/translation="MSERYHCYSLYGTTLEQYNKPLCDLLI"

ORIGIN

Query Match
Best Local Similarity 100.0%; Score 28; DB 2; Length 87;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
1 GACATTATTGTTATAGTTGTATGGAAC 28
|||||
14 GACATTATTGTTATAGTTGTATGGAAC 41

RESULT 7
HPV14512 271 bp DNA linear VRL 14-SHP-1995
LOCUS
DEFINITION Human papillomavirus clone HPV1603 E6 protein (E6) gene, partial
cds.
VERSION U14512.1 GI:984945
KEYWORDS
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
Virus; dsDNA viruses, no RNA stage; Papillomaviridae;
unclassified Papillomaviridae.
1 (bases 1 to 271)
Haegert,D.G., Galutira,D.F. and Youngnuband,B.H.
Sequence variation in the E6 gene of human papillomavirus type 16
Unpublished
2 (bases 1 to 271)
Galutira,D.F.
Direct Submission
Submitted (07-SEP-1994) Dante F. Galutira, Memorial University of
Newfoundland, Discipline of Pathology, Fac. Medicine, St. John's,
Newfoundland, A1B 3Y6, Canada

FEATURES
source
1.271
/organism="Human papillomavirus"
/mol_type="genomic DNA"
/strain="HPV16"
/db_xref="taxon:10566"
/clone="HPV1603"
/tissue_type="cervical tissue from invasive carcinoma"
1..271
/gene="E6"
/note="E6"
<1..>271
/gene="E6"
/codon_start=2
/product="E6 protein"
/protein_id="AAB60566.1"
/db_xref="GI:984946"
/translation="VYDFAPRDLCTIVRDGNPYAVCDKLTLYSKISERYHCYSLYG
TTLEQYNKPLCDLLIRINCQKPLCPBEKQRHLDKKQRFNIRGR"
85
/gene="E6"
/note="E6"
/note="T to G transversion from P16, GenBank Accession
Number K02718, position 310; NCBI GI: 333031"
/replac="c"

ORIGIN

Query Match
Best Local Similarity 100.0%; Score 28; DB 10; Length 271;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
1 GACATTATTGTTATAGTTGTATGGAAC 28
|||||

Db 108 GACATTATTGTTATGTTGATGGAAC 135

RESULT 8
LOCUS HPV14513
DEFINITION Human papillomavirus clone HPV1607 E6 protein (E6) gene, partial

ACCESSION U14513
VERSION U14513.1 GI:984947
KEYWORDS Human papillomavirus
SOURCE Human papillomavirus
ORGANISM Viruses; dsDNA viruses, no RNA stage; Papillomaviridae; unclassified Papillomaviridae.

REFERENCE 1 (bases 1 to 272)
AUTHORS Haegert,D.G., Galutira,D.F. and Youngusband,B.H.
TITLE Sequence variation in the E6 gene of human papillomavirus type 16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 272)
AUTHORS Galutira,D.F.
TITLE Direct Submission
JOURNAL Submitted (07-SEP-1994) Dante F. Galutira, Memorial University of Newfoundland, Discipline of Pathology, Fac. Medicine, St. John's, Newfoundland, A1B 3V6, Canada

FEATURES
source
1..272
/organism="Human papillomavirus"
/mol_type="genomic DNA"
/strain="HPV16"
/db_xref="taxon:10566"
/clone="HPV1607"
/tissue_type="cervical tissue from invasive carcinoma"
1..272
/gene="E6"
/note=">272"
/gene="E6"
/codon_start=2
/product="E6 protein"
/protein_id="AAB60567.2"
/db_xref="GI:12831648"
/translation="VYDFAFRDLWIVYDGNPVAVCDKLFYKISRYHYCYSLYGTTLLEQYNKPLCDLLIRINCQKPLCEPEKQRHDKQRFNIRGR"
31
/gene="E6"
/note="C to G transversion from PA16, GenBank accession Number K02718, position 256; NCBI GI: 335031"
/replace="C"

variation

ORIGIN

Query Match 100.0%; Score 28; DB 10; Length 272;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 GACATTATTGTTATGTTGATGGAAC 28
108 GACATTATTGTTATGTTGATGGAAC 135

Db 108 GACATTATTGTTATGTTGATGGAAC 135

RESULT 9
LOCUS AFA04692
DEFINITION Human papillomavirus type 16 isolate HPV16BCCI E6 protein (E6) and E7 protein (E7) genes, partial cds.
ACCESSION AFA04692
VERSION AFA04692.1 GI:15529569
KEYWORDS Human papillomavirus type 16
SOURCE Human papillomavirus type 16
ORGANISM Viruses; dsDNA viruses, no RNA stage; Papillomaviridae; Alphapapillomavirus.
REFERENCE 1 (bases 1 to 370)
AUTHORS Watts,K.J., Thompson,C.H., Coatsart,Y.E. and Rose,B.R.

TITLE
JOURNAL Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia
PUBMED Int. J. Cancer 97 (6), 868-874 (2002)
11857370
REFERENCE 2 (bases 1 to 370)
AUTHORS Watts,K.J., Thompson,C.H., Coatsart,Y.E. and Rose,B.R.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-2001) Department of Infectious Diseases, University of Sydney, Blackburn Building, D06, Off Western Avenue, Camperdown, Sydney, New South Wales 2006, Australia

FEATURES
source
1..370
/organism="Human papillomavirus type 16"
/mol_type="genomic DNA"
/isolate="HPV16BCCI"
/db_xref="taxon:333760"
1..313
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/note=">313"
/gene="E6"
/codon_start=2
/product="E6 protein"
/protein_id="AA01342.1"
/db_xref="GI:15529571"
/translation="DLICIVYRDGNPVAVCDKLFYKISRYHYCYSLYGTTLLEQF NKPLCDLLIRINCQKPLCEPEKQRHDKQRFNIRGRWGRCMSCCRSRTREQL"
316..>370
/gene="E7"
316..>370
/gene="E7"
/codon_start=1
/product="E7 protein"
/protein_id="AA01341.1"
/db_xref="GI:15529570"
/translation="WRGDTPLHRYMTDLQPE"

ORIGIN

Query Match 100.0%; Score 28; DB 10; Length 370;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 GACATTATTGTTATGTTGATGGAAC 28
87 GACATTATTGTTATGTTGATGGAAC 114

Db 87 GACATTATTGTTATGTTGATGGAAC 114

RESULT 10
LOCUS S51110
DEFINITION S51110 421 bp DNA linear VRL 08-MAY-1993
LOCUS orf E6 [human papillomavirus HPV, type 16, head and neck tumor, Genomic, 421 nt].
ACCESSION S51110
VERSION S51110.1 GI:262061
KEYWORDS Human papillomavirus
SOURCE Human papillomavirus
ORGANISM Viruses; dsDNA viruses, no RNA stage; Papillomaviridae; unclassified Papillomaviridae.

REFERENCE 1 (bases 1 to 421)
AUTHORS Tyán,Y.S., Liu,S.T., Ong,W.R., Chen,M.L., Shu,C.H. and Chang,Y.S.
TITLE Detection of Epstein-Barr virus and human papillomavirus in head and neck tumors
JOURNAL J. Clin. Microbiol. 31 (1), 53-56 (1993)
PUBMED 8380183
REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gi262061 120826] from the original journal article.
COMMENT PCR primer sequences: 1-21 and 400-421.
FEATURES
source
1..421
/organism="Human papillomavirus"
/mol_type="genomic DNA"
/db_xref="taxon:10566"

gene /note="type: 16"
1..421
/gene="orf E6"
ORIGIN

Query Match 100.0%; Score 28; DB 10; Length 421;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACATTATTTGTTATGTTGATGGAAC 28
|||||
Db 231 GACATTATTTGTTATGTTGATGGAAC 258
|||||

RESULT 11
AF404695 451 bp DNA linear VRL 09-OCT-2003
LOCUS Human papillomavirus type 16 isolate HPV16E6CC4 E6 protein (E6) and
DEFINITION E7 protein (E7) genes, partial cds.
ACCESSION AF404695
VERSION AF404695.1 GI:15529578
KEYWORDS
SOURCE Human papillomavirus type 16
ORGANISM Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
REFERENCE 1 (bases 1 to 451)
AUTHORS Watts,K.U., Thompson,C.H., Cossart,Y.E. and Rose,B.R.
TITLE Alpha papillomavirus.
JOURNAL 11857370
PUBMED 2 (bases 1 to 451)
REFERENCES Watts,K.U., Thompson,C.H., Cossart,Y.E. and Rose,B.R.
AUTHORS Direct Submission
TITLE Submitted (31-JUL-2001) Department of Infectious Diseases,
JOURNAL University of Sydney, Blackburn Building, D06, Off Western Avenue,
Camperdown, Sydney, New South Wales 2006, Australia
location/Qualifiers
1..451
/organism="Human papillomavirus type 16"
/mol_type="genomic DNA"
/isolate="HPV16E6CC4"
/db_xref="taxon:333760"
<1..395
/gene="E6"
<1..395
/gene="E6"
/codon_start=3
/product="E6 protein"
/protein_id="AA01347.1"
/db_xref="GI:15529579"
/translation="TTHDILIECYCKQQLRREYGFAPRDLCTVRDGNPYAVCDK
CLKEYSKISEYRHYCYSLYGTLEQYKRPICDLLIRICINCKPLCPREKORHLDKQ
RFHNI RGRWTRCSCRSRRRETQL"
398..>451
/gene="E7"
398..>451
/gene="E7"
/codon_start=1
/product="E7 protein"
/protein_id="AA01348.1"
/db_xref="GI:15529580"
/translation="WHGDTPTLHMYMDLQPE"

ORIGIN

Query Match 100.0%; Score 28; DB 10; Length 451;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACATTATTTGTTATGTTGATGGAAC 28
|||||
Db 169 GACATTATTTGTTATGTTGATGGAAC 196
|||||

RESULT 12
AF404703 451 bp DNA linear VRL 09-OCT-2003
LOCUS Human papillomavirus type 16 isolate HPV16E6CC12 E6 protein (E6)
DEFINITION and E7 protein (E7) genes, partial cds.
ACCESSION AF404703
VERSION AF404703.1 GI:15529602
KEYWORDS
SOURCE Human papillomavirus type 16
ORGANISM Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
REFERENCE 1 (bases 1 to 451)
AUTHORS Watts,K.U., Thompson,C.H., Cossart,Y.E. and Rose,B.R.
TITLE Sequence variation and physical state of human papillomavirus type
JOURNAL 16 cervical cancer isolates from Australia and New Caledonia
Int. J. Cancer 97 (6), 868-874 (2002)
11857370
2 (bases 1 to 451)
REFERENCES Watts,K.U., Thompson,C.H., Cossart,Y.E. and Rose,B.R.
AUTHORS Direct Submission
TITLE Submitted (31-JUL-2001) Department of Infectious Diseases,
JOURNAL University of Sydney, Blackburn Building, D06, Off Western Avenue,
Camperdown, Sydney, New South Wales 2006, Australia
location/Qualifiers
1..451
/organism="Human papillomavirus type 16"
/mol_type="genomic DNA"
/isolate="HPV16E6CC12"
/db_xref="taxon:333760"
<1..395
/gene="E6"
<1..395
/gene="E6"
/codon_start=3
/product="E6 protein"
/protein_id="AA01363.1"
/db_xref="GI:15529603"
/translation="TTHNIIIECYCKQQLRREYDFAPRDLCTVRDGNPYAVCDK
CLKEYSKISEYRHYCYSLYGTLEQYKRPICDLLIRICINCKPLCPREKORHLDKQ
RFHNI RGRWTRCSCRSRRRETQL"
398..>451
/gene="E7"
398..>451
/gene="E7"
/codon_start=1
/product="E7 protein"
/protein_id="AA01364.1"
/db_xref="GI:15529604"
/translation="WHGDTPTLHMYMDLQPE"

ORIGIN

Query Match 100.0%; Score 28; DB 10; Length 451;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACATTATTTGTTATGTTGATGGAAC 28
|||||
Db 169 GACATTATTTGTTATGTTGATGGAAC 196
|||||

RESULT 13
HPU34111 456 bp DNA linear VRL 08-MAR-1996
LOCUS Human papillomavirus type 16, isolate NM T455, early transforming
DEFINITION protein E6 (E6) gene, complete cds.
ACCESSION U34111
VERSION U34111.1 GI:1098727
KEYWORDS
SOURCE Human papillomavirus
ORGANISM Human papillomavirus


```

ORIGIN
CINCKPCLPCEKORHLDKKORFHNIRGHWGRCMSCCSSRTRETOU"

Query Match      100.0%; Score 28; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 GACATTATTGTTATGTTGTATGGAAC 28
|||||
230 GACATTATTGTTATGTTGTATGGAAC 257

RESULT 16
HPU34121
LOCUS
DEFINITION
HPU34121 456 bp DNA linear VRL 08-MAR-1996
Human papillomavirus type 16, isolate OR 4724, early transforming
protein E6 (E6) gene, complete cds.
ACCESSION
U34121
VERSION
U34121.1 GI:1098747
KEYWORDS
SOURCE
Human papillomavirus
Human papillomavirus
Viruses; deDNA viruses, no RNA stage; Papillomaviridae;
unclassified Papillomaviridae.
REFERENCE
1 (bases 1 to 456)
Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildesheim,A.
and Jenison,S.A.
Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the
E6, I2, and L1 coding segments
J. Virol. 69 (12), 7743-7753 (1995)
JOURNAL
PUBMED
7494284
REFERENCE
2 (bases 1 to 456)
Farmer,A.D.
Direct Submision
Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National
Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
Alamos, NM 87501, USA
FEATURES
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Location/Qualifiers
1..456
/organism="Human papillomavirus"
/mol_type="genomic DNA"
/isolate="OR 4724"
/db_xref="taxon:10566"
/note="collected by cervical lavage at Kaiser Permanente,
Portland, Oregon, United States."
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/db_xref="GI:1098748"
/translation="MEQDQERPRKLPOLCTELQTTIHDIIECYCKQOLRRBYVD
PARPLCTYRGNPYAVCDKLTYSKSRHXYSGTTLBQYKPLCDLLIR
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ORIGIN
Query Match      100.0%; Score 28; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 GACATTATTGTTATGTTGTATGGAAC 28
|||||
230 GACATTATTGTTATGTTGTATGGAAC 257

RESULT 17
HPU34123
LOCUS
DEFINITION
HPU34123 456 bp DNA linear VRL 08-MAR-1996
Human papillomavirus type 16, isolate OR 5110, early transforming
protein E6 (E6) gene, complete cds.

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ACCESSION
U34123
VERSION
U34123.1 GI:1098751
KEYWORDS
Human papillomavirus
SOURCE
Human papillomavirus
Human papillomavirus
Viruses; deDNA viruses, no RNA stage; Papillomaviridae;
unclassified Papillomaviridae.
REFERENCE
1 (bases 1 to 456)
Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildesheim,A.
and Jenison,S.A.
Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the
E6, I2, and L1 coding segments
J. Virol. 69 (12), 7743-7753 (1995)
JOURNAL
PUBMED
7494284
REFERENCE
2 (bases 1 to 456)
Farmer,A.D.
Direct Submision
Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National
Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
Alamos, NM 87501, USA
FEATURES
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Location/Qualifiers
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/organism="Human papillomavirus"
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Portland, Oregon, United States."
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/db_xref="GI:1098752"
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ORIGIN
Query Match      100.0%; Score 28; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
230 GACATTATTGTTATGTTGTATGGAAC 257

RESULT 18
HPU34124
LOCUS
DEFINITION
HPU34124 456 bp DNA linear VRL 08-MAR-1996
Human papillomavirus type 16, isolate OR 5428, early transforming
protein E6 (E6) gene, complete cds.
ACCESSION
U34124
VERSION
U34124.1 GI:1098753
KEYWORDS
Human papillomavirus
Human papillomavirus
Viruses; deDNA viruses, no RNA stage; Papillomaviridae;
unclassified Papillomaviridae.
REFERENCE
1 (bases 1 to 456)
Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildesheim,A.
and Jenison,S.A.
Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the
E6, I2, and L1 coding segments
J. Virol. 69 (12), 7743-7753 (1995)
JOURNAL
PUBMED
7494284
REFERENCE
2 (bases 1 to 456)
Farmer,A.D.

```

TITLE Direct Submission
JOURNAL Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los Alamos, NM 87501, USA

FEATURES
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/mol_type="genomic DNA"
/isolate="OR 5428"
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ORIGIN
Query Match 100.0%; Score 28; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACATTATGTTATAGTTTGTATGGAAC 28
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230 GACATTATGTTATAGTTTGTATGGAAC 257

Db 230 GACATTATGTTATAGTTTGTATGGAAC 257

RESULT 19
HPV34126 456 bp DNA linear VRL 08-MAR-1996
LOCUS Human papillomavirus type 16, isolate OR 6170, early transforming
DEFINITION protein E6 (E6) gene, complete cds.
ACCESSION U34126
VERSION U34126.1 GI:1098757
KEYWORDS
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
Virusess; dsDNA viruses, no RNA stage; Papillomaviridae;
unclassified Papillomaviridae.
REFERENCE 1 (bases 1 to 456)
Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildesheim,A. and Jensen,S.A.
Human papillomavirus type 16 variant lineages in United States populations characterized by nucleotide sequence analysis of the E6, E2, and E1 coding segments
J. Virol. 69 (12), 7743-7753 (1995)
7494284
2 (bases 1 to 456)
Farmer,A.D.
Direct Submission
Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los Alamos, NM 87501, USA
Location/Qualifiers
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/mol_type="genomic DNA"
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/note="collected by cervical lavage at Kaiser Permanente, Portland, Oregon, United States."
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/codon_start=1

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CDS

/product="early transforming protein E6"
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/db_xref="GI:1098758"
/translation="MFQDQERPRKLPQLCTELQTTIHIIIECYCKQQLRRBYDFAFRLCIVRDGNPYAVCDKCLFKYSISIRHYCSLYGTTLEQQNKPLCDLLIR CINCKPLCPBEKQRHLDKQRFNIRGRMTGRCMSCCRSRTRETL"

ORIGIN
Query Match 100.0%; Score 28; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACATTATGTTATAGTTTGTATGGAAC 28
|||||
230 GACATTATGTTATAGTTTGTATGGAAC 257

Db 230 GACATTATGTTATAGTTTGTATGGAAC 257

RESULT 20
HPV34129 456 bp DNA linear VRL 08-MAR-1996
LOCUS Human papillomavirus type 16, isolate OR 7574, early transforming
DEFINITION protein E6 (E6) gene, complete cds.
ACCESSION U34129
VERSION U34129.1 GI:1098763
KEYWORDS
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
Virusess; dsDNA viruses, no RNA stage; Papillomaviridae;
unclassified Papillomaviridae.
REFERENCE 1 (bases 1 to 456)
Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildesheim,A. and Jensen,S.A.
Human papillomavirus type 16 variant lineages in United States populations characterized by nucleotide sequence analysis of the E6, E2, and E1 coding segments
J. Virol. 69 (12), 7743-7753 (1995)
7494284
2 (bases 1 to 456)
Farmer,A.D.
Direct Submission
Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los Alamos, NM 87501, USA
Location/Qualifiers
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/mol_type="genomic DNA"
/isolate="OR 7574"
/db_xref="taxon:10566"
/note="collected by cervical lavage at Kaiser Permanente, Portland, Oregon, United States."
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACATTATGTTATAGTTTGTATGGAAC 28
|||||
230 GACATTATGTTATAGTTTGTATGGAAC 257

Db 230 GACATTATGTTATAGTTTGTATGGAAC 257

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Query Match	100.0%;	Score 28;	DB 2;	Length 477;
Best Local Similarity	100.0%;	Pred. No. 0.031;		
Matches	28;	Conservative 0;	Mismatches 0;	Indels 0;
Qy	1	GACATTATGTTATGATTGATGAAC	28	
Db	251	GACATTATGTTATGATTGATGAAC	278	
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LOCUS	AX057038	477 bp	DNA	linear
DEFINITION	Sequence 1 from Patent WO0075336.			PAT 17-JUN-2001
ACCESSION	AX057038			
VERSION	AX057038.1	GI:12309879		
KEYWORDS				
SOURCE	Human papillomavirus			
ORGANISM	Human papillomavirus			
REFERENCE	1	Choppin,J., Bourgault Villade,I., Guillet,J.G., Connan,F. and		
AUTHORS		Ferries,B.		
TITLE		Proteinfragmente die verschiedene epitope der hpv proteine e6 und		
JOURNAL		e7 umfassen, ihre herstellung und verwendungen insbesondere zur		
FEATURES		implung		
source		Patent: WO 0075336-A 1 14-DEC-2000;		
		Biovector Therapeutics S.A. (FR) ; Institut National de la Sante et		
		de la Recherche Medicale (INSERM) (FR)		
CDS		location/Qualifiers		
	1..477	/organism="Human papillomavirus"		
		/mol_type="unassigned DNA"		
		/db_xref="taxon:10566"		
	1..477	/note="unnamed protein product"		
		/codon_start=1		
		/protein_id="CAC22410.1"		
		/db_xref="GI:12309880"		
		/translation="MHQKRTAMFODPOERPRKLPQCTELQTTIHDIIECVCKQQL		
		LRRVDFPARDLCTIVRDNPAPVCCKPKYSKISBYHNYCSYIGTLEQYKPK		
		LDLILRCINQKPLCPBEKQRHLDKKQRFHNRGRWTRGCMSCRSSRTRRTQL"		
ORIGIN				
Query Match	100.0%;	Score 28;	DB 2;	Length 477;
Best Local Similarity	100.0%;	Pred. No. 0.031;		
Matches	28;	Conservative 0;	Mismatches 0;	Indels 0;
Qy	1	GACATTATGTTATGATTGATGAAC	28	
Db	251	GACATTATGTTATGATTGATGAAC	278	
RESULT 24				
LOCUS	AX766063	477 bp	DNA	linear
DEFINITION	Sequence 7 from Patent WO03008573.			PAT 25-JUN-2003
ACCESSION	AX766063			
VERSION	AX766063.1	GI:32260136		
KEYWORDS				
SOURCE	Human papillomavirus type 16			
ORGANISM	Human papillomavirus type 16			
REFERENCE	1	Alphapapillomavirus.		
AUTHORS	1	Miner,A.J.		
TITLE		Silencing of gene expression		
JOURNAL		Patent: WO 03008573-A 7 30-JUN-2003;		
FEATURES		Miner, Anne Josephine (GB)		
source		location/Qualifiers		
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Query Match 100.0%; Score 28; DB 2; Length 477;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACATTATTTAGTTGATGGAAC 28
|||||
Db 251 GACATTATTTAGTTGATGGAAC 278

RESULT 25
AF486299 477 bp DNA linear VRL 12-AUG-2002
LOCUS Human papillomavirus type 16 strain As-P isolate PMH-Q24 E6 protein
DEFINITION (E6) gene, complete cds.
ACCESSION AF486299
VERSION AF486299.1 GI:19744647
KEYWORDS
SOURCE Human papillomavirus type 16
ORGANISM Human papillomavirus type 16
REFERENCE 1 (bases 1 to 477)
AUTHORS Chan, P.K.S., Lam, C.W., Cheung, T.H., Li, W.W.H., Lo, K.W.K.,
TITLE Human papillomavirus type 16
JOURNAL Human papillomavirus type 16 intertypic variant infection and risk
AUTHORS Chan, M.Y.M., Cheung, J.L.K., Xu, L.Y., and Cheng, A.F.
TITLE for cervical neoplasia in Southern China
JOURNAL J. Infect. Dis. 186 (5), 696-700 (2002)
AUTHORS 2 (bases 1 to 477)
TITLE Human papillomavirus type 16
JOURNAL Human papillomavirus type 16
AUTHORS Chan, P.K.S., Lam, C.W., Cheung, T.H., Li, W.W.H., Lo, K.W.K.,
TITLE Direct Submision
JOURNAL Submitted (22-FEB-2002) Department of Microbiology, The Chinese
AUTHORS University of Hong Kong, Prince of Wales Hospital, Shatin, N.T.,
TITLE Hong Kong SAR, China
FEATURES
source location/Qualifiers
1..477
/organism="Human papillomavirus type 16"
/mol_type="genomic DNA"
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/country="China"
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carcinoma of the cervix"
1..477
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LRREYDPAFDLCIVRDGNPAVDCDKLTKYSKISRYRHVCYSLYGTTLEQYQNK
LCDLIRICINQKPLCEPKRKHLDKQRFNIRGRWGRCMSCRSRTRRTOL"

ORIGIN

Query Match 100.0%; Score 28; DB 10; Length 477;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACATTATTTAGTTGATGGAAC 28
|||||
Db 251 GACATTATTTAGTTGATGGAAC 278

RESULT 26

AF486300 477 bp DNA linear VRL 12-AUG-2002
LOCUS Human papillomavirus type 16 strain As-P isolate PMH-Q59 E6 protein
DEFINITION (E6) gene, complete cds.
ACCESSION AF486300
VERSION AF486300.1 GI:19744649
KEYWORDS
SOURCE Human papillomavirus type 16
ORGANISM Human papillomavirus type 16
REFERENCE 1 (bases 1 to 477)
AUTHORS Chan, P.K.S., Lam, C.W., Cheung, T.H., Li, W.W.H., Lo, K.W.K.,
TITLE Human papillomavirus type 16
JOURNAL Human papillomavirus type 16 intertypic variant infection and risk
AUTHORS Chan, M.Y.M., Cheung, J.L.K., Xu, L.Y., and Cheng, A.F.
TITLE for cervical neoplasia in Southern China
JOURNAL J. Infect. Dis. 186 (5), 696-700 (2002)
AUTHORS 2 (bases 1 to 477)
TITLE Human papillomavirus type 16
JOURNAL Human papillomavirus type 16
AUTHORS Chan, P.K.S., Lam, C.W., Cheung, T.H., Li, W.W.H., Lo, K.W.K.,
TITLE Direct Submision
JOURNAL Submitted (22-FEB-2002) Department of Microbiology, The Chinese
AUTHORS University of Hong Kong, Prince of Wales Hospital, Shatin, N.T.,
TITLE Hong Kong SAR, China
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/organism="Human papillomavirus type 16"
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ORIGIN

Query Match 100.0%; Score 28; DB 10; Length 477;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACATTATTTAGTTGATGGAAC 28
|||||
Db 251 GACATTATTTAGTTGATGGAAC 278

RESULT 27

AF486301 477 bp DNA linear VRL 12-AUG-2002
LOCUS Human papillomavirus type 16 strain As-P isolate OEH-2076 E6
DEFINITION (E6) gene, complete cds.
ACCESSION AF486301
VERSION AF486301.1 GI:19744651
KEYWORDS
SOURCE Human papillomavirus type 16
ORGANISM Human papillomavirus type 16
REFERENCE 1 (bases 1 to 477)
AUTHORS Chan, P.K.S., Lam, C.W., Cheung, T.H., Li, W.W.H., Lo, K.W.K.,
TITLE Human papillomavirus type 16
JOURNAL Human papillomavirus type 16 intertypic variant infection and risk
AUTHORS Chan, M.Y.M., Cheung, J.L.K., Xu, L.Y., and Cheng, A.F.
TITLE for cervical neoplasia in Southern China
JOURNAL J. Infect. Dis. 186 (5), 696-700 (2002)
AUTHORS 2 (bases 1 to 477)
TITLE Human papillomavirus type 16
JOURNAL Human papillomavirus type 16
AUTHORS Chan, P.K.S., Lam, C.W., Cheung, T.H., Li, W.W.H., Lo, K.W.K.,
TITLE Direct Submision
JOURNAL Submitted (22-FEB-2002) Department of Microbiology, The Chinese
AUTHORS University of Hong Kong, Prince of Wales Hospital, Shatin, N.T.,
TITLE Hong Kong SAR, China
FEATURES
source location/Qualifiers
1..477
/organism="Human papillomavirus type 16"
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/strain="As-P"
/isolate="PMH-Q59"
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carcinoma of the cervix"
1..477
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1..477
/gene="E6"
/note="oncprotein; transforming; trans-activating;
p53-binding"
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/db_xref="GI:19744650"
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LRREYDPAFDLCIVRDGNPAVDCDKLTKYSKISRYRHVCYSLYGTTLEQYQNK
LCDLIRICINQKPLCEPKRKHLDKQRFNIRGRWGRCMSCRSRTRRTOL"

ORIGIN

Query Match 100.0%; Score 28; DB 10; Length 477;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACATTATTTAGTTGATGGAAC 28
|||||
Db 251 GACATTATTTAGTTGATGGAAC 278

RESULT 28

TITLE Human papillomavirus type 16 intratypic variant infection and risk
JOURNAL J. Infect. Dis. 186 (5), 696-700 (2002)
REFERENCE 2 (bases 1 to 477)
AUTHORS Chan, P.K.S., Lam, C.W., Cheung, T.H., Li, W.W.H., Lo, K.W.K.,
Chan, M.Y.M., Cheung, J.L.K., Xu, L.Y. and Cheng, A.F.
TITLE Direct Submision
JOURNAL Submitted (22-FEB-2002) Department of Microbiology, The Chinese
University of Hong Kong, Prince of Wales Hospital, Shatin, N.T.,
Hong Kong SAR, China

FEATURES
source
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/organism="Human papillomavirus type 16"
/mol_type="genomic DNA"
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/isolate="QEH-2076"
/db_xref="taxon:333760"
/country="China"
/note="Isolated from a patient with cervical
intraepithelial neoplasia grade II"

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1..477
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1..477
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/note="oncoprotein; transforming; trans-activating;
p53-binding"
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/db_xref="GI:19744652"
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ORIGIN
Query Match 100.0%; Score 28; DB 10; Length 477;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACATTATTGTTATAGTTGTATGGAAC 28
|||||
251 GACATTATTGTTATAGTTGTATGGAAC 278
|||||

RESULT 28
AF486302 477 bp DNA linear VRL 12-AUG-2002
LOCUS Human papillomavirus type 16 strain As-P isolate PWH-Q81 E6 protein
DEFINITION (E6) gene, complete cds.
ACCESSION AF486302
VERSION AF486302.1 GI:19744653
KEYWORDS
ORGANISM Human papillomavirus type 16
SOURCE Human papillomavirus type 16
Virusess; daDNA viruses, no RNA stage; Papillomaviridae;
Alphapapillomavirus.
1 (bases 1 to 477)
/organism="Human papillomavirus type 16"
/mol_type="genomic DNA"
/strain="As-C131"
/isolate="QEH-173"
/db_xref="taxon:333760"
/country="China"
/note="Isolated from a patient with intraepithelial
neoplasia grade I"

REFERENCE
AUTHORS Chan, P.K.S., Lam, C.W., Cheung, T.H., Li, W.W.H., Lo, K.W.K.,
Chan, M.Y.M., Cheung, J.L.K., Xu, L.Y. and Cheng, A.F.
TITLE Human papillomavirus type 16 intratypic variant infection and risk
JOURNAL Submitted (22-FEB-2002) Department of Microbiology, The Chinese
University of Hong Kong, Prince of Wales Hospital, Shatin, N.T.,
Hong Kong SAR, China

FEATURES
source
1..477
/organism="Human papillomavirus type 16"
/mol_type="genomic DNA"

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/isolate="PWH-Q81"
/db_xref="taxon:333760"
/country="China"
/note="Isolated from a patient with invasive squamous cell
carcinoma of the cervix"

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p53-binding"
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ORIGIN
Query Match 100.0%; Score 28; DB 10; Length 477;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACATTATTGTTATAGTTGTATGGAAC 28
|||||
251 GACATTATTGTTATAGTTGTATGGAAC 278
|||||

RESULT 29
AF486303 477 bp DNA linear VRL 12-AUG-2002
LOCUS Human papillomavirus type 16 strain As-C131 isolate QEH-173 E6
DEFINITION protein (E6) gene, complete cds.
ACCESSION AF486303
VERSION AF486303.1 GI:19744655
KEYWORDS
ORGANISM Human papillomavirus type 16
SOURCE Human papillomavirus type 16
Virusess; daDNA viruses, no RNA stage; Papillomaviridae;
Alphapapillomavirus.
1 (bases 1 to 477)
/organism="Human papillomavirus type 16"
/mol_type="genomic DNA"
/strain="As-C131"
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/note="Isolated from a patient with intraepithelial
neoplasia grade I"

REFERENCE
AUTHORS Chan, P.K.S., Lam, C.W., Cheung, T.H., Li, W.W.H., Lo, K.W.K.,
Chan, M.Y.M., Cheung, J.L.K., Xu, L.Y. and Cheng, A.F.
TITLE Human papillomavirus type 16 intratypic variant infection and risk
JOURNAL Submitted (22-FEB-2002) Department of Microbiology, The Chinese
University of Hong Kong, Prince of Wales Hospital, Shatin, N.T.,
Hong Kong SAR, China

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AUTHORS      1 (bases 1 to 477)
              Chan, P.K.S., Lam, C.W., Cheung, T.H., Li, W.W.H., Lo, K.W.K.,
              Chan, M.Y.M., Cheung, J.L.K., Xu, L.Y., and Cheng, A.F.
TITLE        Human papillomavirus type 16 intratypic variant infection and risk
              for cervical neoplasia in Southern China
JOURNAL      J. Infect. Dis. 186 (5), 696-700 (2002)
REFERENCE    2 (bases 1 to 477)
AUTHORS      Chan, P.K.S., Lam, C.W., Cheung, T.H., Li, W.W.H., Lo, K.W.K.,
              Chan, M.Y.M., Cheung, J.L.K., Xu, L.Y., and Cheng, A.F.
TITLE        Direct Submision
JOURNAL      Submitted (22-FEB-2002) Department of Microbiology, The Chinese
              University of Hong Kong, Prince of Wales Hospital, Shatin, N.T.,
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DEFINITION   protein (E6) gene, complete cds.
ACCESSION    AF486307
VERSION      AF486307.1 GI:19744663
KEYWORDS
SOURCE       Human papillomavirus type 16
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TITLE        Human papillomavirus type 16 intratypic variant infection and risk
              for cervical neoplasia in Southern China
JOURNAL      J. Infect. Dis. 186 (5), 696-700 (2002)
REFERENCE    2 (bases 1 to 477)
AUTHORS      Chan, P.K.S., Lam, C.W., Cheung, T.H., Li, W.W.H., Lo, K.W.K.,
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TITLE        Direct Submission
JOURNAL      Submitted (22-FEB-2002) Department of Microbiology, The Chinese
              University of Hong Kong, Prince of Wales Hospital, Shatin, N.T.,
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LOCUS        Human papillomavirus type 16 strain As-A178 isolate QEH-186 E6
DEFINITION   protein (E6) gene, complete cds.
ACCESSION    AF486308
VERSION      AF486308.1 GI:19744665
KEYWORDS
SOURCE       Human papillomavirus type 16
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ORGANISM     1 (bases 1 to 477)
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              Chan, M.Y.M., Cheung, J.L.K., Xu, L.Y., and Cheng, A.F.
TITLE        Human papillomavirus type 16 intratypic variant infection and risk
              for cervical neoplasia in Southern China
JOURNAL      J. Infect. Dis. 186 (5), 696-700 (2002)
REFERENCE    2 (bases 1 to 477)
AUTHORS      Chan, P.K.S., Lam, C.W., Cheung, T.H., Li, W.W.H., Lo, K.W.K.,
              Chan, M.Y.M., Cheung, J.L.K., Xu, L.Y., and Cheng, A.F.
TITLE        Direct Submission
JOURNAL      Submitted (22-FEB-2002) Department of Microbiology, The Chinese
              University of Hong Kong, Prince of Wales Hospital, Shatin, N.T.,
              Hong Kong SAR, China
FEATURES
location/Qualifiers

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Db 251 GACATTATGTTATAGTTGTATGGAAC 278

RESULT 35
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LOCUS Human papillomavirus type 16 strain As-A267 isolate PMH-066 E6
DEFINITION AF486309
ACCESSION AF486309
KEYWORDS AF486309.1 GI:19744667
SOURCE Human papillomavirus type 16
ORGANISM Human papillomavirus type 16
Virus; dsDNA viruses, no RNA stage; Papillomaviridae;
Alphapapillomavirus.
1 (bases 1 to 477)
Chan, P.K.S., Lam, C.W., Cheung, T.H., Li, W.W.H., Lo, K.W.K.,
Chan, M.Y.M., Cheung, J.L.K., Xu, L.Y. and Cheng, A.F.
Human papillomavirus type 16 intratypic variant infection and risk
for cervical neoplasia in Southern China
J. Infect. Dis. 186 (5), 696-700 (2002)
2 (bases 1 to 477)
Chan, P.K.S., Lam, C.W., Cheung, T.H., Li, W.W.H., Lo, K.W.K.,
Chan, M.Y.M., Cheung, J.L.K., Xu, L.Y. and Cheng, A.F.
Direct Submission
Submitted (22-FEB-2002) Department of Microbiology, The Chinese
University of Hong Kong, Prince of Wales Hospital, Shatin, N.T.,
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Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0.031;
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RESULT 36
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LOCUS Human papillomavirus type 16 strain E-P isolate PMH-042 E6 protein
DEFINITION AF486310
ACCESSION AF486310
KEYWORDS AF486310.1 GI:19744669
SOURCE Human papillomavirus type 16
ORGANISM Human papillomavirus type 16
Virus; dsDNA viruses, no RNA stage; Papillomaviridae;
Alphapapillomavirus.
1 (bases 1 to 477)
Chan, P.K.S., Lam, C.W., Cheung, T.H., Li, W.W.H., Lo, K.W.K.,
Chan, M.Y.M., Cheung, J.L.K., Xu, L.Y. and Cheng, A.F.
Human papillomavirus type 16 intratypic variant infection and risk
for cervical neoplasia in Southern China
J. Infect. Dis. 186 (5), 696-700 (2002)
2 (bases 1 to 477)
Chan, P.K.S., Lam, C.W., Cheung, T.H., Li, W.W.H., Lo, K.W.K.,
Chan, M.Y.M., Cheung, J.L.K., Xu, L.Y. and Cheng, A.F.
Direct Submission
Submitted (22-FEB-2002) Department of Microbiology, The Chinese
University of Hong Kong, Prince of Wales Hospital, Shatin, N.T.,
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Location/Qualifiers
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Db 251 GACATTATGTTATAGTTGTATGGAAC 278

RESULT 37
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LOCUS Human papillomavirus type 16 strain E-P isolate PMH-Q15 E6 protein
DEFINITION AF486311
ACCESSION AF486311
KEYWORDS AF486311.1 GI:19744671
SOURCE Human papillomavirus type 16

ORGANISM Human papillomavirus type 16
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Alphapapillomavirus.
REFERENCE 1 (bases 1 to 477)
AUTHORS Chan, P.K.S., Lam, C.W., Cheung, T.H., Li, W.W.H., Lo, K.W.K.,
Chan, M.Y.M., Cheung, J.L.K., Xu, L.Y., and Cheng, A.F.
TITLE Human papillomavirus type 16 intraepithelial neoplasia and risk
for cervical neoplasia in Southern China
JOURNAL J. Infect. Dis. 186 (5), 696-700 (2002)
REFERENCE 2 (bases 1 to 477)
AUTHORS Chan, P.K.S., Lam, C.W., Cheung, T.H., Li, W.W.H., Lo, K.W.K.,
Chan, M.Y.M., Cheung, J.L.K., Xu, L.Y., and Cheng, A.F.
TITLE Direct Submission
JOURNAL Submitted (22-FEB-2002) Department of Microbiology, The Chinese
University of Hong Kong, Prince of Wales Hospital, Shatin, N.T.,
Hong Kong SAR, China
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DEFINITION (E6) gene, complete cds.
ACCESSION AF486312
VERSION AF486312.1 GI:19744673
KEYWORDS Human papillomavirus type 16
SOURCE Human papillomavirus type 16
ORGANISM Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Alphapapillomavirus.
REFERENCE 1 (bases 1 to 477)
AUTHORS Chan, P.K.S., Lam, C.W., Cheung, T.H., Li, W.W.H., Lo, K.W.K.,
Chan, M.Y.M., Cheung, J.L.K., Xu, L.Y., and Cheng, A.F.
TITLE Human papillomavirus type 16 intraepithelial neoplasia and risk
for cervical neoplasia in Southern China
JOURNAL J. Infect. Dis. 186 (5), 696-700 (2002)
REFERENCE 2 (bases 1 to 477)
AUTHORS Chan, P.K.S., Lam, C.W., Cheung, T.H., Li, W.W.H., Lo, K.W.K.,
Chan, M.Y.M., Cheung, J.L.K., Xu, L.Y., and Cheng, A.F.
TITLE Direct Submission
JOURNAL Submitted (22-FEB-2002) Department of Microbiology, The Chinese

University of Hong Kong, Prince of Wales Hospital, Shatin, N.T.,
Hong Kong SAR, China
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RESULT 39
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LOCUS Human papillomavirus type 16 strain E-P isolate QEH-453 E6 protein
DEFINITION (E6) gene, complete cds.
ACCESSION AF486313
VERSION AF486313.1 GI:19744675
KEYWORDS Human papillomavirus type 16
SOURCE Human papillomavirus type 16
ORGANISM Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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REFERENCE 1 (bases 1 to 477)
AUTHORS Chan, P.K.S., Lam, C.W., Cheung, T.H., Li, W.W.H., Lo, K.W.K.,
Chan, M.Y.M., Cheung, J.L.K., Xu, L.Y., and Cheng, A.F.
TITLE Human papillomavirus type 16 intraepithelial neoplasia and risk
for cervical neoplasia in Southern China
JOURNAL J. Infect. Dis. 186 (5), 696-700 (2002)
REFERENCE 2 (bases 1 to 477)
AUTHORS Chan, P.K.S., Lam, C.W., Cheung, T.H., Li, W.W.H., Lo, K.W.K.,
Chan, M.Y.M., Cheung, J.L.K., Xu, L.Y., and Cheng, A.F.
TITLE Direct Submission
JOURNAL Submitted (22-FEB-2002) Department of Microbiology, The Chinese
University of Hong Kong, Prince of Wales Hospital, Shatin, N.T.,
Hong Kong SAR, China
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DEFINITION
ACCESSION AF486315
VERSION AF486315
KEYWORDS
SOURCE
ORGANISM Human papillomavirus type 16
Human papillomavirus type 16
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Alphapapillomavirus.
1 (bases 1 to 477)
Chan, P.K.S., Lam, C.W., Cheung, T.H., Li, W.W.H., Lo, K.W.K.,
Chan, M.Y.M., Cheung, J.L.K., Xu, L.Y. and Cheng, A.F.
Human papillomavirus type 16 intratypic variant infection and risk
for cervical neoplasia in Southern China
J. Infect. Dis. 186 (5), 696-700 (2002)
2 (bases 1 to 477)
Chan, P.K.S., Lam, C.W., Cheung, T.H., Li, W.W.H., Lo, K.W.K.,
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University of Hong Kong, Prince of Wales Hospital, Shatin, N.T.,
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DEFINITION
ACCESSION AF486316
VERSION AF486316
KEYWORDS
SOURCE
ORGANISM Human papillomavirus type 16
Human papillomavirus type 16
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Alphapapillomavirus.
1 (bases 1 to 477)
Chan, P.K.S., Lam, C.W., Cheung, T.H., Li, W.W.H., Lo, K.W.K.,
Chan, M.Y.M., Cheung, J.L.K., Xu, L.Y. and Cheng, A.F.
Human papillomavirus type 16 intratypic variant infection and risk
for cervical neoplasia in Southern China
J. Infect. Dis. 186 (5), 696-700 (2002)
2 (bases 1 to 477)
Chan, P.K.S., Lam, C.W., Cheung, T.H., Li, W.W.H., Lo, K.W.K.,
Chan, M.Y.M., Cheung, J.L.K., Xu, L.Y. and Cheng, A.F.
Direct Submision
Submitted (22-FEB-2002) Department of Microbiology, The Chinese
University of Hong Kong, Prince of Wales Hospital, Shatin, N.T.,
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Location/Qualifiers
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ORIGIN

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RESULT 42
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DEFINITION
ACCESSION AF486317

VERSION AF486317.1 GI:19744683
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REFERENCE 1 (bases 1 to 477)
AUTHORS Chan, P.K.S., Lam, C.W., Cheung, T.H., Li, W.W.H., Lo, K.W.K., Chan, M.Y.M., Cheung, J.L.K., Xu, L.Y. and Cheng, A.F.
TITLE Human papillomavirus type 16 intratypic variant infection and risk for cervical neoplasia in Southern China
JOURNAL J. Infect. Dis. 186 (5), 696-700 (2002)
2 (bases 1 to 477)
AUTHORS Chan, P.K.S., Lam, C.W., Cheung, T.H., Li, W.W.H., Lo, K.W.K., Chan, M.Y.M., Cheung, J.L.K., Xu, L.Y. and Cheng, A.F.
TITLE Direct Submission
JOURNAL Submitted (22-FEB-2002) Department of Microbiology, The Chinese University of Hong Kong, Prince of Wales Hospital, Shatin, N.T., Hong Kong SAR, China
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DEFINITION Human papillomavirus type 16 complete cds.
ACCESSION AF486318
VERSION AF486318.1 GI:19744685
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SOURCE Human papillomavirus type 16
ORGANISM Viruses; dsDNA viruses, no RNA stage; Papillomaviridae; Alphapapillomavirus.
REFERENCE 1 (bases 1 to 477)
AUTHORS Chan, P.K.S., Lam, C.W., Cheung, T.H., Li, W.W.H., Lo, K.W.K., Chan, M.Y.M., Cheung, J.L.K., Xu, L.Y. and Cheng, A.F.
TITLE Human papillomavirus type 16 intratypic variant infection and risk for cervical neoplasia in Southern China
JOURNAL J. Infect. Dis. 186 (5), 696-700 (2002)
2 (bases 1 to 477)
AUTHORS Chan, P.K.S., Lam, C.W., Cheung, T.H., Li, W.W.H., Lo, K.W.K.,

Chan, M.Y.M., Cheung, J.L.K., Xu, L.Y. and Cheng, A.F.
TITLE Direct Submission
JOURNAL Submitted (22-FEB-2002) Department of Microbiology, The Chinese University of Hong Kong, Prince of Wales Hospital, Shatin, N.T., Hong Kong SAR, China
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DEFINITION Human papillomavirus type 16 complete cds.
ACCESSION AF486319
VERSION AF486319.1 GI:19744687
KEYWORDS Human papillomavirus type 16
SOURCE Human papillomavirus type 16
ORGANISM Viruses; dsDNA viruses, no RNA stage; Papillomaviridae; Alphapapillomavirus.
REFERENCE 1 (bases 1 to 477)
AUTHORS Chan, P.K.S., Lam, C.W., Cheung, T.H., Li, W.W.H., Lo, K.W.K., Chan, M.Y.M., Cheung, J.L.K., Xu, L.Y. and Cheng, A.F.
TITLE Human papillomavirus type 16 intratypic variant infection and risk for cervical neoplasia in Southern China
JOURNAL J. Infect. Dis. 186 (5), 696-700 (2002)
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AUTHORS Chan, P.K.S., Lam, C.W., Cheung, T.H., Li, W.W.H., Lo, K.W.K., Chan, M.Y.M., Cheung, J.L.K., Xu, L.Y. and Cheng, A.F.
TITLE Direct Submission
JOURNAL Submitted (22-FEB-2002) Department of Microbiology, The Chinese University of Hong Kong, Prince of Wales Hospital, Shatin, N.T., Hong Kong SAR, China
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ORGANISM Human papillomavirus type 16
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AUTHORS Chan, P.K.S., Lam, C.W., Cheung, T.H., Li, W.W.H., Lo, K.W.K., Chan, M.Y.M., Cheung, J.L.K., Xu, L.Y., and Cheng, A.F.
TITLE Human papillomavirus type 16 intra-typic variant infection and risk for cervical neoplasia in Southern China
JOURNAL J. Infect. Dis. 186 (5), 696-700 (2002)
REFERENCE 2 (bases 1 to 477)
AUTHORS Chan, P.K.S., Lam, C.W., Cheung, T.H., Li, W.W.H., Lo, K.W.K., Chan, M.Y.M., Cheung, J.L.K., Xu, L.Y., and Cheng, A.F.
TITLE Direct Submission
JOURNAL Submitted (22-FEB-2002) Department of Microbiology, The Chinese University of Hong Kong, Prince of Wales Hospital, Shatin, N.T., Hong Kong SAR, China
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DEFINITION Human papillomavirus type 16 isolate HPV16ECC11 E6 protein (E6)
ACCESSION AF404702
VERSION AF404702.1 GI:15529599
KEYWORDS
SOURCE Human papillomavirus type 16
ORGANISM Human papillomavirus type 16
REFERENCE 1 (bases 1 to 488)
AUTHORS Watts, K.J., Thompson, C.H., Cossart, Y.E. and Rose, B.R.
TITLE Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia
JOURNAL Int. J. Cancer 97 (6), 868-874 (2002)

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REFERENCE 2 (bases 1 to 488)
AUTHORS Watts, K.J., Thompson, C.H., Cossart, Y.E. and Rose, B.R.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-2001) Department of Infectious Diseases, University of Sydney, Blackburn Building, D06, Off Western Avenue, Camperdown, Sydney, New South Wales 2006, Australia
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LOCUS Sequence 11 from patent US 6004557.
DEFINITION AR095319
ACCESSION AR095319
VERSION AR095319.1 GI:10023090
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 519)
AUTHORS Edwards, S., John, C., Cox, J., Cooper, J., Webb, E., Ann, and Frazer, I.
TITLE Variants of human papillomavirus antigens
JOURNAL Patent: US 6004557-A 11 21-DEC-1999;
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REFERENCE      1 (bases 1 to 519)
AUTHORS       Edwards,S,John., Cox,J,Cooper., Webb,B,Ann. and Frazer,I.
TITLE         Variants of human papillomavirus antigens
JOURNAL       Patent: US 6004557-A 13 21-DEC-1999;
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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

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Perfect score: 28
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Total number of hits satisfying chosen parameters: 12732272

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Post-processing: Minimum Match 0%

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Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
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121	28	100.0	780	10	AF187869	AF187869 Human pap	194	26.4	94.3	138	2	DD187319	DD187319 SPLICSO
122	28	100.0	790	2	I88813	I88813 Sequence	195	26.4	94.3	149	2	DD187314	DD187314 SPLICSO
123	28	100.0	801	2	AR095318	AR095318 Sequence	196	26.4	94.3	298	10	AF404704	AF404704 Human pap
124	28	100.0	801	2	AR173471	AR173471 Sequence	197	26.4	94.3	370	10	AF404692	AF404692 Human pap
125	28	100.0	822	2	A98742	A98742 Sequence	198	26.4	94.3	22	2	DD178592	DD178592 METHOD FO
126	28	100.0	822	2	BD080312	BD080312 Vaccine.	199	26.4	94.3	22	2	AX802492	AX802492 Sequence
127	28	100.0	822	2	BD103161	BD103161 Vaccine.	200	26.4	94.3	22	2	AX802975	AX802975 Sequence
128	28	100.0	822	2	AR183573	AR183573 Sequence	201	26.4	94.3	22	2	AX803252	AX803252 Sequence
129	28	100.0	822	2	AX020926	AX020926 Sequence	202	26.4	94.3	30	2	AR129425	AR129425 Sequence
130	28	100.0	822	2	A98748	A98748 Sequence	203	26.4	94.3	53	2	DD178764	DD178764 METHOD FO
131	28	100.0	879	2	BD080315	BD080315 Vaccine.	204	26.4	94.3	53	2	AX802664	AX802664 Sequence
132	28	100.0	879	2	BD103164	BD103164 Vaccine.	205	26.4	94.3	53	2	AX802976	AX802976 Sequence
133	28	100.0	879	2	AR183576	AR183576 Sequence	206	26.4	94.3	53	2	AC154096	AC154096 Phytoph
134	28	100.0	879	2	AX020932	AX020932 Sequence	207	26.4	94.3	53	2	AC099332	AC099332 Homo sapi
135	28	100.0	921	10	HPA388069	HPA388069 Human pap	208	26.4	94.3	53	2	AC092058	AC092058 Homo sapi
136	28	100.0	939	2	AX403959	AX403959 Sequence	209	26.4	94.3	53	2	AC120234	AC120234 Rattus no
137	28	100.0	939	2	AX460903	AX460903 Sequence	210	26.4	94.3	53	2	AC120234_1	AC120234_1 Rattus no
138	28	100.0	1000	2	A07622	A07622 Amplified	211	26.4	94.3	53	2	AX803254	AX803254 Sequence
139	28	100.0	1000	2	I18920	I18920 Sequence	212	26.4	94.3	53	2	AC130927	AC130927 Rattus no
140	28	100.0	1116	2	A98744	A98744 Sequence	213	26.4	94.3	53	2	AR099822	AR099822 Sequence
141	28	100.0	1116	2	BD080313	BD080313 Vaccine.	214	26.4	94.3	53	2	AR142234	AR142234 Sequence
142	28	100.0	1116	2	BD103162	BD103162 Vaccine.	215	26.4	94.3	53	2	I34495	I34495 Sequence
143	28	100.0	1116	2	AR183574	AR183574 Sequence	216	26.4	94.3	53	2	I57330	I57330 Sequence
144	28	100.0	1116	2	AX020928	AX020928 Sequence	217	26.4	94.3	53	2	I73208	I73208 Sequence
145	28	100.0	1173	2	A98752	A98752 Sequence	218	26.4	94.3	53	2	AR142057	AR142057 Sequence
146	28	100.0	1173	2	BD080317	BD080317 Vaccine.	219	26.4	94.3	53	2	I59924	I59924 Sequence
147	28	100.0	1173	2	BD103166	BD103166 Vaccine.	220	26.4	94.3	53	2	I86782	I86782 Sequence
148	28	100.0	1173	2	AR183578	AR183578 Sequence	221	26.4	94.3	53	2	I95807	I95807 Sequence
149	28	100.0	1173	2	AX020936	AX020936 Sequence	222	26.4	94.3	53	2	AR708786	AR708786 Sequence
150	28	100.0	1267	10	HPA242681	HPA242681 Human pap	223	26.4	94.3	53	2	AC156905	AC156905 Bos tau
151	28	100.0	1267	10	HPA388056	HPA388056 Human pap	224	26.4	94.3	53	2	ALU713989	ALU713989 Mouse DNA
152	28	100.0	1267	10	HPA388057	HPA388057 Human pap	225	26.4	94.3	53	2	AC174977	AC174977 Bos tau
153	28	100.0	1267	10	HPA388058	HPA388058 Human pap	226	26.4	94.3	53	2	AC114051	AC114051 Rattus no
154	28	100.0	1267	10	HPA388059	HPA388059 Human pap	227	26.4	94.3	53	2	AC115778	AC115778 Mus muscu
155	28	100.0	1267	10	HPA388060	HPA388060 Human pap	228	26.4	94.3	53	2	AC158303	AC158303 Mus muscu
156	28	100.0	1267	10	HPA388061	HPA388061 Human pap	229	26.4	94.3	53	2	AC161169	AC161169 Mus muscu
157	28	100.0	1267	10	HPA388062	HPA388062 Human pap	230	26.4	94.3	53	2	AR129446	AR129446 Sequence
158	28	100.0	1267	10	HPA388063	HPA388063 Human pap	231	26.4	94.3	53	2	AC018958	AC018958 Homo sapi
159	28	100.0	1267	10	HPA388064	HPA388064 Human pap	232	26.4	94.3	53	2	AC018958	AC018958 Homo sapi
160	28	100.0	1267	10	HPA388065	HPA388065 Human pap	233	26.4	94.3	53	2	AC068278	AC068278 Homo sapi
161	28	100.0	1267	10	HPA388066	HPA388066 Human pap	234	26.4	94.3	53	2	AC019035	AC019035 Homo sapi
162	28	100.0	1267	10	HPA388067	HPA388067 Human pap	235	26.4	94.3	53	2	DD178594	DD178594 METHOD FO
163	28	100.0	1267	10	HPA388068	HPA388068 Human pap	236	26.4	94.3	53	2	AX802494	AX802494 Sequence
164	28	100.0	3531	10	AF001599	AF001599 Human pap	237	26.4	94.3	53	2	AX802979	AX802979 Sequence

C 238	20	71.4	23	2	BD227561	311	19	67.9	453	2	C0069257	Sequence
C 239	20	71.4	23	2	AR476267	312	19	67.9	453	2	C0096287	Sequence
C 240	20	71.4	24	2	BD017592	313	19	67.9	453	2	C0202739	Sequence
C 241	20	71.4	24	2	BD017593	314	19	67.9	453	2	C0256922	Sequence
C 242	20	71.4	24	2	117084	315	19	67.9	453	2	C0330879	Sequence
C 243	20	71.4	24	2	117085	316	19	67.9	533	2	AX230117	Sequence
C 244	20	71.4	51	2	DD178766	317	19	67.9	594	2	C0058669	Sequence
C 245	20	71.4	51	2	AX802666	318	19	67.9	594	2	C0109032	Sequence
C 246	20	71.4	51	2	AX802980	319	19	67.9	594	2	C0147663	Sequence
C 247	20	71.4	73945	12	AC101549	320	19	67.9	594	2	C0207443	Sequence
C 248	20	71.4	121416	12	CT573055	321	19	67.9	594	2	C0230911	Sequence
C 249	20	71.4	124281	5	AL136101	322	19	67.9	609	2	C0269059	Sequence
C 250	20	71.4	126589	12	AC173645	323	19	67.9	594	7	BV234777	Sequence
C 251	20	71.4	159035	5	AC092584	324	19	67.9	687	2	C0751610	Sequence
C 252	20	71.4	163186	5	AC015994	325	19	67.9	803	10	PHR67	Sequence
C 253	20	71.4	173452	5	AC003013	326	19	67.9	924	2	C0078586	Sequence
C 254	20	71.4	175482	6	AC132947	327	19	67.9	924	2	C0183596	Sequence
C 255	20	71.4	176730	12	AC073994	328	19	67.9	924	2	C0207970	Sequence
C 256	20	71.4	179884	6	AC121318	329	19	67.9	924	2	C0306749	Sequence
C 257	20	71.4	243163	12	AC098002	330	19	67.9	1089	2	C0821780	Sequence
C 258	19.8	70.7	2671	11	BC072164	331	19	67.9	1868	4	AP304366	Sequence
C 259	19.8	70.7	185866	6	AC109510	332	19	67.9	1961	2	C0069411	Sequence
C 260	19.8	70.7	213363	6	AC164399	333	19	67.9	1961	2	C0173728	Sequence
C 261	19.8	70.7	225655	6	AC099690	334	19	67.9	1961	2	C0202870	Sequence
C 262	19.6	70.0	551	7	BV462142	335	19	67.9	1961	2	C0294250	Sequence
C 263	19.6	70.0	641	7	BV602988	336	19	67.9	2353	2	C0054455	Sequence
C 264	19.6	70.0	831	7	BV494107	337	19	67.9	2353	2	C0073696	Sequence
C 265	19.6	70.0	1096	6	RATREB1	338	19	67.9	2353	2	C0104581	Sequence
C 266	19.6	70.0	30000	2	DD164679	339	19	67.9	2353	2	C0143291	Sequence
C 267	19.6	70.0	30000	2	AX695899	340	19	67.9	2353	2	C0178780	Sequence
C 268	19.6	70.0	40989	15	AF204805	341	19	67.9	2353	2	C0203126	Sequence
C 269	19.6	70.0	68567	5	AL389915	342	19	67.9	2353	2	C0226485	Sequence
C 270	19.6	70.0	78229	5	AL139140	343	19	67.9	2353	2	C0264626	Sequence
C 271	19.6	70.0	108484	12	AC177279	344	19	67.9	2353	2	C0301716	Sequence
C 272	19.6	70.0	142650	5	AC112656	345	19	67.9	2353	2	C0338925	Sequence
C 273	19.6	70.0	160431	12	AC118586	346	19	67.9	2720	5	HSB805169	Sequence
C 274	19.6	70.0	168936	12	AC024992	347	19	67.9	2811	5	AB220481	Sequence
C 275	19.6	70.0	181720	12	AC073283	348	19	67.9	4362	5	AB039667	Sequence
C 276	19.6	70.0	184225	12	AC173915	349	19	67.9	4419	5	BC112167	Sequence
C 277	19.6	70.0	189203	12	AC019125	350	19	67.9	4888	2	C0720083	Sequence
C 278	19.6	70.0	191983	5	AF274858	351	19	67.9	4895	2	CS056094	Sequence
C 279	19.6	70.0	200059	12	AC153674	352	19	67.9	4895	2	CS108411	Sequence
C 280	19.6	70.0	211193	12	AC155491	353	19	67.9	4895	5	AF195657	Sequence
C 281	19.6	70.0	230917	12	AC159760	354	19	67.9	7851	10	PHV35CG	Sequence
C 282	19.6	70.0	244251	12	AC125865	355	19	67.9	7879	2	HPV35H	Sequence
C 283	19.6	70.0	247743	12	AC103091	356	19	67.9	8307	2	AX676351	Sequence
C 284	19.6	70.0	290627	12	AC165991	357	19	67.9	8307	15	BACWAPX	Sequence
C 285	19.6	70.0	324745	13	U41276	358	19	67.9	17057	15	BACHYTPP	Sequence
C 286	19.2	68.6	41039	13	U41276	359	19	67.9	28954	15	BACHYTPP	Sequence
C 287	19.2	68.6	110000	12	AC164608	360	19	67.9	35252	12	AC101051	Sequence
C 288	19.2	68.6	110000	15	CP000075	361	19	67.9	35984	12	AC140910	Sequence
C 289	19.2	68.6	110000	15	CP000107	362	19	67.9	36383	5	HSB6C3	Sequence
C 290	19.2	68.6	110000	15	AE016796	363	19	67.9	36560	5	AF195658	Sequence
C 291	19.2	68.6	110000	15	BA000038	364	19	67.9	38119	13	AF125956	Sequence
C 292	19.2	68.6	110000	15	AX950851	365	19	67.9	38902	5	AY963685	Sequence
C 293	19.2	68.6	113845	6	AL935325	366	19	67.9	42688	13	CBRG15A11	Sequence
C 294	19.2	68.6	206044	6	AC138210	367	19	67.9	46913	12	AP001878	Sequence
C 295	19.2	68.6	224712	6	AC169668	368	19	67.9	67817	11	BX950227	Sequence
C 296	19.2	68.6	240778	12	AC105584	369	19	67.9	87054	11	BX511074	Sequence
C 297	19	67.9	19	2	C0832282	370	19	67.9	94558	11	BX927353	Sequence
C 298	19	67.9	19	2	C0880065	371	19	67.9	95528	5	AC096678	Sequence
C 299	19	67.9	19	2	C0880461	372	19	67.9	103950	5	AC034235	Sequence
C 300	19	67.9	19	2	C0832283	373	19	67.9	108566	12	AC098193	Sequence
C 301	19	67.9	19	2	C0832283	374	19	67.9	110000	4	AP008218	Sequence
C 302	19	67.9	19	2	C0880066	375	19	67.9	110000	4	AE016955	Sequence
C 303	19	67.9	19	2	C0880066	376	19	67.9	110000	4	AE017349	Sequence
C 304	19	67.9	19	2	DD057309	377	19	67.9	110000	4	AE017349	Sequence
C 305	19	67.9	19	2	DD057310	378	19	67.9	110000	12	AC098192	Sequence
C 306	19	67.9	19	2	DD057311	379	19	67.9	110000	12	AC140833	Sequence
C 307	19	67.9	19	2	DD057312	380	19	67.9	110000	12	AP006468	Sequence
C 308	19	67.9	19	2	DD057313	381	19	67.9	115991	12	AC166314	Sequence
C 309	19	67.9	19	2	DD057314	382	19	67.9	120624	4	AY973543	Sequence
C 310	19	67.9	19	2	DD057314	383	19	67.9	125479	5	HSJ244P24	Sequence

676	18.4	65.7	110000	15	BA000019_43	Continuation (44 o	749	18.4	65.7	199759	6	AP006505	AP006505 Mus muscu
677	18.4	65.7	110000	15	BA000019_44	Continuation (45 o	750	18.4	65.7	200000	5	AP000493	AP000493 Homo sapi
678	18.4	65.7	112361	5	AC027316	Homo sapi	751	18.4	65.7	202108	12	AC113218	AC113218 Rattus no
679	18.4	65.7	112670	5	AL589165	Homo sapi	752	18.4	65.7	203697	12	AC157906	AC157906 Mus muscu
680	18.4	65.7	113028	5	HS68D15	Homo sapi	753	18.4	65.7	204098	6	AC162176	AC162176 Mus muscu
681	18.4	65.7	113974	5	AC018763	Homo sapi	754	18.4	65.7	205222	6	AC123534	AC123534 Mus muscu
682	18.4	65.7	122839	5	AL161898	Homo sapi	755	18.4	65.7	206825	12	AC141064	AC141064 Homo sapi
683	18.4	65.7	126753	6	AL1731655	Mus muscu	756	18.4	65.7	206925	12	AC177893	AC177893 Zee maye
684	18.4	65.7	129098	5	HS46H23	Homo sapi	757	18.4	65.7	207436	12	AC140823	AC140823 Homo sapi
685	18.4	65.7	132449	5	AL365272	Homo sapi	758	18.4	65.7	207686	12	AC156812	AC156812 Bos tauru
686	18.4	65.7	133691	5	AC074347	Homo sapi	759	18.4	65.7	207757	12	AC166450	AC166450 Bos tauru
687	18.4	65.7	134245	5	HS1052M9	Homo sapi	760	18.4	65.7	209271	6	AP006504	AP006504 Mus muscu
688	18.4	65.7	135299	5	AC091857	Homo sapi	761	18.4	65.7	209336	6	AC108840	AC108840 Mus muscu
689	18.4	65.7	137942	6	AL362290	Homo sapi	762	18.4	65.7	209999	6	AL731711	AL731711 Mouse DNA
690	18.4	65.7	139630	5	AL6465745	Mus muscu	763	18.4	65.7	210672	12	HS179115	HS179115
691	18.4	65.7	138653	5	AL355381	Homo sapi	764	18.4	65.7	211076	6	AC107611	AC107611 Rattus no
692	18.4	65.7	140549	5	AP006192	Homo sapi	765	18.4	65.7	211515	5	AC144479	AC144479 Pan trogl
693	18.4	65.7	141594	11	BX469928	Zebrafish	766	18.4	65.7	211662	6	AC161375	AC161375 Mus muscu
694	18.4	65.7	143167	12	AC182015	Atelerix	767	18.4	65.7	213050	15	AL646079	AL646079 Rattus no
695	18.4	65.7	143200	5	AC008413	Homo sapi	768	18.4	65.7	213550	12	AC135904	AC135904 Rattus no
696	18.4	65.7	144781	4	AC135426	Oryza sat	769	18.4	65.7	220212	12	AC141603	AC141603 Homo sapi
697	18.4	65.7	146687	5	AC110592	Homo sapi	770	18.4	65.7	220853	12	AC167604	AC167604 Bos tauru
698	18.4	65.7	147899	12	AC128194	Rattus no	771	18.4	65.7	222655	6	AC153541	AC153541 Mus muscu
699	18.4	65.7	152610	6	AC166051	Homo sapi	772	18.4	65.7	222880	12	AC172805	AC172805 Bos tauru
700	18.4	65.7	156630	12	AC177752	Strongylo	773	18.4	65.7	223110	6	AC123752	AC123752 Mus muscu
701	18.4	65.7	157034	6	AC145397	Rattus no	774	18.4	65.7	223536	12	CT027544	CT027544 Danto xer
702	18.4	65.7	157034	12	AC125237	Homo sapi	775	18.4	65.7	224009	12	AC131058	AC131058 Mus muscu
703	18.4	65.7	158357	5	CNS07BPC	Homo sapi	776	18.4	65.7	224622	6	AC165953	AC165953 Mus muscu
704	18.4	65.7	159567	5	CNS07BPC	Homo sapi	777	18.4	65.7	226645	12	AC094273	AC094273 Rattus no
705	18.4	65.7	160177	11	BS936343	Zebrafish	778	18.4	65.7	229134	12	AC096974	AC096974 Rattus no
706	18.4	65.7	162058	11	BSX30081	Zebrafish	779	18.4	65.7	229474	12	AC165510	AC165510 Bos tauru
707	18.4	65.7	162441	5	AL356321	Homo sapi	780	18.4	65.7	230288	12	AC122977	AC122977 Rattus no
708	18.4	65.7	163283	5	AL355606	Homo sapi	781	18.4	65.7	230788	12	AC114017	AC114017 Rattus no
709	18.4	65.7	164404	12	AC027149	Homo sapi	782	18.4	65.7	231376	11	AC146753	AC146753 Gallus ga
710	18.4	65.7	164605	12	AC113605	Homo sapi	783	18.4	65.7	232105	12	AC159779	AC159779 Bos tauru
711	18.4	65.7	164659	12	AC126577	Rattus no	784	18.4	65.7	232961	12	AC119317	AC119317 Rattus no
712	18.4	65.7	165235	6	AC145398	Rattus no	785	18.4	65.7	233038	12	AC118403	AC118403 Rattus no
713	18.4	65.7	166381	12	AC116943	Pan trogl	786	18.4	65.7	237729	12	AC098284	AC098284 Rattus no
714	18.4	65.7	166656	12	AC025331	Homo sapi	787	18.4	65.7	238988	12	AC096344	AC096344 Rattus no
715	18.4	65.7	169327	12	AC080110	Homo sapi	788	18.4	65.7	241544	12	AL713879	AL713879 Homo sapi
716	18.4	65.7	169892	6	AC154812	Mus muscu	789	18.4	65.7	244594	12	AC112470	AC112470 Rattus no
717	18.4	65.7	170398	12	AC013540	Homo sapi	790	18.4	65.7	245229	12	AC099093	AC099093 Rattus no
718	18.4	65.7	170425	11	BX465867	Zebrafish	791	18.4	65.7	245369	12	AC096044	AC096044 Rattus no
719	18.4	65.7	171255	5	AL691447	Homo sapi	792	18.4	65.7	245617	12	AC095526	AC095526 Rattus no
720	18.4	65.7	172945	5	AC108009	Homo sapi	793	18.4	65.7	249765	12	AC129855	AC129855 Rattus no
721	18.4	65.7	173804	5	HS1030M6	Homo sapi	794	18.4	65.7	251149	12	AC109774	AC109774 Rattus no
722	18.4	65.7	173945	11	BS322597	Zebrafish	795	18.4	65.7	252519	12	AC126215	AC126215 Rattus no
723	18.4	65.7	174085	6	AC163342	Mus muscu	796	18.4	65.7	253411	12	AC128606	AC128606 Rattus no
724	18.4	65.7	174600	6	AC110534	Mus muscu	797	18.4	65.7	253777	12	AC165904	AC165904 Bos tauru
725	18.4	65.7	174924	12	CT033833	Danto xer	798	18.4	65.7	256974	12	AC103221	AC103221 Rattus no
726	18.4	65.7	176435	12	AC149874	Xenopus t	799	18.4	65.7	258862	6	CT009577	CT009577 Mouse DNA
727	18.4	65.7	176843	12	AC026655	Homo sapi	800	18.4	65.7	260224	12	AC130084	AC130084 Rattus no
728	18.4	65.7	177101	12	BX470137	Danto xer	801	18.4	65.7	263706	12	AC097149	AC097149 Rattus no
729	18.4	65.7	178006	6	AC164068	Mus muscu	802	18.4	65.7	266718	12	AC098602	AC098602 Rattus no
730	18.4	65.7	178864	5	AC022535	Homo sapi	803	18.4	65.7	271368	12	AC170401	AC170401 Bos tauru
731	18.4	65.7	178896	6	AC122504	Mus muscu	804	18.4	65.7	278136	12	AC152273	AC152273 Bos tauru
732	18.4	65.7	180752	12	AC167845	Bos tauru	805	18.4	65.7	290052	12	AC160578	AC160578 Bos tauru
733	18.4	65.7	181501	12	AC016005	Homo sapi	806	18.4	65.7	301479	5	AC136590	AC136590 Homo sapi
734	18.4	65.7	183535	5	AC137551	Homo sapi	807	18.4	65.7	329752	12	AC105591	AC105591 Rattus no
735	18.4	65.7	183894	6	AC129935	Mus muscu	808	18.4	65.7	340000	5	AP001725	AP001725 Homo sapi
736	18.4	65.7	184510	6	AC101894	Homo sapi	809	18.4	65.7	340000	5	AP001725	AP001725 Homo sapi
737	18.4	65.7	184876	5	AC008473	Homo sapi	810	18.4	65.7	340000	5	AP001725	AP001725 Homo sapi
738	18.4	65.7	185121	6	AC102907	Mus muscu	811	18.4	65.7	340000	5	AP001725	AP001725 Homo sapi
739	18.4	65.7	185920	5	AC009399	Homo sapi	812	18.4	65.7	340000	5	AP001725	AP001725 Homo sapi
740	18.4	65.7	188920	12	AC140709	Homo sapi	813	18.4	65.7	340000	5	AP001725	AP001725 Homo sapi
741	18.4	65.7	190613	12	AC011692	Homo sapi	814	18.4	65.7	340000	5	AP001725	AP001725 Homo sapi
742	18.4	65.7	192707	12	AC116250	Rattus no	815	18.4	65.7	340000	5	AP001725	AP001725 Homo sapi
743	18.4	65.7	195296	12	AC156652	Bos tauru	816	18.4	65.7	340000	5	AP001725	AP001725 Homo sapi
744	18.4	65.7	195457	12	AC128064	Bos tauru	817	18.4	65.7	340000	5	AP001725	AP001725 Homo sapi
745	18.4	65.7	196470	5	BS000203	Pan trogl	818	18.4	65.7	340000	5	AP001725	AP001725 Homo sapi
746	18.4	65.7	196715	12	AC141600	Homo sapi	819	18.4	65.7	340000	5	AP001725	AP001725 Homo sapi
747	18.4	65.7	197153	6	AC141966	Rattus no	820	18.4	65.7	340000	5	AP001725	AP001725 Homo sapi
748	18.4	65.7	199634	6	AL591209	Mouse DNA	821	18.4	65.7	340000	5	AP001725	AP001725 Homo sapi

968	18	64.3	78428	12	AC174546	AC174546 Strongylo
c 969	18	64.3	89039	11	BX548062	BX548062 Zebrafish
970	18	64.3	100427	5	AC004048	AC004048 Homo sapi
c 971	18	64.3	108441	12	AC150445	AC150445 Medicago
c 972	18	64.3	109222	6	AC116371	AC116371 Mus muscu
c 973	18	64.3	109968	5	AC131151	AC131151 Homo sapi
c 974	18	64.3	110000	12	AC098940	AC098940 Rattus no
c 975	18	64.3	110000	12	AC102394	AC102394 12 of
976	18	64.3	110000	15	CP000091	CP000091 7 of
977	18	64.3	110000	15	CP000110	CP000110 14 of
978	18	64.3	110000	15	CP000110	CP000110 14 of
c 979	18	64.3	110000	15	CP000117	CP000117 56 of
c 980	18	64.3	110000	15	CP000153	CP000153 10 of
c 981	18	64.3	114304	12	AC174308	AC174308 Medicago
c 982	18	64.3	118263	5	CNS01DRM	Al117667 Human chr
c 983	18	64.3	118684	5	AC025335	AC025335 Homo sapi
984	18	64.3	121017	5	AC087388	AC087388 Homo sapi
985	18	64.3	122057	12	AC177365	AC177365 Strongylo
c 986	18	64.3	127266	5	AC023672	AC023672 Homo sapi
987	18	64.3	128189	12	AC176261	AC176261 Strongylo
988	18	64.3	129477	11	BX927161	BX927161 Zebrafish
989	18	64.3	131365	4	AC140027	AC140027 Medicago
990	18	64.3	133485	6	AC118213	AC118213 Mus muscu
c 991	18	64.3	133819	12	AC178603	AC178603 Strongylo
992	18	64.3	134914	5	AC004542	AC004542 Homo sapi
993	18	64.3	135894	5	AC145425	AC145425 Homo sapi
c 994	18	64.3	136809	6	AL683892	AL683892 Mouse DNA
c 995	18	64.3	139077	11	AL935038	AL935038 Zebrafish
c 996	18	64.3	139342	10	AF325155	AF325155 Spodopter
c 997	18	64.3	139529	12	AC176009	AC176009 Strongylo
c 998	18	64.3	140222	11	CR385090	CR385090 Zebrafish
c 999	18	64.3	141146	12	AC179298	AC179298 Strongylo
1000	18	64.3	142477	5	AC109781	AC109781 Homo sapi

ALIGNMENTS

RESULT 1	AR063359	28 bp	DNA	linear	PAT 29-SEP-1999
LOCUS	AR063359	Sequence 7 from patent US 5846701.			
DEFINITION	AR063359				
ACCESSION	AR063359.1	GI:5992667			
VERSION					
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 28)				
TITLE	Kacian,D.Louis. and McAllister,D.Lisa.				
JOURNAL	Method for suppressing inhibition of enzyme-mediated reactions by				
FEATURES	ionic detergents using high concentration of non-ionic detergent				
source	Patent: US 5846701-A 7 08-DEC-1998;				
	Location/Qualifiers				
	1..28				
	/organism="unknown"				
	/mol_type="unassigned DNA"				

ORIGIN					
Query Match	100.0%;	Score 28;	DB 2;	Length 28;	
Best Local Similarity	100.0%;	Pred. No. 0.002;			
Matches	28;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	GAACAGCAATACAAACCGTTGTG	28		
Db	1	GAACAGCAATACAAACCGTTGTG	28		
RESULT 2	AR349065	28 bp	DNA	linear	PAT 17-AUG-2003
LOCUS	AR349065	Sequence 5 from patent US 6583278.			
DEFINITION	AR349065				
ACCESSION	AR349065				

VERSION	AR349065.1	GI:33749770			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 28)				
TITLE	Nucleic acid probes complementary to human papilloma virus nucleic				
JOURNAL	acid				
FEATURES	Patent: US 6583278-A 5 24-JUN-2003;				
source	Gen-Probe Incorporated; San Diego, CA				
	Location/Qualifiers				
	1..28				
	/organism="unknown"				
	/mol_type="genomic DNA"				
ORIGIN					
Query Match	100.0%;	Score 28;	DB 2;	Length 28;	
Best Local Similarity	100.0%;	Pred. No. 0.002;			
Matches	28;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	GAACAGCAATACAAACCGTTGTG	28		
Db	1	GAACAGCAATACAAACCGTTGTG	28		
RESULT 3	AR349066/c	28 bp	DNA	linear	PAT 17-AUG-2003
LOCUS	AR349066	Sequence 6 from patent US 6583278.			
DEFINITION	AR349066				
ACCESSION	AR349066				
VERSION	AR349066.1	GI:33749771			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 28)				
TITLE	Carter,N.M.				
JOURNAL	Nucleic acid probes complementary to human papilloma virus nucleic				
FEATURES	acid				
source	Patent: US 6583278-A 6 24-JUN-2003;				
	Gen-Probe Incorporated; San Diego, CA				
	Location/Qualifiers				
	1..28				
	/organism="unknown"				
	/mol_type="genomic DNA"				
ORIGIN					
Query Match	100.0%;	Score 28;	DB 2;	Length 28;	
Best Local Similarity	100.0%;	Pred. No. 0.002;			
Matches	28;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	GAACAGCAATACAAACCGTTGTG	28		
Db	1	GAACAGCAATACAAACCGTTGTG	28		
RESULT 4	AR349067	28 bp	DNA	linear	PAT 17-AUG-2003
LOCUS	AR349067	Sequence 7 from patent US 6583278.			
DEFINITION	AR349067				
ACCESSION	AR349067				
VERSION	AR349067.1	GI:33749772			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 28)				
TITLE	Carter,N.M.				
JOURNAL	Nucleic acid probes complementary to human papilloma virus nucleic				
	acid				
	Patent: US 6583278-A 7 24-JUN-2003;				
	Gen-Probe Incorporated; San Diego, CA				

FEATURES Location/Qualifiers
source 1..28
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 28; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACAGCAATACAAACCGTGTGTG 28
1 GAACAGCAATACAAACCGTGTGTG 28

Db 1 GAACAGCAATACAAACCGTGTGTG 28

RESULT 5
AR349068/c 28 bp DNA linear PAT 17-AUG-2003
LOCUS AR349068
DEFINITION Sequence 8 from patent US 6583278.
ACCESSION AR349068
VERSION AR349068.1 GI:33749773
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Carter,N.M.
TITLE Nucleic acid probes complementary to human papilloma virus nucleic acid
JOURNAL Patent: US 6583278-A 8 24-JUN-2003;
Gen-Probe Incorporated; San Diego, CA

FEATURES
source Location/Qualifiers
1..28
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 28; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACAGCAATACAAACCGTGTGTG 28
28 GAACAGCAATACAAACCGTGTGTG 1

Db 28 GAACAGCAATACAAACCGTGTGTG 1

RESULT 6
AR577462 87 bp DNA linear PAT 14-DEC-2004
LOCUS AR577462
DEFINITION Sequence 7 from patent US 6783763.
ACCESSION AR577462
VERSION AR577462.1 GI:56580067
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 87)
AUTHORS Choplin,J., Villada,I.B., Guillet,J.-G., Connan,F. and Ferries,B.
TITLE Polypeptidic proteinic fragments of the E6 and E7 HPV proteins,
production and use thereof in vaccines
JOURNAL Patent: US 6783763-A 7 31-AUG-2004;
Peptide Immune Ligands and Institut National de la Sante et de la
Recherche Medicale (INSERM); Labège, Cedex;

FEATURES
source Location/Qualifiers
1..87
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 28; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACAGCAATACAAACCGTGTGTG 28
49 GAACAGCAATACAAACCGTGTGTG 76

Db 49 GAACAGCAATACAAACCGTGTGTG 76

RESULT 7
AX057044 87 bp DNA linear PAT 17-JAN-2001
LOCUS AX057044
DEFINITION Sequence 7 from Patent WO0075336.
ACCESSION AX057044
VERSION AX057044.1 GI:12309885
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Choplin,J., Bourgault Villada,I., Guillet,J.G., Connan,F. and
Ferries,B.
TITLE Proteinfraegmente die verschiedene epitope der hpv proteine e6 und
e7 umfassen, ihre herstellung und verwendungen insbesondere zur
impfung
JOURNAL Patent: WO 0075336-A 7 14-DEC-2000;
Biovector Therapeutics S.A. (FR) ; Institut National de la Sante et
de la Recherche Medicale (INSERM) (FR)

FEATURES
source Location/Qualifiers
1..87
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="fragment de la sequence codant pour E6 de HPV et
sequence peptidique correspondance"
1..>87
/note="unnamed protein product"
/codon_start=1
/transl_table=1
/protein_id="CAC22413.1"
/db_xref="GI:12309886"
/translation="MSERYRHYCVSLVYTTLEQYKRLCDLLT"

ORIGIN
Query Match 100.0%; Score 28; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACAGCAATACAAACCGTGTGTG 28
49 GAACAGCAATACAAACCGTGTGTG 76

Db 49 GAACAGCAATACAAACCGTGTGTG 76

RESULT 8
HPV14515 245 bp DNA linear VRL 15-FEB-2001
LOCUS HPV14515
DEFINITION Human papillomavirus clone HPV1629 E6 gene, partial
cds.
ACCESSION U14515
VERSION U14515.1 GI:984951
KEYWORDS
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
REFERENCE 1 (bases 1 to 245)
AUTHORS Haegert,D.G., Galutira,D.F. and Younghsband,B.H.
TITLE Sequence variation in the E6 gene of human papillomavirus type 16
JOURNAL Unpublished
AUTHORS Galutira,D.F.
TITLE Direct Submission
JOURNAL Submitted (07-SEP-1994) Dante F. Galutira, Memorial University of
Newfoundland, Discipline of Pathology, Fac. Medicine, St. John's,
Newfoundland, A1B 3V6, Canada

FEATURES
source Location/Qualifiers

source 1. .245
/organism="Human papillomavirus"
/mol_type="genomic DNA"
/strain="HPV16"
/db_xref="taxon:10566"
/clone="HPV1629"
/tissue_type="cervical tissue from invasive carcinoma"
1. .245
/gene="B6"
/note="A to G transition from PA16, GenBank Accession Number K02718, position 286; NCBI gi: 333031"
/replace="t"
64
/gene="B6"
/note="A to G transition from PA16, GenBank Accession Number K02718, position 289; NCBI gi: 333031"
/replace="a"
110
/gene="B6"
/note="C to T transition from PA16, GenBank Accession Number K02718, position 335; NCBI gi: 333031"
/replace="c"
125
/gene="B6"
/note="T to G transversion from PA16, GenBank Accession Number K02718, position 350; NCBI gi: 333031"
/replace="t"
139
/gene="B6"
/note="A to T transversion from PA16, GenBank Accession Number K02718, position 364; NCBI gi: 333031"
/replace="a"
ORIGIN
Query Match 100.0%; Score 28; DB 10; Length 245;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAACAGCAATACAAACCGTTGTGTG 28
|||||
Db 143 GAACAGCAATACAAACCGTTGTGTG 170
RESULT 9
HPV14511 253 bp DNA linear VRL 15-FEB-2001
LOCUS Human papillomavirus clone HPV1601 E6 protein (E6) gene, partial
DEFINITION cds.
ACCESSION U14511
VERSION U14511.1 GI:984943
KEYWORDS
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
unclassified Papillomaviridae;
viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
REFERENCE 1 (bases 1 to 253)
AUTHORS Haegert,D.G., Galutira,D.F. and Younghusband,B.H.
TITLE Sequence variation in the E6 gene of human papillomavirus type 16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 253)
AUTHORS Galutira,D.F.
TITLE Direct Submission
JOURNAL Submitted (07-SEP-1994) Dante F. Galutira, Memorial University of

FEATURES
source Newfoundland, Discipline of Pathology, Fac. Medicine, St. John's, Newfoundland, A1B 3V6, Canada
Location/Qualifiers
1. .253
/organism="Human papillomavirus"
/mol_type="genomic DNA"
/strain="HPV16"
/db_xref="taxon:10566"
/clone="HPV1601"
/cell_line="Caaki and Siha"
/tissue_type="cervical"
1. .253
/gene="B6"
/note="A to G transition from PA16, GenBank Accession Number K02718, position 350; NCBI gi: 333031"
/replace="t"
115
/gene="B6"
/note="T to G transversion from PA16, GenBank Accession Number K02718, position 350; NCBI gi: 333031"
/replace="t"
ORIGIN
Query Match 100.0%; Score 28; DB 10; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAACAGCAATACAAACCGTTGTGTG 28
|||||
Db 133 GAACAGCAATACAAACCGTTGTGTG 160
RESULT 10
HPV14512 271 bp DNA linear VRL 14-SEP-1995
LOCUS Human papillomavirus clone HPV1603 E6 protein (E6) gene, partial
DEFINITION cds.
ACCESSION U14512
VERSION U14512.1 GI:984945
KEYWORDS
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
unclassified Papillomaviridae;
viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
REFERENCE 1 (bases 1 to 271)
AUTHORS Haegert,D.G., Galutira,D.F. and Younghusband,B.H.
TITLE Sequence variation in the E6 gene of human papillomavirus type 16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 271)
AUTHORS Galutira,D.F.
TITLE Direct Submission
JOURNAL Submitted (07-SEP-1994) Dante F. Galutira, Memorial University of Newfoundland, Discipline of Pathology, Fac. Medicine, St. John's, Newfoundland, A1B 3V6, Canada
FEATURES
source Location/Qualifiers
1. .271
/organism="Human papillomavirus"
/mol_type="genomic DNA"
/strain="HPV16"
/db_xref="taxon:10566"
/clone="HPV1603"
/tissue_type="cervical tissue from invasive carcinoma"
1. .271
/gene="B6"
/note="A to G transition from PA16, GenBank Accession Number K02718, position 350; NCBI gi: 333031"
/replace="t"
/product="B6 protein"

variation
/protein_id="AAB60566.1"
/db_xref="GI:984946"
/translation="VYDPAFRLDCTIVRDGNPYAVCDKCLKFYSKISEYRHYCYSLYG
TTLEQQYNKPLCDLLIRNCINQKPLCEBEKQRLDKKQRFHNIRGR"
85
/gene="E6"
/note="T to G transversion from PA16, GenBank Accession
Number K02718, position 310; NCBI gi: 333031"
/replace="t"

ORIGIN
Query Match 100.0%; Score 28; DB 10; Length 271;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACAGCAATACAAACCGTTGTGTG 28
|||||
143 GAACAGCAATACAAACCGTTGTGTG 170

RESULT 11
HPV14513 272 bp DNA linear VRL 15-FEB-2001
LOCUS
DEFINITION Human papillomavirus clone HPV1607 E6 protein (E6) gene, partial
cds.
ACCESSION U14513 GI:984947
VERSION
KEYWORDS
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
unclassified Papillomaviridae.
REFERENCE 1 (bases 1 to 272) Dante F. Galutira, D.F. and Younghusband, B.H.
Haegert, D.G., Galutira, D.F. and Younghusband, B.H.
Sequence variation in the E6 gene of human papillomavirus type 16
Unpublished
2 (bases 1 to 272)
Galutira, D.F.
Direct Submission
Submitted (07-SEP-1994) Dante F. Galutira, Memorial University of
Newfoundland, Discipline of Pathology, Fac. Medicine, St. John's,
Newfoundland, A1B 3V6, Canada
location/Qualifiers
1. 272
/organism="Human papillomavirus"
/mol_type="genomic DNA"
/strain="HPV16"
/db_xref="taxon:10566"
/clone="HPV1607"
/tissue_type="cervical tissue from invasive carcinoma"
1. 272
/gene="E6"
/gene="E6"
/gene="E6"
/codon_start=2
/product="E6 protein"
/protein_id="AAB60567.2"
/db_xref="GI:12831648"
/translation="VYDPAFRLDCTIVRDGNPYAVCDKCLKFYSKISEYRHYCYSLYG
TTLEQQYNKPLCDLLIRNCINQKPLCEBEKQRLDKKQRFHNIRGR"
31
/gene="E6"
/note="C to G transversion from PA16, GenBank Accession
Number K02718, position 256; NCBI gi: 333031"
/replace="c"

ORIGIN
Query Match 100.0%; Score 28; DB 10; Length 272;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACAGCAATACAAACCGTTGTGTG 28
|||||

Db 143 GAACAGCAATACAAACCGTTGTGTG 170

RESULT 12
HPV14514 273 bp DNA linear VRL 15-FEB-2001
LOCUS
DEFINITION Human papillomavirus clone HPV1627 E6 protein (E6) gene, partial
cds.
ACCESSION U14514 GI:984949
VERSION
KEYWORDS
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
unclassified Papillomaviridae.
REFERENCE 1 (bases 1 to 273)
Haegert, D.G., Galutira, D.F. and Younghusband, B.H.
Sequence variation in the E6 gene of human papillomavirus type 16
Unpublished
2 (bases 1 to 273)
Galutira, D.F.
Direct Submission
Submitted (07-SEP-1994) Dante F. Galutira, Memorial University of
Newfoundland, Discipline of Pathology, Fac. Medicine, St. John's,
Newfoundland, A1B 3V6, Canada
location/Qualifiers
1. 273
/organism="Human papillomavirus"
/mol_type="genomic DNA"
/strain="HPV16"
/db_xref="taxon:10566"
/clone="HPV1627"
/tissue_type="cervical tissue from invasive carcinoma"
1. 273
/gene="E6"
/gene="E6"
/gene="E6"
/codon_start=2
/product="E6 protein"
/protein_id="AAB60568.2"
/db_xref="GI:12831649"
/translation="VYDPAFRLDCTIVRDGNPYAVCDKCLKFYSKISEYRHYCYSLYG
TTLEQQYNKPLCDLLIRNCINQKPLCEBEKQRLDKKQRFHNIRGR"
61
/gene="E6"
/note="T to A transversion from PA16, GenBank Accession
Number K02718, position 286; NCBI gi: 333031"
/replace="t"
64
/gene="E6"
/note="A to G transversion from PA16, GenBank Accession
Number K02718, position 289; NCBI gi: 333031"
/replace="a"
110
/gene="E6"
/note="C to T transversion from PA16, GenBank Accession
Number K02718, position 335; NCBI gi: 333031"
/replace="c"

ORIGIN
Query Match 100.0%; Score 28; DB 10; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACAGCAATACAAACCGTTGTGTG 28
|||||
143 GAACAGCAATACAAACCGTTGTGTG 170

Db 143 GAACAGCAATACAAACCGTTGTGTG 170

RESULT 13
HPV14516 274 bp DNA linear VRL 14-SEP-1995
LOCUS
DEFINITION Human papillomavirus clone HPV1649 E6 protein (E6) gene, partial

Accession	cds
U14516	U14516
U14516.1	GI:984953
KEYWORDS	
SOURCE	
ORGANISM	Human papillomavirus Human papillomavirus Human papillomavirus Virus; dsDNA viruses, no RNA stage; Papillomaviridae; unclassified Papillomaviridae.
REFERENCE	
AUTHORS	1 (bases 1 to 374)
TITLE	Hager, D.G., Galutira, D.F. and Youngusband, B.H.
REFERENCE	Sequence variation in the B6 gene of human papillomavirus type 16
AUTHORS	2 (bases 1 to 274)
TITLE	Galutira, D.F.
JOURNAL	Direct Submission
Submitted (07-SEP-1994)	Dante F. Galutira, Memorial University of
Newfoundland, Discipline of Pathology, Fac. Medicine, St. John's,	
Newfoundland, A1B 3X6, Canada	
Location/Qualifiers	
FEATURES	
source	1..274
	/organism="Human papillomavirus"
	/mol_type="genomic DNA"
	/strain="HPV16"
	/db_xref="taxon:10566"
	/clone="HPV1649"
	/tissue_type="cervical tissue from invasive carcinoma"
	1..274
	/gene="B6"
	<1..>274
	/gene="B6"
	/codon_start=2
	/product="B6 protein"
	/protein_id="AAB60570.1"
	/db_xref="GI:984954"
	/translation="VYDPAPFRLDLCIVRDGNPAVCDKLFYSKISRYRYCYSVYGV
	TTLTQQYNKPLCDLLINCINCQKRLCPBEKQRHLDKXQRFNINGRW"
	61
variation	/gene="B6"
	/note="T to A transversion from PA16, GenBank Accession
	Number K02718, position 286; NCBI gi: 333031"
	/replace="c"
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variation	/gene="B6"
	/note="A to G transversion from PA16, GenBank Accession
	Number K02718, position 289; NCBI gi: 333031"
	/replace="a"
	110
variation	/gene="B6"
	/note="C to T transition from PA16, GenBank Accession
	Number K02718, position 335; NCBI gi: 333031"
	/replace="c"
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variation	/gene="B6"
	/note="T to G transversion from PA16, GenBank Accession
	Number K02718, position 350; NCBI gi: 333031"
	/replace="c"
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Query Match	100.0%; Score 28; DB 10; Length 274;
Best Local Similarity	100.0%; Pred. NO. 0.0024;
Matches	28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 GAACGACATACACAAACCGTTGGT 28
DB	143 GAACGACATACAAACCGTTGGT 170
RESULT 14	
LOCUS	551110 421 bp DNA linear VRL 08-MAY-1993
DEFINITION	orf B6 [human papillomavirus HPV, type 16, head and neck tumor,
Genomic, 421 nt].	
ACCESSION	551110

VERSION	SS1110.1	GI:262061
KEYWORDS		
SOURCE		
ORGANISM	Human papillomavirus	
	Human papillomavirus	
	Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;	
REFERENCE	unclassified Papillomaviridae.	
AUTHORS	1 (bases 1 to 421)	
TITLE	Yuan,Y.S., Liu,S.T., Ong,W.R., Chen,M.L., Shu,C.H. and Chang,Y.S.	
JOURNAL	Detection of Epstein-Barr virus and human papillomavirus in head	
PUBMED	and neck tumors	
REMARK	J. Clin. Microbiol. 31 (1), 53-56 (1993)	
COMMENT	8380183	
FEATURES	GenBank staff at the National Library of Medicine created this	
	entry [NCBI gisbg 120826] from the original journal article.	
	PCR primer sequences: 1-21 and 400-421.	
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source	1..421	
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	/db_xref="taxon:10566"	
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	/gene="orf E6"	
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	Best Local Similarity	100.0%; Pied. No. 0.0025;
	Matches	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	1 GAACAGCAATTCACAACCGTGTGTCG 28	
Dd	266 GAACAGCAATTCACAACCGTGTGTCG 293	
RESULT_15		
AF404695	451 bp	DNA linear VRL 09-OCT-2003
DEFINITION	Human papillomavirus type 16 isolate HPV16B6C4 E6 protein (E6) and	
ACCESSION	E7 protein (E7) genes, partial cds.	
VERSION	AF404695	
KEYWORDS	AF404695.1 GI:15529578	
SOURCE		
ORGANISM	Human papillomavirus type 16	
	Human papillomavirus type 16	
	Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;	
	Alphapapillomavirus.	
REFERENCE	1 (bases 1 to 451)	
AUTHORS	Watts,K.J., Thompson,C.H., Coscart,Y.E. and Rose,B.R.	
TITLE	Sequence variation and physical state of human papillomavirus type	
JOURNAL	16 cervical cancer isolates from Australia and New Caledonia	
PUBMED	Int. J. Cancer 97 (6), 868-874 (2002)	
REMARK	11837370	
AUTHORS	2 (bases 1 to 451)	
TITLE	Watts,K.J., Thompson,C.H., Coscart,Y.E. and Rose,B.R.	
JOURNAL	Direct Submission	
PUBMED	Submitted (31-JUL-2001) Department of Infectious Diseases,	
REMARK	University of Sydney, Blackburn Building, D06, Off Western Avenue,	
JOURNAL	Camperdown, Sydney, New South Wales 2006, Australia	
FEATURES	Location/Qualifiers	
source	1..451	
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CDS	/codon_start=3	
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	/db_xref="GI:15529579"	
	/translation="TIHDIILECYCKQOLLREVYGFAPRDLCTIYRDGNPYAVCDK	

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398..>451
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/product="E7 protein"
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/db_xref="GI:15529580"
/translation="MHGDTPTLHEYMIDLQPE"

ORIGIN

Query Match 100.0%; Score 28; DB 10; Length 451;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 GAACAGCAATACAAACCAACCGTTGTGTG 28
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204 GAACAGCAATACAAACCAACCGTTGTGTG 231

Db

RESULT 16
AF404696 451 bp DNA linear VRL 09-OCT-2003
LOCUS Human papillomavirus type 16 isolate HVI6B6CC5 E6 protein (E6) and
DEFINITION E7 protein (E7) genes, partial cds.
ACCESSION AF404696
VERSION AF404696.1 GI:15529581
KEYWORDS
SOURCE Human papillomavirus type 16
ORGANISM Human papillomavirus type 16
VIRUSES; deDNA viruses, no RNA stage; Papillomaviridae;
Alphapapillomavirus.
1 (bases 1 to 451)
REFERENCE Watters,K.J., Thompson,C.H., Cossart,Y.E. and Rose,B.R.
AUTHORS Sequence variation and physical state of human papillomavirus type
TITLE 16 cervical cancer isolates from Australia and New Caledonia
JOURNAL Int. J. Cancer 97 (6), 868-874 (2002)
PUBMED 11857370
2 (bases 1 to 451)
REFERENCE Watters,K.J., Thompson,C.H., Cossart,Y.E. and Rose,B.R.
AUTHORS Direct Submission
TITLE Submitted (31-JUL-2001) Department of Infectious Diseases,
JOURNAL University of Sydney, Blackburn Building, D06, Off Western Avenue,
Camperdown, Sydney, New South Wales 2006, Australia
location/Qualifiers
1. 451
/organism="Human papillomavirus type 16"
/mol_type="genomic DNA"
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/protein_id="AL01349.1"
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398..>451
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/db_xref="GI:15529583"
/translation="MHGDTPTLHEYMIDLQPE"

ORIGIN

Query Match 100.0%; Score 28; DB 10; Length 451;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 GAACAGCAATACAAACCAACCGTTGTGTG 28
|||||
204 GAACAGCAATACAAACCAACCGTTGTGTG 231

Db

RESULT 17
AF404699 451 bp DNA linear VRL 09-OCT-2003
LOCUS Human papillomavirus type 16 isolate HVI6B6CC8 E6 protein (E6) and
DEFINITION E7 protein (E7) genes, partial cds.
ACCESSION AF404699
VERSION AF404699.1 GI:15529590
KEYWORDS
SOURCE Human papillomavirus type 16
ORGANISM Human papillomavirus type 16
VIRUSES; deDNA viruses, no RNA stage; Papillomaviridae;
Alphapapillomavirus.
1 (bases 1 to 451)
REFERENCE Watters,K.J., Thompson,C.H., Cossart,Y.E. and Rose,B.R.
AUTHORS Sequence variation and physical state of human papillomavirus type
TITLE 16 cervical cancer isolates from Australia and New Caledonia
JOURNAL Int. J. Cancer 97 (6), 868-874 (2002)
PUBMED 11857370
2 (bases 1 to 451)
REFERENCE Watters,K.J., Thompson,C.H., Cossart,Y.E. and Rose,B.R.
AUTHORS Direct Submission
TITLE Submitted (31-JUL-2001) Department of Infectious Diseases,
JOURNAL University of Sydney, Blackburn Building, D06, Off Western Avenue,
Camperdown, Sydney, New South Wales 2006, Australia
location/Qualifiers
1. 451
/organism="Human papillomavirus type 16"
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398..>451
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/codon_start=1
/product="E7 protein"
/protein_id="AL01356.1"
/db_xref="GI:15529592"
/translation="MHGDTPTLHEYMIDLQPE"

ORIGIN

Query Match 100.0%; Score 28; DB 10; Length 451;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 GAACAGCAATACAAACCAACCGTTGTGTG 28
|||||
204 GAACAGCAATACAAACCAACCGTTGTGTG 231

Db

RESULT 18
AF404700

LOCUS AF404700 451 bp DNA linear VRL 09-OCT-2003
DEFINITION Human papillomavirus type 16 isolate HPV16ECC9 E6 protein (E6) and
E7 protein (E7) genes, partial cds.
ACCESSION AF404700
VERSION AF404700.1 GI:15529593
KEYWORDS
SOURCE
ORGANISM Human papillomavirus type 16
Human papillomavirus type 16
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Alphapapillomavirus.
REFERENCE
AUTHORS 1 (bases 1 to 451)
Watts,K.J., Thompson,C.H., Cossart,Y.E. and Rose,B.R.
TITLE Sequence variation and physical state of human papillomavirus type
16 cervical cancer isolates from Australia and New Caledonia
JOURNAL Int. J. Cancer 97 (6), 868-874 (2002)
PUBMED 11857370
REFERENCE
AUTHORS 2 (bases 1 to 451)
Watts,K.J., Thompson,C.H., Cossart,Y.E. and Rose,B.R.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-2001) Department of Infectious Diseases,
University of Sydney, Blackburn Building, D06, Off Western Avenue,
Camperdown, Sydney, New South Wales 2006, Australia
Location/Qualifiers
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/product="E6 protein"
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398..>451
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ORIGIN
Query Match 100.0%; Score 28; DB 10; Length 451;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACAGCAATACAAACCGTTGTGTG 28
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Db 204 GAACAGCAATACAAACCGTTGTGTG 231
|||||

RESULT 19
AF404701 451 bp DNA linear VRL 09-OCT-2003
LOCUS AF404701
DEFINITION Human papillomavirus type 16 isolate HPV16ECC10 E6 protein (E6)
and E7 protein (E7) genes, partial cds.
ACCESSION AF404701
VERSION AF404701.1 GI:15529596
KEYWORDS
SOURCE
ORGANISM Human papillomavirus type 16
Human papillomavirus type 16
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Alphapapillomavirus.
REFERENCE
AUTHORS 1 (bases 1 to 451)
Watts,K.J., Thompson,C.H., Cossart,Y.E. and Rose,B.R.

TITLE Sequence variation and physical state of human papillomavirus type
16 cervical cancer isolates from Australia and New Caledonia
JOURNAL Int. J. Cancer 97 (6), 868-874 (2002)
PUBMED 11857370
REFERENCE
AUTHORS 2 (bases 1 to 451)
Watts,K.J., Thompson,C.H., Cossart,Y.E. and Rose,B.R.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-2001) Department of Infectious Diseases,
University of Sydney, Blackburn Building, D06, Off Western Avenue,
Camperdown, Sydney, New South Wales 2006, Australia
Location/Qualifiers
1..451
/organism="Human papillomavirus type 16"
/mol_type="Genomic DNA"
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398..>451
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ORIGIN
Query Match 100.0%; Score 28; DB 10; Length 451;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACAGCAATACAAACCGTTGTGTG 28
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Db 204 GAACAGCAATACAAACCGTTGTGTG 231
|||||

RESULT 20
AF404703 451 bp DNA linear VRL 09-OCT-2003
LOCUS AF404703
DEFINITION Human papillomavirus type 16 isolate HPV16ECC12 E6 protein (E6)
and E7 protein (E7) genes, partial cds.
ACCESSION AF404703
VERSION AF404703.1 GI:15529602
KEYWORDS
SOURCE
ORGANISM Human papillomavirus type 16
Human papillomavirus type 16
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Alphapapillomavirus.
REFERENCE
AUTHORS 1 (bases 1 to 451)
Watts,K.J., Thompson,C.H., Cossart,Y.E. and Rose,B.R.
TITLE Sequence variation and physical state of human papillomavirus type
16 cervical cancer isolates from Australia and New Caledonia
JOURNAL Int. J. Cancer 97 (6), 868-874 (2002)
PUBMED 11857370
REFERENCE
AUTHORS 2 (bases 1 to 451)
Watts,K.J., Thompson,C.H., Cossart,Y.E. and Rose,B.R.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-2001) Department of Infectious Diseases,
University of Sydney, Blackburn Building, D06, Off Western Avenue,
Camperdown, Sydney, New South Wales 2006, Australia
Location/Qualifiers
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ORIGIN
Query Match 100.0%; Score 28; DB 10; Length 451;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAACAGCAATACACAAACCGTTGTGTG 28
Db 204 GAACAGCAATACACAAACCGTTGTGTG 231
RESULT 21
LOCUS AR167393 456 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 29 from patent US 6287569.
ACCESSION AR167393
VERSION AR167393.1 GI:17903171
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 456)
AUTHORS Kijpse, T.J., and Wu, Y.
TITLE Vaccines with enhanced intracellular processing
JOURNAL Patent: US 6287569-A 29 11-SEP-2001;
FEATURES
source location/Qualifiers
1..456
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 100.0%; Score 28; DB 2; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAACAGCAATACACAAACCGTTGTGTG 28
Db 265 GAACAGCAATACACAAACCGTTGTGTG 292
RESULT 22
LOCUS AR177943 456 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 6 from patent US 6313373.
ACCESSION AR177943
VERSION AR177943.1 GI:17920298
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
REFERENCE 1 (bases 1 to 456)
AUTHORS Eckert, R.L., and Crish, J.F.
TITLE Tissue specific promoters and transgenic mouse for the screening of
pharmaceuticals
JOURNAL Patent: US 6313373-A 6 06-NOV-2001;
FEATURES
source location/Qualifiers
1..456
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 100.0%; Score 28; DB 2; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAACAGCAATACACAAACCGTTGTGTG 28
Db 265 GAACAGCAATACACAAACCGTTGTGTG 292
RESULT 23
LOCUS AF327851 456 bp DNA linear VRL 04-JAN-2001
DEFINITION Human papillomavirus type 16 early transforming protein E6 variant
ACCESSION AF327851
VERSION AF327851.1 GI:12025467
KEYWORDS Human papillomavirus type 16
SOURCE Human papillomavirus type 16
ORGANISM Human papillomavirus type 16
REFERENCE 1 (bases 1 to 456)
AUTHORS Ma, Z., Qian, D., Ma, J., Lin, R., Ming, W., Zhong, Z., Zhang, Q. and
Zhang, F.
TITLE Cloning and Sequencing of HPV16 E6 gene from Cervical Carcinoma
Biopsies in Xinjiang
JOURNAL Shengwu Huaxue Yu Shengwu Wuli Jinzhan (2001) In press
REFERENCE 2 (bases 1 to 456)
AUTHORS Ma, Z. and Zhang, F.
TITLE Direct Submision
JOURNAL Submitted (12-DEC-2000) Department of Biology, University of
Xinjiang, 14 Shengli Road, Urumqi, Xinjiang 830046, P.R. China
FEATURES
source location/Qualifiers
1..456
/organism="Human papillomavirus type 16"
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FAFRDICTIVRDGNPYAVCDKCLKYSKISRYRHCYSLYGTTLEQYNKPCDLLIR
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ORIGIN
Query Match 100.0%; Score 28; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAACAGCAATACACAAACCGTTGTGTG 28
Db 265 GAACAGCAATACACAAACCGTTGTGTG 292

RESULT 24
LOCUS HPJ34107 456 bp DNA linear VRL 08-MAR-1996
DEFINITION Human papillomavirus type 16, isolate NM 4094, early transforming protein E6 (E6) gene, complete cds.
ACCESSION U34107
VERSION U34107.1 GI:1098719
KEYWORDS
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
REFERENCE 1 (bases 1 to 456)
AUTHORS Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildesheim,A. and Jensen,S.A.
TITLE Human papillomavirus type 16 variant lineages in United States populations characterized by nucleotide sequence analysis of the E6, E2, and E1 coding segments
J. Virol. 69 (12), 7743-7753 (1995)
JOURNAL 7494284
PUBMED 2 (bases 1 to 456)
REFERENCE Farmer,A.D.
AUTHORS Direct Submission
TITLE Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los Alamos, NM 87501, USA
FEATURES
source location/Qualifiers
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/organism="Human papillomavirus"
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/note="collected by cervical swab at the University of New Mexico, New Mexico, United States."
1..456
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/product="early transforming protein E6"
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/db_xref="GI:1098720"
/translation="MFQDQERPRKLPHLCTELQTTIHDIIEVCYCKOOLRREYVD FAPRDCIVYRDGNPYAVCDKLPKYSKISERYCYGVSYGTTLEQYVKKPLCDLLIR CINQKPLCEBKQRHLDKQRFNIRGWTGRCHSCCSSRRRTQL"
ORIGIN
Query Match 100.0%; Score 28; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAACAGCAATACAAACCGTTGTG 28
Db 265 GAACAGCAATACAAACCGTTGTG 292
RESULT 25
LOCUS HPJ34108 456 bp DNA linear VRL 08-MAR-1996
DEFINITION Human papillomavirus type 16, isolate NM 9999, early transforming protein E6 (E6) gene, complete cds.
ACCESSION U34108
VERSION U34108.1 GI:1098721
KEYWORDS
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
REFERENCE 1 (bases 1 to 456)
AUTHORS Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildesheim,A. and Jensen,S.A.

TITLE Human papillomavirus type 16 variant lineages in United States populations characterized by nucleotide sequence analysis of the E6, E2, and E1 coding segments
J. Virol. 69 (12), 7743-7753 (1995)
JOURNAL 7494284
PUBMED 2 (bases 1 to 456)
REFERENCE Farmer,A.D.
AUTHORS Direct Submission
TITLE Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los Alamos, NM 87501, USA
FEATURES
source location/Qualifiers
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/isolate="NM 9999"
/db_xref="taxon:10566"
/note="collected by cervical swab at the University of New Mexico, New Mexico, United States."
1..456
/gene="E6"
1..456
/gene="E6"
/codon_start=1
/product="early transforming protein E6"
/protein_id="AA91655.1"
/db_xref="GI:1098722"
/translation="MFQDQERPRKLPHLCTELQTTIHDIIEVCYCKOOLRREYVD FAPRDCIVYRDGNPYAVCDKLPKYSKISERYCYGVSYGTTLEQYVKKPLCDLLIR CINQKPLCEBKQRHLDKQRFNIRGWTGRCHSCCSSRRRTQL"
ORIGIN
Query Match 100.0%; Score 28; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAACAGCAATACAAACCGTTGTG 28
Db 265 GAACAGCAATACAAACCGTTGTG 292
RESULT 26
LOCUS HPJ34109 456 bp DNA linear VRL 08-MAR-1996
DEFINITION Human papillomavirus type 16, isolate NM T197, early transforming protein E6 (E6) gene, complete cds.
ACCESSION U34109
VERSION U34109.1 GI:1098723
KEYWORDS
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
REFERENCE 1 (bases 1 to 456)
AUTHORS Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildesheim,A. and Jensen,S.A.
TITLE Human papillomavirus type 16 variant lineages in United States populations characterized by nucleotide sequence analysis of the E6, E2, and E1 coding segments
J. Virol. 69 (12), 7743-7753 (1995)
JOURNAL 7494284
PUBMED 2 (bases 1 to 456)
REFERENCE Farmer,A.D.
AUTHORS Direct Submission
TITLE Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los Alamos, NM 87501, USA
FEATURES
source location/Qualifiers
1..456
/organism="Human papillomavirus"
/mol_type="genomic DNA"
/isolate="NM T197"
/db_xref="taxon:10566"

gene /note="collected by cervical swab at the University of New Mexico, New Mexico, United States."
1. .456
/gene="E6"
CDS 1. .456
/gene="E6"
/codon_start=1
/product="early transforming protein E6"
/protein_id="AA91656.1"
/db_xref="GI:1098724"
/translation="MFODPQRPKLPOLCTELQTTIHDIILCEVCCKOOLRREYD
FARFDCTIVRDGNPVAVCDKCKFYKISBYRHVCYSVGTTLLEQYNNPLCDLLIR
CINCKRPLCEBKQRHDKQRPHNIRGWTGRCMSCRSRTRRETOL"

ORIGIN
Query Match 100.0%; Score 28; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 265 GAACAGCAATACAAACCGTTGTGTG 292

RESULT 27
HPU34110 456 bp DNA linear VRL 08-MAR-1996
LOCUS Human papillomavirus type 16, isolate NM T446, early transforming
DEFINITION protein E6 (E6) gene, complete cds.
ACCESSION U34110.1 GI:1098725
VERSION U34110.1 GI:1098725
KEYWORDS Human papillomavirus
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
Virus(es); dsDNA viruses, no RNA stage; Papillomaviridae;
unclassified Papillomaviridae.
1 (bases 1 to 456)
REFERENCE Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildesheim,A.
AUTHORS and Jenison,S.A.
TITLE Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the
E6, E2, and L1 coding segments
J. Virol. 69 (12), 7743-7753 (1995)
7494284
2 (bases 1 to 456)
REFERENCE Farmer,A.D.
AUTHORS Direct Submission
TITLE Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National
JOURNAL Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
PUBMED Alamos, NM 87501, USA
7494284
CDS 1. .456
/organism="Human papillomavirus"
/mol_type="genomic DNA"
/isolate="NM T446"
/db_xref="taxon:10566"
/note="collected by cervical swab at the University of New Mexico, New Mexico, United States."
1. .456
/gene="E6"
1. .456
/gene="E6"
/codon_start=1
/product="early transforming protein E6"
/protein_id="AA91657.1"
/db_xref="GI:1098726"
/translation="MFODPQRPKLPOLCTELQTTIHDIILCEVCCKOOLRREYD
FARFDCTIVRDGNPVAVCDKCKFYKISBYRHVCYSVGTTLLEQYNNPLCDLLIR
CINCKRPLCEBKQRHDKQRPHNIRGWTGRCMSCRSRTRRETOL"

ORIGIN
Query Match 100.0%; Score 28; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.0025;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACAGCAATACAAACCGTTGTGTG 28
Db 265 GAACAGCAATACAAACCGTTGTGTG 292

RESULT 28
HPU34111 456 bp DNA linear VRL 08-MAR-1996
LOCUS Human papillomavirus type 16, isolate NM T455, early transforming
DEFINITION protein E6 (E6) gene, complete cds.
ACCESSION U34111
VERSION U34111.1 GI:1098727
KEYWORDS Human papillomavirus
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
Virus(es); dsDNA viruses, no RNA stage; Papillomaviridae;
unclassified Papillomaviridae.
1 (bases 1 to 456)
REFERENCE Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildesheim,A.
AUTHORS and Jenison,S.A.
TITLE Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the
E6, E2, and L1 coding segments
J. Virol. 69 (12), 7743-7753 (1995)
7494284
2 (bases 1 to 456)
REFERENCE Farmer,A.D.
AUTHORS Direct Submission
TITLE Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National
JOURNAL Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
PUBMED Alamos, NM 87501, USA
7494284
CDS 1. .456
/organism="Human papillomavirus"
/mol_type="genomic DNA"
/isolate="NM T455"
/db_xref="taxon:10566"
/note="collected by cervical swab at the University of New Mexico, New Mexico, United States."
1. .456
/gene="E6"
1. .456
/gene="E6"
/codon_start=1
/product="early transforming protein E6"
/protein_id="AA91658.1"
/db_xref="GI:1098728"
/translation="MFODPQRPKLPOLCTELQTTIHDIILCEVCCKOOLRREYD
FARFDCTIVRDGNPVAVCDKCKFYKISBYRHVCYSVGTTLLEQYNNPLCDLLIR
CINCKRPLCEBKQRHDKQRPHNIRGWTGRCMSCRSRTRRETOL"

ORIGIN
Query Match 100.0%; Score 28; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACAGCAATACAAACCGTTGTGTG 28
Db 265 GAACAGCAATACAAACCGTTGTGTG 292

RESULT 29
HPU34112 456 bp DNA linear VRL 08-MAR-1996
LOCUS Human papillomavirus type 16, isolate NM T529, early transforming
DEFINITION protein E6 (E6) gene, complete cds.
ACCESSION U34112.1 GI:1098729
VERSION U34112.1 GI:1098729
KEYWORDS Human papillomavirus
SOURCE Human papillomavirus
ORGANISM Human papillomavirus

viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
unclassified Papillomaviridae.
1 (bases 1 to 456)
Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildebrandt,A.
and Jenson,S.A.
Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the
E6, E2, and L1 coding segments
J. Virol. 69 (12), 7743-7753 (1995)
7494284

JOURNAL
PUBMED
2 (bases 1 to 456)
Farmer,A.D.
Direct Submission
Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National
Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
Alamos, NM 87501, USA

FEATURES
source
1..456
/organism="Human papillomavirus"
/mol_type="genomic DNA"
/isolate="NM T529"
/db_xref="taxon:10566"
/note="collected by cervical swab at the University of New
Mexico, New Mexico, United States."
1..456
/gene="E6"
1..456
/gene="E6"
/codon_start=1
/product="early transforming protein E6"
/protein_id="AA91659.1"
/db_xref="GI:1098730"
/translation="MFODQPERPRKLPDLCTELQTTIHDIIECYCKQQLRREYVD
FARDCIVRDGNPYAVCDKCLKFYSKISERYCYSLYGTTLBOQYNKPLCDLLIR
CINQKPLCEBKORHDKKQRFHNIRGRTGCMSCSKSRTRSTQL"

ORIGIN
Query Match 100.0%; Score 28; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 GAACAGCAATACAAACCGTTGTGTG 28
|||||
265 GAACAGCAATACAAACCGTTGTGTG 292
|||||

RESULT 30
HPJ34113 456 bp DNA linear VRL 08-MAR-1996
LOCUS
DEFINITION Human papillomavirus type 16, isolate OR 0198, early transforming
protein E6 (E6) gene, complete cds.
U34113
U34113.1 GI:1098731

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Human papillomavirus
Human papillomavirus
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
unclassified Papillomaviridae.
1 (bases 1 to 456)
Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildebrandt,A.
and Jenson,S.A.
Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the
E6, E2, and L1 coding segments
J. Virol. 69 (12), 7743-7753 (1995)
7494284

JOURNAL
PUBMED
2 (bases 1 to 456)
Farmer,A.D.
Direct Submission
Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National
Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
Alamos, NM 87501, USA
Location/Qualifiers

FEATURES
source

source
1..456
/organism="Human papillomavirus"
/mol_type="genomic DNA"
/isolate="OR 0198"
/db_xref="taxon:10566"
/note="collected by cervical lavage at Kaiser Permanente,
Portland, Oregon, United States."
1..456
/gene="E6"
1..456
/gene="E6"
/codon_start=1
/product="early transforming protein E6"
/protein_id="AA91660.1"
/db_xref="GI:1098732"
/translation="MFODQPERPRKLPDLCTELQTTIHDIIECYCKQQLRREYVD
FARDCIVRDGNPYAVCDKCLKFYSKISERYCYSLYGTTLBOQYNKPLCDLLIR
CINQKPLCEBKORHDKKQRFHNIRGRTGCMSCSKSRTRSTQL"

ORIGIN
Query Match 100.0%; Score 28; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 GAACAGCAATACAAACCGTTGTGTG 28
|||||
265 GAACAGCAATACAAACCGTTGTGTG 292
|||||

RESULT 31
HPJ34114 456 bp DNA linear VRL 08-MAR-1996
LOCUS
DEFINITION Human papillomavirus type 16, isolate OR 1905, early transforming
protein E6 (E6) gene, complete cds.
U34114
U34114.1 GI:1098733

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Human papillomavirus
Human papillomavirus
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
unclassified Papillomaviridae.
1 (bases 1 to 456)
Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildebrandt,A.
and Jenson,S.A.
Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the
E6, E2, and L1 coding segments
J. Virol. 69 (12), 7743-7753 (1995)
7494284

JOURNAL
PUBMED
2 (bases 1 to 456)
Farmer,A.D.
Direct Submission
Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National
Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
Alamos, NM 87501, USA
Location/Qualifiers

FEATURES
source
1..456
/organism="Human papillomavirus"
/mol_type="genomic DNA"
/isolate="OR 1905"
/db_xref="taxon:10566"
/note="collected by cervical lavage at Kaiser Permanente,
Portland, Oregon, United States."
1..456
/gene="E6"
1..456
/gene="E6"
/codon_start=1
/product="early transforming protein E6"
/protein_id="AA91661.1"
/db_xref="GI:1098734"
/translation="MFODQPERPRKLPDLCTELQTTIHDIIECYCKQQLRREYVD
FARDCIVRDGNPYAVCDKCLKFYSKISERYCYSLYGTTLBOQYNKPLCDLLIR

ORIGIN CINCQKPLCEBKORHLDKORFNHNGRWTGRCMSCRSSRTRETL"

Query Match 100.0%; Score 28; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACAGCAATACAAACCGTTGTG 28
|||||
Db 265 GAACAGCAATACAAACCGTTGTG 292

RESULT 32
HPU34115 456 bp DNA linear VRL 08-MAR-1996
LOCUS Human papillomavirus type 16, isolate OR 2087, early transforming
DEFINITION protein E6 (E6) gene, complete cds.
ACCESSION U34115
VERSION U34115.1 GI:1098735
KEYWORDS
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
Virusess; dsDNA viruses, no RNA stage; Papillomaviridae;
unclassified Papillomaviridae.
1 (bases 1 to 456)
REFERENCE Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildesheim,A.
AUTHORS and Jenison,S.A.
TITLE Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the
E6, I2, and I1 coding segments
J. Virol. 69 (12), 7743-7753 (1995)
7494284
2 (bases 1 to 456)
REFERENCE Farmer,A.D.
AUTHORS Direct Submission
TITLE Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National
JOURNAL Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
Alamos, NM 87501, USA
FEATURES
source Location/Qualifiers
1. 456
/organism="Human papillomavirus"
/mol_type="genomic DNA"
/isolate="OR 2087"
/db_xref="taxon:10566"
/note="collected by cervical lavage at Kaiser Permanente,
Portland, Oregon, United States."
1. 456
/gene="E6"
1. 456
/gene="E6"
1. 456
/gene="E6"
/codon_start=1
/product="early transforming protein E6"
/protein_id="AA91662.1"
/db_xref="GI:1098736"
/translation="MFQDPOBRPRKLPOLCTELQTTIHIIIECVCKQOOLRREYD
FAPRDLCTIVRDGNPVAVCCKLKFYSKISBYRYCYSGVGTTEQQYNRPCLDLRL
CINCQKPLCEBKORHLDKORFNHNGRWTGRCMSCRSSRTRETL"

ORIGIN

Query Match 100.0%; Score 28; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACAGCAATACAAACCGTTGTG 28
|||||
Db 265 GAACAGCAATACAAACCGTTGTG 292

RESULT 33
HPU34116 456 bp DNA linear VRL 08-MAR-1996
LOCUS Human papillomavirus type 16, isolate OR 3136, early transforming
DEFINITION protein E6 (E6) gene, complete cds.

ACCESSION U34116
VERSION U34116.1 GI:1098737
KEYWORDS
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
Virusess; dsDNA viruses, no RNA stage; Papillomaviridae;
unclassified Papillomaviridae.
1 (bases 1 to 456)
REFERENCE Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildesheim,A.
AUTHORS and Jenison,S.A.
TITLE Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the
E6, I2, and I1 coding segments
J. Virol. 69 (12), 7743-7753 (1995)
7494284
2 (bases 1 to 456)
REFERENCE Farmer,A.D.
AUTHORS Direct Submission
TITLE Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National
JOURNAL Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
Alamos, NM 87501, USA
FEATURES
source Location/Qualifiers
1. 456
/organism="Human papillomavirus"
/mol_type="genomic DNA"
/isolate="OR 3136"
/db_xref="taxon:10566"
/note="collected by cervical lavage at Kaiser Permanente,
Portland, Oregon, United States."
1. 456
/gene="E6"
1. 456
/gene="E6"
1. 456
/gene="E6"
/codon_start=1
/product="early transforming protein E6"
/protein_id="AA91663.1"
/db_xref="GI:1098738"
/translation="MFQDPOBRPRKLPOLCTELQTTIHIIIECVCKQOOLRREYD
FAPRDLCTIVRDGNPVAVCCKLKFYSKISBYRYCYSGVGTTEQQYNRPCLDLRL
CINCQKPLCEBKORHLDKORFNHNGRWTGRCMSCRSSRTRETL"

ORIGIN

Query Match 100.0%; Score 28; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACAGCAATACAAACCGTTGTG 28
|||||
Db 265 GAACAGCAATACAAACCGTTGTG 292

RESULT 34
HPU34117 456 bp DNA linear VRL 08-MAR-1996
LOCUS Human papillomavirus type 16, isolate OR 3473, early transforming
DEFINITION protein E6 (E6) gene, complete cds.
ACCESSION U34117
VERSION U34117.1 GI:1098739
KEYWORDS
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
Virusess; dsDNA viruses, no RNA stage; Papillomaviridae;
unclassified Papillomaviridae.
1 (bases 1 to 456)
REFERENCE Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildesheim,A.
AUTHORS and Jenison,S.A.
TITLE Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the
E6, I2, and I1 coding segments
J. Virol. 69 (12), 7743-7753 (1995)
7494284
2 (bases 1 to 456)
REFERENCE Farmer,A.D.

RESULT 37
HPU34120 456 bp DNA linear VRL 08-MAR-1996
LOCUS Human papillomavirus type 16, isolate OR 4716, early transforming
DEFINITION protein E6 (E6) gene, complete cds.
ACCESSION U34120
VERSION U34120.1 GI:1098745
KEYWORDS
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
REFERENCE
AUTHORS Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildesheim,A.
and Jenison,S.A.
TITLE Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the
E6, I2, and L1 coding segments
JOURNAL J. Virol. 69 (12), 7743-7753 (1995)
PUBMED 7494284
REFERENCE 2 (bases 1 to 456)
AUTHORS Farmer,A.D.
TITLE Direct Submission
JOURNAL Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National
Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
Alamos, NM 87501, USA
FEATURES
source
1. 456
/organism="Human papillomavirus"
/mol_type="genomic DNA"
/isolate="OR 4716"
/db_xref="taxon:10566"
/note="collected by cervical lavage at Kaiser Permanente,
Portland, Oregon, United States."
1. 456
/gene="E6"
1. 456
/codon_start=1
/product="early transforming protein E6"
/protein_id="AA91667.1"
/db_xref="GI:1098746"
/translation="MPQDQPERPKLPOLCTELQTHIIEICVCKQQLRREYD
FARPLDCTIVRDGNPVAVCDKCLKFKYSIRYKCYSLVCTTEQQYNKPLCDLLR
CINQKPLCEBKORHLDKORFHNIRMTGRCMSCRSRTRETL"

ORIGIN
Query Match 100.0%; Score 28; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAACGACATACACAAACCGTTGTG 28
|||||
Db 265 GAACGACATACACAAACCGTTGTG 292
|||||

RESULT 38
HPU34121 456 bp DNA linear VRL 08-MAR-1996
LOCUS Human papillomavirus type 16, isolate OR 4724, early transforming
DEFINITION protein E6 (E6) gene, complete cds.
ACCESSION U34121
VERSION U34121.1 GI:1098747
KEYWORDS
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
REFERENCE
AUTHORS Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildesheim,A.
and Jenison,S.A.
TITLE Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the

JOURNAL
PUBMED 7494284
REFERENCE 2 (bases 1 to 456)
AUTHORS Farmer,A.D.
TITLE Direct Submission
JOURNAL Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National
Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
Alamos, NM 87501, USA
FEATURES
source
1. 456
/organism="Human papillomavirus"
/mol_type="genomic DNA"
/isolate="OR 4724"
/db_xref="taxon:10566"
/note="collected by cervical lavage at Kaiser Permanente,
Portland, Oregon, United States."
1. 456
/gene="E6"
1. 456
/codon_start=1
/product="early transforming protein E6"
/protein_id="AA91668.1"
/db_xref="GI:1098748"
/translation="MPQDQPERPKLPOLCTELQTHIIEICVCKQQLRREYD
FARPLDCTIVRDGNPVAVCDKCLKFKYSIRYKCYSLVCTTEQQYNKPLCDLLR
CINQKPLCEBKORHLDKORFHNIRMTGRCMSCRSRTRETL"

ORIGIN
Query Match 100.0%; Score 28; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAACGACATACACAAACCGTTGTG 28
|||||
Db 265 GAACGACATACACAAACCGTTGTG 292
|||||

RESULT 39
HPU34122 456 bp DNA linear VRL 08-MAR-1996
LOCUS Human papillomavirus type 16, isolate OR 4997, early transforming
DEFINITION protein E6 (E6) gene, complete cds.
ACCESSION U34122
VERSION U34122.1 GI:1098749
KEYWORDS
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
REFERENCE
AUTHORS Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildesheim,A.
and Jenison,S.A.
TITLE Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the
E6, I2, and L1 coding segments
JOURNAL J. Virol. 69 (12), 7743-7753 (1995)
PUBMED 7494284
REFERENCE 2 (bases 1 to 456)
AUTHORS Farmer,A.D.
TITLE Direct Submission
JOURNAL Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National
Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
Alamos, NM 87501, USA
FEATURES
source
1. 456
/organism="Human papillomavirus"
/mol_type="genomic DNA"
/isolate="OR 4997"
/db_xref="taxon:10566"
/note="collected by cervical lavage at Kaiser Permanente,
Portland, Oregon, United States."

gene 1. .456
/gene="B6"
CDS 1. .456
/gene="B6"
/codon_start=1
/product="early transforming protein B6"
/protein_id="AA91669.1"
/db_xref="GI:1098750"
/translation="MFQDQPERPRKLPLCTELQTTIHILIECVCKOQLRREYVD
FARDCIVYRDGNPFAVCDKCLKFYSKISRYHGYSLYGTLLBQYINPPLCDLLIR
CINCKPLCEBKHRLDKKORFHNIKRWGTGCMSCCRSRTRETOL"

ORIGIN

Query Match 100.0%; Score 28; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACAGCAATACAAACCGTTGTGTG 28
|||||
265 GAACAGCAATACAAACCGTTGTGTG 292

Db

RESULT 40
HPJ34123 456 bp DNA linear VRL 08-MAR-1996
LOCUS Human papillomavirus type 16, isolate OR 5110, early transforming
DEFINITION protein B6 (B6) gene, complete cds.
ACCESSION U34123
KEYWORDS U34123.1 GI:1098751
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
unclassified Papillomaviridae.
REFERENCE 1 (bases 1 to 456)
Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildesheim,A.
and Jenison,S.A.
Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the
E6, E2, and L1 coding segments
J. Virol. 69 (12), 7743-7753 (1995)
7494284
2 (bases 1 to 456)
Farmer,A.D.
Direct Submission
Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National
Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
Alamos, NM 87501, USA
Location/Qualifiers
1. .456
/organism="Human papillomavirus"
/mol_type="genomic DNA"
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Portland, Oregon, United States."
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/translation="MFQDQPERPRKLPLCTELQTTIHILIECVCKOQLRREYVD
FARDCIVYRDGNPFAVCDKCLKFYSKISRYHGYSLYGTLLBQYINPPLCDLLIR
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ORIGIN

Query Match 100.0%; Score 28; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACAGCAATACAAACCGTTGTGTG 28
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265 GAACAGCAATACAAACCGTTGTGTG 292

Db

RESULT 41
HPJ34124 456 bp DNA linear VRL 08-MAR-1996
LOCUS Human papillomavirus type 16, isolate OR 5428, early transforming
DEFINITION protein B6 (B6) gene, complete cds.
ACCESSION U34124
KEYWORDS U34124.1 GI:1098753
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
unclassified Papillomaviridae.
REFERENCE 1 (bases 1 to 456)
Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildesheim,A.
and Jenison,S.A.
Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the
E6, E2, and L1 coding segments
J. Virol. 69 (12), 7743-7753 (1995)
7494284
2 (bases 1 to 456)
Farmer,A.D.
Direct Submission
Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National
Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
Alamos, NM 87501, USA
Location/Qualifiers
1. .456
/organism="Human papillomavirus"
/mol_type="genomic DNA"
/isolate="OR 5428"
/db_xref="taxon:10566"
/note="collected by cervical lavage at Kaiser Permanente,
Portland, Oregon, United States."
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/protein_id="AA91671.1"
/db_xref="GI:1098754"
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CINCKPLCEBKHRLDKKORFHNIKRWGTGCMSCCRSRTRETOL"

ORIGIN

Query Match 100.0%; Score 28; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACAGCAATACAAACCGTTGTGTG 28
|||||
265 GAACAGCAATACAAACCGTTGTGTG 292

Db

RESULT 42
HPJ34125 456 bp DNA linear VRL 08-MAR-1996
LOCUS Human papillomavirus type 16, isolate OR 6106, early transforming
DEFINITION protein B6 (B6) gene, complete cds.
ACCESSION U34125
KEYWORDS U34125.1 GI:1098755
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
unclassified Papillomaviridae.

REFERENCE 1 (bases 1 to 456)
AUTHORS Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildesheim,A.
and Jenison,S.A.
TITLE Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the
E6, I2, and L1 coding segments
JOURNAL J. Virol. 69 (12), 7743-7753 (1995)
PUBMED 7494284
REFERENCE 2 (bases 1 to 456)
AUTHORS Farmer,A.D.
TITLE Direct Submission
JOURNAL Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National
Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
Alamos, NM 87501, USA
FEATURES
SOURCE Location/Qualifiers
1..456
/organism="Human papillomavirus"
/mol_type="genomic DNA"
/isolate="OR 6170"
/db_xref="taxon:10566"
/note="collected by cervical lavage at Kaiser Permanente,
Portland, Oregon, United States."
gene 1..456
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/product="early transforming protein E6"
/protein_id="AA91672.1"
/db_xref="GI:1098756"
/translation="MFQDPERPRKLPDLCTELQTTIHDIILECVYCKQQLRREYD
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CINQKPLCEBKORHLDKORFHNIRGRTGRCMSCRSSRRTRRQTL"
ORIGIN
Query Match 100.0%; Score 28; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAACAGCAATACAAACCGTGTGTG 28
|||||
Db 265 GAACAGCAATACAAACCGTGTGTG 292
RESULT 43
HPJ34126 456 bp DNA linear VRL 08-MAR-1996
LOCUS Human papillomavirus type 16, isolate OR 6170, early transforming
DEFINITION protein E6 (E6) gene, complete cds.
ACCESSION U34126
VERSION U34126.1 GI:1098757
KEYWORDS Human papillomavirus
SOURCE Human papillomavirus
ORGANISM Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
unclassified Papillomaviridae.
REFERENCE 1 (bases 1 to 456)
AUTHORS Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildesheim,A.
and Jenison,S.A.
TITLE Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the
E6, I2, and L1 coding segments
JOURNAL J. Virol. 69 (12), 7743-7753 (1995)
PUBMED 7494284
REFERENCE 2 (bases 1 to 456)
AUTHORS Farmer,A.D.
TITLE Direct Submission
JOURNAL Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National
Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
Alamos, NM 87501, USA
FEATURES
SOURCE Location/Qualifiers
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/isolate="OR 6170"
/db_xref="taxon:10566"
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Portland, Oregon, United States."
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/codon_start=1
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/protein_id="AA91674.1"
/db_xref="GI:1098760"
/translation="MFQDPERPRKLPDLCTELQTTIHDIILECVYCKQQLRREYD
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ORIGIN
Query Match 100.0%; Score 28; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAACAGCAATACAAACCGTGTGTG 28
|||||
Db 265 GAACAGCAATACAAACCGTGTGTG 292
RESULT 44
HPJ34127 456 bp DNA linear VRL 08-MAR-1996
LOCUS Human papillomavirus type 16, isolate OR 6311, early transforming
DEFINITION protein E6 (E6) gene, complete cds.
ACCESSION U34127
VERSION U34127.1 GI:1098759
KEYWORDS Human papillomavirus
SOURCE Human papillomavirus
ORGANISM Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
unclassified Papillomaviridae.
REFERENCE 1 (bases 1 to 456)
AUTHORS Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildesheim,A.
and Jenison,S.A.
TITLE Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the
E6, I2, and L1 coding segments
JOURNAL J. Virol. 69 (12), 7743-7753 (1995)
PUBMED 7494284
REFERENCE 2 (bases 1 to 456)
AUTHORS Farmer,A.D.
TITLE Direct Submission
JOURNAL Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National
Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
Alamos, NM 87501, USA
FEATURES
SOURCE Location/Qualifiers
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/organism="Human papillomavirus"
/mol_type="genomic DNA"
/isolate="OR 6311"
/db_xref="taxon:10566"
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Portland, Oregon, United States."
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/gene="E6"
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/codon_start=1
/product="early transforming protein E6"
/protein_id="AA91674.1"
/db_xref="GI:1098760"
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CINQKPLCEBKORHLDKORFHNIRGRTGRCMSCRSSRRTRRQTL"
ORIGIN

REFERENCE 1 (bases 1 to 456)
AUTHORS Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildesheim,A.
and Jenison,S.A.
TITLE Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the
E6, I2, and L1 coding segments
JOURNAL J. Virol. 69 (12), 7743-7753 (1995)
PUBMED 7494284
REFERENCE 2 (bases 1 to 456)
AUTHORS Farmer,A.D.
TITLE Direct Submission
JOURNAL Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National
Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
Alamos, NM 87501, USA
FEATURES
SOURCE Location/Qualifiers
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/mol_type="genomic DNA"
/isolate="OR 6170"
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Portland, Oregon, United States."
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ORIGIN
Query Match 100.0%; Score 28; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAACAGCAATACAAACCGTGTGTG 28
|||||
Db 265 GAACAGCAATACAAACCGTGTGTG 292
RESULT 44
HPJ34127 456 bp DNA linear VRL 08-MAR-1996
LOCUS Human papillomavirus type 16, isolate OR 6311, early transforming
DEFINITION protein E6 (E6) gene, complete cds.
ACCESSION U34127
VERSION U34127.1 GI:1098759
KEYWORDS Human papillomavirus
SOURCE Human papillomavirus
ORGANISM Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
unclassified Papillomaviridae.
REFERENCE 1 (bases 1 to 456)
AUTHORS Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildesheim,A.
and Jenison,S.A.
TITLE Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the
E6, I2, and L1 coding segments
JOURNAL J. Virol. 69 (12), 7743-7753 (1995)
PUBMED 7494284
REFERENCE 2 (bases 1 to 456)
AUTHORS Farmer,A.D.
TITLE Direct Submission
JOURNAL Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National
Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
Alamos, NM 87501, USA
FEATURES
SOURCE Location/Qualifiers
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/mol_type="genomic DNA"
/isolate="OR 6311"
/db_xref="taxon:10566"
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Portland, Oregon, United States."
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1..456
/codon_start=1
/product="early transforming protein E6"
/protein_id="AA91674.1"
/db_xref="GI:1098760"
/translation="MFQDPERPRKLPDLCTELQTTIHDIILECVYCKQQLRREYD
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CINQKPLCEBKORHLDKORFHNIRGRTGRCMSCRSSRRTRRQTL"
ORIGIN

Query Match 100.0%; Score 28; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACAGCAATACAAACCGTTGTGTG 28
Db 265 GAACAGCAATACAAACCGTTGTGTG 292

RESULT 45
HPU34128 456 bp DNA linear VRL 08-MAR-1996
LOCUS Human papillomavirus type 16, isolate OR 7145, early transforming
DEFINITION protein E6 (E6) gene, complete cds.
ACCESSION U34128.1 GI:1098761
KEYWORDS Human papillomavirus
SOURCE Human papillomavirus
ORGANISM unclassified Papillomaviridae;
REFERENCE 1 (bases 1 to 456)
AUTHORS Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildesheim,A.
and Jenison,S.A.
TITLE Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the
E6, L2, and L1 coding segments
J. Virol. 69 (12), 7743-7753 (1995)
7494284
2 (bases 1 to 456)
PUBMED Farmer,A.D.
REFERENCE Direct Submission
AUTHORS Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National
JOURNAL Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
Alamos, NM 87501, USA
LOCATION/Qualifiers
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Portland, Oregon, United States."
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FAFRDLCIVRDGNPYAVCDCKLFYSKSEYRYCYSLYGTLEQYNNPLCDLLIR
CINQKRLCPBEKQRHLDKKQRFHNIRGWTGRCMSCRSSRTRRETQL"

ORIGIN
Query Match 100.0%; Score 28; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACAGCAATACAAACCGTTGTGTG 28
Db 265 GAACAGCAATACAAACCGTTGTGTG 292

RESULT 46
HPU34129 456 bp DNA linear VRL 08-MAR-1996
LOCUS Human papillomavirus type 16, isolate OR 7574, early transforming
DEFINITION protein E6 (E6) gene, complete cds.
ACCESSION U34129.1 GI:1098763

KEYWORDS
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
unclassified Papillomaviridae;
REFERENCE 1 (bases 1 to 456)
AUTHORS Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildesheim,A.
and Jenison,S.A.
TITLE Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the
E6, L2, and L1 coding segments
J. Virol. 69 (12), 7743-7753 (1995)
7494284
2 (bases 1 to 456)
PUBMED Farmer,A.D.
REFERENCE Direct Submission
AUTHORS Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National
JOURNAL Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
Alamos, NM 87501, USA
LOCATION/Qualifiers
FEATURES
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Portland, Oregon, United States."
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/db_xref="GI:1098764"
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FAFRDLCIVRDGNPYAVCDCKLFYSKSEYRYCYSLYGTLEQYNNPLCDLLIR
CINQKRLCPBEKQRHLDKKQRFHNIRGWTGRCMSCRSSRTRRETQL"

ORIGIN
Query Match 100.0%; Score 28; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACAGCAATACAAACCGTTGTGTG 28
Db 265 GAACAGCAATACAAACCGTTGTGTG 292

RESULT 47
HPU34130 456 bp DNA linear VRL 08-MAR-1996
LOCUS Human papillomavirus type 16, isolate OR 7587, early transforming
DEFINITION protein E6 (E6) gene, complete cds.
ACCESSION U34130.1 GI:1098765
KEYWORDS Human papillomavirus
SOURCE Human papillomavirus
ORGANISM unclassified Papillomaviridae;
REFERENCE 1 (bases 1 to 456)
AUTHORS Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildesheim,A.
and Jenison,S.A.
TITLE Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the
E6, L2, and L1 coding segments
J. Virol. 69 (12), 7743-7753 (1995)
7494284
2 (bases 1 to 456)
PUBMED Farmer,A.D.
REFERENCE Direct Submission
AUTHORS Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National
JOURNAL Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
Alamos, NM 87501, USA
LOCATION/Qualifiers

FEATURES
source
Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los Alamos, NM 87501, USA
location/Qualifiers
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/db_xref="taxon:10566"
/note="collected by cervical lavage at Kaiser Permanente, Portland, Oregon, United States."
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/translation="MFQDPERPKLPDLCTELQTTIHDIILECVYKQOLLREYD FAPRDLCTIVRDGNPYAVCDKFKYSKISEYRYCVSLGTTLEQYNNPDLCLLR CINQKRLCEBERQRLDKQRPHNIRGRWTGRCMSCRSSRTRERQL"

ORIGIN
Query Match 100.0%; Score 28; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACAGCAATACAAACCGTTGTG 28
|||||
265 GAACAGCAATACAAACCGTTGTG 292

RESULT 48
HPU34131 456 bp DNA linear VRL 08-MAR-1996
LOCUS Human papillomavirus type 16, isolate OR 7632, early transforming
DEFINITION protein E6 (E6) gene, complete cds.
VERSION U34131.1 GI:1098767
KEYWORDS Human papillomavirus
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
unclassified Papillomaviridae;
REFERENCE 1 (bases 1 to 456)
Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildesheim,A. and Jensen,S.A.
Human papillomavirus type 16 variant lineages in United States populations characterized by nucleotide sequence analysis of the E6, E2, and L1 coding segments
J. Virol. 69 (12), 7743-7753 (1995)
7494284
2 (bases 1 to 456)
Farmer,A.D.
Direct Submission
Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los Alamos, NM 87501, USA
location/Qualifiers
1..456
/organism="Human papillomavirus"
/mol_type="genomic DNA"
/isolate="OR 7632"
/db_xref="taxon:10566"
/note="collected by cervical lavage at Kaiser Permanente, Portland, Oregon, United States."
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/gene="E6"
/codon_start=1
/product="early transforming protein E6"
/protein_id="AA91678.1"

gene
CDS

/db_xref="GI:1098768"
/translation="MFQDPERPKLPDLCTELQTTIHDIILECVYKQOLLREYD FAPRDLCTIVRDGNPYAVCDKFKYSKISEYRYCVSLGTTLEQYNNPDLCLLR CINQKRLCEBERQRLDKQRPHNIRGRWTGRCMSCRSSRTRERQL"

ORIGIN
Query Match 100.0%; Score 28; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACAGCAATACAAACCGTTGTG 28
|||||
265 GAACAGCAATACAAACCGTTGTG 292

RESULT 49
HPU34132 456 bp DNA linear VRL 08-MAR-1996
LOCUS Human papillomavirus type 16, isolate OR 8160, early transforming
DEFINITION protein E6 (E6) gene, complete cds.
VERSION U34132.1 GI:1098769
KEYWORDS Human papillomavirus
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
unclassified Papillomaviridae;
REFERENCE 1 (bases 1 to 456)
Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildesheim,A. and Jensen,S.A.
Human papillomavirus type 16 variant lineages in United States populations characterized by nucleotide sequence analysis of the E6, E2, and L1 coding segments
J. Virol. 69 (12), 7743-7753 (1995)
7494284
2 (bases 1 to 456)
Farmer,A.D.
Direct Submission
Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los Alamos, NM 87501, USA
location/Qualifiers
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/db_xref="taxon:10566"
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1..456
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ORIGIN
Query Match 100.0%; Score 28; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACAGCAATACAAACCGTTGTG 28
|||||
265 GAACAGCAATACAAACCGTTGTG 292

RESULT 50
HPU34133

LOCUS HP034133 456 bp DNA linear VRL 08-MAR-1996
 DEFINITION Human papillomavirus type 16, isolate OR 8329, early transforming
 protein E6 (E6) gene, complete cds.
 ACCESSION U34133
 VERSION U34133.1 GI:1098771
 KEYWORDS
 SOURCE Human papillomavirus
 ORGANISM Human papillomavirus
 Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 unclassified Papillomaviridae.
 REFERENCE 1 (bases 1 to 456)
 AUTHORS Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildesheim,A.
 and Jenison,S.A.
 TITLE Human papillomavirus type 16 variant lineages in United States
 populations characterized by nucleotide sequence analysis of the
 E6, L2, and L1 coding segments
 JOURNAL J. Virol. 69 (12), 7743-7753 (1995)
 PUBMED 7494284
 REFERENCE 2 (bases 1 to 456)
 AUTHORS Farmer,A.D.
 TITLE Direct Submission
 JOURNAL Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National
 Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
 Alamos, NM 87501, USA
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 /organism="Human papillomavirus"
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 /db_xref="taxon:10566"
 /note="collected by cervical lavage at Kaiser Permanente,
 Portland, Oregon, United States."
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 CINQKPLCPBEKQRLDKKQRFHNRGWTGRQWMSCCRSSRTREITOL"
 ORIGIN
 Query Match 100.0%; Score 28; DB 10; Length 456;
 Best Local Similarity 100.0%; Pred. No. 0.0025;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GAACAGCAATACAAACCGTTGTGTG 28
 DB 265 GAACAGCAATACAAACCGTTGTGTG 292

Search completed: May 24, 2006, 06:53:50
 Job time : 915.046 secs

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2006, 05:46:37 ; Search time 638.284 Seconds
(without alignments)
2103.915 Million cell updates/sec

Title: US-10-601-913-85

Perfect score: 21
Sequence: 1 CAGGACACAGTGGCTTTGAC 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 1000 summaries

Database :

GenEmbl: *
1: gb_env: *
2: gb_pat: *
3: gb_ph: *
4: gb_pl: *
5: gb_pr: *
6: gb_ro: *
7: gb_atc: *
8: gb_ey: *
9: gb_un: *
10: gb_vl: *
11: gb_ov: *
12: gb_hcg: *
13: gb_in: *
14: gb_cm: *
15: gb_da: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	21	100.0	21	2	AR349146 Sequence
3	21	100.0	21	2	AR349147 Sequence
4	21	100.0	21	2	AR349148 Sequence
5	21	100.0	104	2	DD187316 SPICRISO
6	21	100.0	138	2	DD187319 SPICRISO
7	21	100.0	170	10	HPUS9980 Human papil
8	21	100.0	245	10	HPUS9980 Human papil
9	21	100.0	253	10	HPU14515 Human papil
10	21	100.0	271	10	HPU14512 Human papil
11	21	100.0	272	10	HPU14513 Human papil
12	21	100.0	273	10	HPU14514 Human papil
13	21	100.0	274	10	HPU14516 Human papil
14	21	100.0	298	10	AF404704 Human pap
15	21	100.0	370	10	AF404692 Human pap
16	21	100.0	421	10	SS1110 Orf B6 (hum
17	21	100.0	451	10	AF404695 Human pap
18	21	100.0	451	10	AF404696 Human pap

19	21	100.0	451	10	AF404699 Human pap
20	21	100.0	451	10	AF404700 Human pap
21	21	100.0	451	10	AF404701 Human pap
22	21	100.0	451	10	AF404703 Human pap
23	21	100.0	456	2	AR167393 Sequence
24	21	100.0	456	2	AR177943 Sequence
25	21	100.0	456	10	AF327851 Human pap
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65	21	100.0	473	10	AF404694 Human pap
66	21	100.0	477	2	CS113240 Sequence
67	21	100.0	477	2	AR577459 Sequence
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C 94	21	100.0	477	10	AF486324	Human pap	C 167	21	100.0	1267	10	HPA388065	AJ388065	Human pap
C 95	21	100.0	477	10	AF486325	Human pap	C 168	21	100.0	1267	10	HPA388066	AJ388066	Human pap
C 96	21	100.0	477	10	DQ323982	Human pap	C 169	21	100.0	1267	10	HPA388067	AJ388067	Human pap
C 97	21	100.0	482	10	AF404658	Human pap	C 170	21	100.0	1267	10	HPA388068	AJ388068	Human pap
C 98	21	100.0	488	10	AF404702	Human pap	C 171	21	100.0	3531	2	HPA388069	AJ388069	Human pap
C 99	21	100.0	519	2	AR095319	Sequence	C 172	21	100.0	7902	2	AF001599	AF001599	Sequence
C 100	21	100.0	519	2	AR173472	Sequence	C 173	21	100.0	7904	2	AX800450	AX800450	Sequence
C 101	21	100.0	540	2	AF404705	Human pap	C 174	21	100.0	7904	2	BD070940	BD070940	Sequence
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C 104	21	100.0	543	10	AF404706	Human pap	C 177	21	100.0	7904	2	CS195904	CS195904	Sequence
C 105	21	100.0	570	10	AY112663	Human pap	C 178	21	100.0	7904	2	I70142	I70142	Sequence
C 106	21	100.0	592	10	AY098923	Human pap	C 179	21	100.0	7904	2	I70143	I70143	Sequence
C 107	21	100.0	596	10	AY098919	Human pap	C 180	21	100.0	7904	2	I72345	I72345	Sequence
C 108	21	100.0	598	2	CO410317	Sequence	C 181	21	100.0	7904	2	AX763489	AX763489	Sequence
C 109	21	100.0	600	10	AY098922	Human pap	C 182	21	100.0	7904	10	AF125673	AF125673	Human pap
C 110	21	100.0	601	10	AY098918	Human pap	C 183	21	100.0	7904	10	AF472509	AF472509	Human pap
C 111	21	100.0	602	10	AY112662	Human pap	C 184	21	100.0	7904	10	AF536179	AF536179	Human pap
C 112	21	100.0	654	10	AF548023	Human pap	C 185	21	100.0	7905	10	PPH16	PPH16	Human pap
C 113	21	100.0	693	10	AF469198	Human pap	C 186	21	100.0	7905	10	AF534061	AF534061	Human pap
C 114	21	100.0	741	10	AF469197	Human pap	C 187	21	100.0	7906	10	HPH89348	HPH89348	Human pap
C 115	21	100.0	743	2	CO414264	Sequence	C 188	21	100.0	7906	10	AF536180	AF536180	Human pap
C 116	21	100.0	745	2	AX188300	Sequence	C 189	21	100.0	7906	10	AF686579	AF686579	Human pap
C 117	21	100.0	755	10	AY089951	Human pap	C 190	21	100.0	7906	10	AF686580	AF686580	Human pap
C 118	21	100.0	755	10	AY089952	Human pap	C 191	21	100.0	7906	10	AF686581	AF686581	Human pap
C 119	21	100.0	755	10	AY089953	Human pap	C 192	21	100.0	7906	10	AF686584	AF686584	Human pap
C 120	21	100.0	755	10	AY089954	Human pap	C 193	21	100.0	7907	10	AY686582	AY686582	Human pap
C 121	21	100.0	755	10	AY089955	Human pap	C 194	21	100.0	7907	10	AY686583	AY686583	Human pap
C 122	21	100.0	776	2	I19491	Sequence	C 195	21	100.0	7908	10	AF472508	AF472508	Human pap
C 123	21	100.0	779	2	AR199235	Sequence	C 196	21	95.2	20	2	A21235	A21235	Sequence
C 124	21	100.0	780	10	AF187867	Human pap	C 197	21	95.2	20	2	BD236838	BD236838	Sequence
C 125	21	100.0	780	10	AF187868	Human pap	C 198	21	95.2	20	2	CO814785	CO814785	Sequence
C 126	21	100.0	780	10	AF187868	Human pap	C 199	21	95.2	20	2	AR267070	AR267070	Sequence
C 127	21	100.0	780	10	AF187869	Human pap	C 200	21	95.2	20	2	AR652060	AR652060	Sequence
C 128	21	100.0	790	2	I88813	Sequence	C 201	21	95.2	20	2	AX030354	AX030354	Sequence
C 129	21	100.0	801	2	AR095318	Sequence	C 202	21	95.2	20	2	AX379361	AX379361	Sequence
C 130	21	100.0	801	2	AR173471	Sequence	C 203	21	95.2	21	2	DD178908	DD178908	METHOD
C 131	21	100.0	822	2	A98742	Sequence	C 204	21	95.2	21	2	AX802808	AX802808	Sequence
C 132	21	100.0	822	2	BD080312	Vaccine.	C 205	21	92.4	477	10	AF486319	AF486319	Human pap
C 133	21	100.0	822	2	BD103161	Vaccine.	C 206	21	90.5	20	2	E05240	E05240	Part of DNA
C 134	21	100.0	822	2	AR183573	Sequence	C 207	21	90.5	20	2	AX805231	AX805231	Sequence
C 135	21	100.0	822	2	AX020926	Sequence	C 208	21	90.5	29	2	AR142033	AR142033	Sequence
C 136	21	100.0	879	2	A98748	Sequence	C 209	21	90.5	29	2	I59900	I59900	Sequence
C 137	21	100.0	879	2	BD080315	Vaccine.	C 210	21	90.5	29	2	I86758	I86758	Sequence
C 138	21	100.0	879	2	BD103164	Vaccine.	C 211	21	90.5	29	2	I95783	I95783	Sequence
C 139	21	100.0	879	2	AR183576	Sequence	C 212	21	90.5	29	2	AR708762	AR708762	Sequence
C 140	21	100.0	879	2	AX020932	Sequence	C 213	21	90.5	194799	5	AC006430	AC006430	Homo sapi
C 141	21	100.0	921	10	HPA388069	Human pap	C 214	21	87.6	89	2	DD187320	DD187320	SPLICHOSE
C 142	21	100.0	939	2	AX403959	Sequence	C 215	21	799	5	AY650345	AY650345	Maccaca fa	
C 143	21	100.0	999	2	AX460903	Sequence	C 216	21	1596	2	CO731442	CO731442	Sequence	
C 144	21	100.0	1000	2	A076522	Amplified 8	C 217	21	87.6	2317	2	CO719194	CO719194	Sequence
C 145	21	100.0	1000	2	I18920	Sequence	C 218	21	87.6	2317	2	CO824165	CO824165	Sequence
C 146	21	100.0	1116	2	A98744	Sequence	C 219	21	87.6	2545	5	HDWCABA	HDWCABA	Sequence
C 147	21	100.0	1116	2	BD080313	Vaccine.	C 220	21	87.6	2550	2	I34431	I34431	Homo sapien
C 148	21	100.0	1116	2	BD103162	Vaccine.	C 221	21	87.6	2550	2	I46829	I46829	Sequence
C 149	21	100.0	1116	2	AR183574	Sequence	C 222	21	87.6	2550	2	I55098	I55098	Sequence
C 150	21	100.0	1116	2	AX020928	Sequence	C 223	21	87.6	2742	2	CS162382	CS162382	Sequence
C 151	21	100.0	1154	10	PPH16E	Sequence	C 224	21	87.6	2742	5	AB035305	AB035305	Homo sapi
C 152	21	100.0	1173	2	A98752	Sequence	C 225	21	87.6	2812	6	MMCCAD8	MMCCAD8	Homo sapi
C 153	21	100.0	1173	2	BD080317	Vaccine.	C 226	21	87.6	2929	6	AX933856	AX933856	Sequence
C 154	21	100.0	1173	2	BD103166	Vaccine.	C 227	21	87.6	3126	6	AB010436	AB010436	Rattus ra
C 155	21	100.0	1173	2	AR183578	Sequence	C 228	21	87.6	3136	2	I34425	I34425	Sequence
C 156	21	100.0	1173	2	AX020936	Sequence	C 229	21	87.6	3136	2	I55092	I55092	Sequence
C 157	21	100.0	1267	10	HPA242681	Human pap	C 230	21	87.6	3502	5	AK124734	AK124734	Homo sapi
C 158	21	100.0	1267	10	HPA388056	Human pap	C 231	21	87.6	3552	6	BC057581	BC057581	Mus muscu
C 159	21	100.0	1267	10	HPA388057	Human pap	C 232	21	87.6	4334	6	BC060200	BC060200	Mus muscu
C 160	21	100.0	1267	10	HPA388058	Human pap	C 233	21	87.6	138810	6	AC103397	AC103397	Mus muscu
C 161	21	100.0	1267	10	HPA388059	Human pap	C 234	21	87.6	171239	12	AC010652	AC010652	Homo sapi
C 162	21	100.0	1267	10	HPA388060	Human pap	C 235	21	87.6	173905	5	AC092125	AC092125	Homo sapi
C 163	21	100.0	1267	10	HPA388061	Human pap	C 236	21	87.6	177751	12	AC016844	AC016844	Homo sapi
C 164	21	100.0	1267	10	HPA388062	Human pap	C 237	21	87.6	190333	5	AC092129	AC092129	Homo sapi

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388	16.8	80.0	780	13	ALJ632071	Suberites	AC096845	Takifugu
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451	16.8	80.0	110000	15	CR522870_24	Continuatio	BS000226	Pan trogl
452	16.8	80.0	110000	15	AB015928_52	Continuatio	BS000226	Pan trogl
453	16.8	80.0	110000	15	BA000040_36	Continuatio	BS000226	Pan trogl
454	16.8	80.0	110746	12	CT027659	Danio rer	BS000226	Pan trogl
455	16.8	80.0	114670	11	BX363530	Zebrafish	BS000226	Pan trogl
456	16.8	80.0	120376	11	CR381573	Zebrafish	BS000226	Pan trogl


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c 968 16.2 77.1 76228 12 AC016338
c 969 16.2 77.1 76540 5 AC003678
c 970 16.2 77.1 77313 5 AC110757
c 971 16.2 77.1 77573 5 AY572796
c 972 16.2 77.1 79594 5 AL138805
c 973 16.2 77.1 81542 5 AC100830
c 974 16.2 77.1 82010 5 BS000122
c 975 16.2 77.1 82514 5 AC004137
c 976 16.2 77.1 86480 5 CR759904
c 977 16.2 77.1 86480 5 CR759868
c 978 16.2 77.1 86576 5 AL929403
c 979 16.2 77.1 87364 12 AC138702
c 980 16.2 77.1 88484 5 AL335794
c 981 16.2 77.1 89177 5 AC136000
c 982 16.2 77.1 89214 5 AC093009
c 983 16.2 77.1 92134 12 AC018406
c 984 16.2 77.1 92487 6 BX511247
c 985 16.2 77.1 92644 12 AF186995
c 986 16.2 77.1 93292 5 CR759829
c 987 16.2 77.1 93732 12 AC136444
c 988 16.2 77.1 95930 5 AC106033
c 989 16.2 77.1 96037 12 AC171163
c 990 16.2 77.1 96120 5 AC093669
c 991 16.2 77.1 96798 5 AL356420
c 992 16.2 77.1 96877 12 AC017776
c 993 16.2 77.1 97466 5 BX005422
c 994 16.2 77.1 98835 5 AC073195
c 995 16.2 77.1 99088 5 AC093401
c 996 16.2 77.1 100000 5 AP000092
c 997 16.2 77.1 100000 5 AP000153
c 998 16.2 77.1 100000 5 AP000196
c 999 16.2 77.1 100293 5 AP006259
1000 16.2 77.1 100316 5 AC004556
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ALIGNMENTS

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RESULT 1
AR349145 21 bp DNA linear PAT 17-AUG-2003
LOCUS AR349145 Sequence 85 from patent US 6583278.
ACCESSION AR349145
VERSION AR349145.1 GI:33749850
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Carter,N.M.
TITLE Nucleic acid probes complementary to human papilloma virus nucleic
JOURNAL Patent: US 6583278-A 85 24-JUN-2003;
FEATURES Gen-Probe Incorporated; San Diego, CA
SOURCE Location/Qualifiers
source 1..21
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 21; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGACACAGTGCGCTTTTGAC 21
Db 1 CAGGACACAGTGCGCTTTTGAC 21

RESULT 2
AR349146 21 bp DNA linear PAT 17-AUG-2003
LOCUS AR349146/c
DEFINITION Sequence 86 from patent US 6583278.
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ACCESSION AR349146
VERSION AR349146.1 GI:33749851
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Carter,N.M.
TITLE Nucleic acid probes complementary to human papilloma virus nucleic
JOURNAL Patent: US 6583278-A 86 24-JUN-2003;
FEATURES Gen-Probe Incorporated; San Diego, CA
SOURCE Location/Qualifiers
source 1..21
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 21; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGACACAGTGCGCTTTTGAC 21
Db 21 CAGGACACAGTGCGCTTTTGAC 1
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RESULT 3
AR349147 21 bp DNA linear PAT 17-AUG-2003
LOCUS AR349147 Sequence 87 from patent US 6583278.
ACCESSION AR349147
VERSION AR349147.1 GI:33749852
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Carter,N.M.
TITLE Nucleic acid probes complementary to human papilloma virus nucleic
JOURNAL Patent: US 6583278-A 87 24-JUN-2003;
FEATURES Gen-Probe Incorporated; San Diego, CA
SOURCE Location/Qualifiers
source 1..21
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 21; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGACACAGTGCGCTTTTGAC 21
Db 1 CAGGACACAGTGCGCTTTTGAC 21

RESULT 4
AR349148 21 bp DNA linear PAT 17-AUG-2003
LOCUS AR349148/c
DEFINITION Sequence 88 from patent US 6583278.
ACCESSION AR349148
VERSION AR349148.1 GI:33749853
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Carter,N.M.
TITLE Nucleic acid probes complementary to human papilloma virus nucleic
JOURNAL Patent: US 6583278-A 88 24-JUN-2003;
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Gen-Probe Incorporated; San Diego, CA

FEATURES
source
1. .21
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db

RESULT 5
DD187316 104 bp DNA linear PAT 19-JAN-2006
DEFINITION SPICEOSOME MEDIATED RNA TRANS-SPLICING.
DD187316
KEYWORDS DD187316.1 GI:85643668
JP 2005176849-A/118.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences: artificial sequences.

REFERENCE 1 (bases 1 to 104)
AUTHORS Walsh, C., Chao, H., Mansfield, G.S., Pataraju, M., Baker, C.C.,
GarciaAmbiano, M.A. and Mitchell, L.G.
TITLE SPICEOSOME MEDIATED RNA TRANS-SPLICING
JOURNAL Patent: JP 2005176849-A 118 07-JUL-2005;
INTRON INC

COMMENT OS Artificial Sequence
PN JP 2005176849-A/118
PD 07-JUL-2005
PR 07-JAN-2005 JP 2005003076
PR 08-JAN-2001 US 09/756095, 08-JAN-2001 US 09/756096, PR
08-JAN-2001 US 09/756097, 20-APR-2001 US 09/838858, PR
29-AUG-2001 US 09/941492
PI christopher walsh, hengjun chao, gary s mansfield, madata pi
ptaraju,
PI carl c baker, mariano a garcia-blanco, lloyd g mitchell CC
Binding domain of human papilloma virus PTM
FH Key Location/Qualifiers

FEATURES
source
1. .104
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 100.0%; Score 21; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGACACAGTGGCTTTGAC 21
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4 CAGGACACAGTGGCTTTGAC 24

Db

RESULT 6
DD187319 138 bp DNA linear PAT 19-JAN-2006
DEFINITION SPICEOSOME MEDIATED RNA TRANS-SPLICING.
DD187319
KEYWORDS DD187319.1 GI:85643671
JP 2005176849-A/121.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences: artificial sequences.

REFERENCE 1 (bases 1 to 138)
AUTHORS Walsh, C., Chao, H., Mansfield, G.S., Pataraju, M., Baker, C.C.,
GarciaAmbiano, M.A. and Mitchell, L.G.

SPICEOSOME MEDIATED RNA TRANS-SPLICING
Patent: JP 2005176849-A 121 07-JUL-2005;
INTRON INC

COMMENT OS Artificial Sequence
PN JP 2005176849-A/121
PD 07-JUL-2005
PR 07-JAN-2005 JP 2005003076
PR 08-JAN-2001 US 09/756095, 08-JAN-2001 US 09/756096, PR
08-JAN-2001 US 09/756097, 20-APR-2001 US 09/838858, PR
29-AUG-2001 US 09/941492
PI christopher walsh, hengjun chao, gary s mansfield, madata pi
ptaraju,
PI carl c baker, mariano a garcia-blanco, lloyd g mitchell CC
Binding domain of human papilloma virus PTM
FH Key Location/Qualifiers

FEATURES
source
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"

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Query Match 100.0%; Score 21; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGACACAGTGGCTTTGAC 21
|||||
39 CAGGACACAGTGGCTTTGAC 59

Db

RESULT 7
HPUS9900/c 170 bp mRNA linear VRL 06-JUN-1996
LOCUS HPUS9900
DEFINITION Human papillomavirus type 16 mutant442, major E6E7 splice variant
mRNA, partial cds.
ACCESSION US9900
VERSION US9900.1 GI:1405361
KEYWORDS Human papillomavirus type 16
SOURCE Human papillomavirus type 16
ORGANISM Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
AlphaPapillomavirus.
REFERENCE 1 (bases 1 to 170)
AUTHORS Shipky, R., Siwkowski, A. and Hampel, A.
TITLE Direct Submission
JOURNAL Submitted (03-JUN-1996) Biology, N.I.U., Montgomery Hall #319,
DeKalb, IL 60115, USA

FEATURES
source
1. .170
/organism="Human papillomavirus type 16"
/mol_type="mRNA"
/strain="SiHA"
/db_xref="taxon:333760"
/map="155-506 in the genomic map"
/note="The mutation at site 442 in the E6E7 major splice
variant was verified with a series of clones and PCR batch
sequencing"
1. .81
/note="truncated E6 protein product of the major splice
variant"
/codon_start=1
/product="E6E7"
/protein_id="AA03505.1"
/db_xref="GI:1405362"
/translation="ELQYTHDIILCYCKQQLRRVY"
1. .72
73. .>170
105
/note="site of mutation (nucleotide 442 in genome); This
mutation results in an amino acid change from E to D when
the full-size transcript is translated"

ORIGIN
exon
exon
misc_feature

Query Match 100.0%; Score 21; DB 10; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGACACAGTGGCTTTTGAC 21
|||||
DB 104 CAGGACACAGTGGCTTTTGAC 84

RESULT 8
HPV14515/c 245 bp DNA linear VRL 15-FEB-2001
LOCUS Human papillomavirus clone HPV1629 B6 protein (B6) gene, partial
DEFINITION cds.
ACCESSION U14515
VERSION U14515.1 GI:984951
KEYWORDS
SOURCE Human papillomavirus
ORGANISM Viruses; deDNA viruses, no RNA stage; Papillomaviridae;

REFERENCE 1 (bases 1 to 245)
AUTHORS Haegert,D.G., Galutira,D.F. and Younghusband,B.H.
JOURNAL Sequence variation in the B6 gene of human papillomavirus type 16
REFERENCE 2 (bases 1 to 245)
AUTHORS Galutira,D.F.
TITLE Direct Submision
SUBMITTED (07-SEP-1994) Dante F. Galutira, Memorial University of
Newfoundland, Discipline of Pathology, Fac. Medicine, St. John's,
Newfoundland, A1B 3V6, Canada
LOCATION/Qualifiers

1. .245
/organism="Human papillomavirus"
/mol_type="genomic DNA"
/strain="HPV16"
/db_xref="taxon:10566"
/clone="HPV1629"
/issue_type="cervical tissue from invasive carcinoma"

FEATURES

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1. .245
/organism="Human papillomavirus"
/mol_type="genomic DNA"
/strain="HPV16"
/db_xref="taxon:10566"
/clone="HPV1629"
/issue_type="cervical tissue from invasive carcinoma"
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/db_xref="GI:12831650"
/translation="VYDFAFRDLCIVYRDGNPYAVCDKCLKFYSKISBYRYCYSVYGG
TTLBOQYNKPLCDLIRINCCKPLCPESKORHLDRK"
61
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Number K02718, position 286; NCBI gi: 333031"
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Number K02718, position 289; NCBI gi: 333031"
/replace="a"
110
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/note="C to T transversion from PA16, GenBank Accession
Number K02718, position 335; NCBI gi: 333031"
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125
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/note="T to G transversion from PA16, GenBank Accession
Number K02718, position 350; NCBI gi: 333031"
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139
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/note="A to T transversion from PA16, GenBank Accession

ORIGIN
Number K02718, position 364; NCBI gi: 333031"
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Query Match 100.0%; Score 21; DB 10; Length 245;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGACACAGTGGCTTTTGAC 21
|||||
DB 215 CAGGACACAGTGGCTTTTGAC 195

RESULT 9
HPV14511/c 253 bp DNA linear VRL 15-FEB-2001
LOCUS Human papillomavirus clone HPV1601 B6 protein (B6) gene, partial
DEFINITION cds.
ACCESSION U14511
VERSION U14511.1 GI:984943
KEYWORDS
SOURCE Human papillomavirus
ORGANISM Viruses; deDNA viruses, no RNA stage; Papillomaviridae;

REFERENCE 1 (bases 1 to 253)
AUTHORS Haegert,D.G., Galutira,D.F. and Younghusband,B.H.
JOURNAL Sequence variation in the B6 gene of human papillomavirus type 16
REFERENCE 2 (bases 1 to 253)
AUTHORS Galutira,D.F.
TITLE Direct Submision
SUBMITTED (07-SEP-1994) Dante F. Galutira, Memorial University of
Newfoundland, Discipline of Pathology, Fac. Medicine, St. John's,
Newfoundland, A1B 3V6, Canada
LOCATION/Qualifiers

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/db_xref="taxon:10566"
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/issue_type="cervical"
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/db_xref="GI:12831647"
/translation="PAFRDLCIVYRDGNPYAVCDKCLKFYSKISBYRYHYGVGTTL
EQQYNKPLCDLIRINCCKPLCPESKORHLDRKRFHNI"
115
/gene="B6"
/note="T to G transversion from PA16, GenBank Accession
Number K02718, position 350; NCBI gi: 333031"
/replace="t"

FEATURES

source
1. .253
/organism="Human papillomavirus"
/mol_type="genomic DNA"
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/issue_type="cervical"
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/db_xref="GI:12831647"
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EQQYNKPLCDLIRINCCKPLCPESKORHLDRKRFHNI"
115
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/note="T to G transversion from PA16, GenBank Accession
Number K02718, position 350; NCBI gi: 333031"
/replace="t"

ORIGIN

Query Match 100.0%; Score 21; DB 10; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGACACAGTGGCTTTTGAC 21
|||||
DB 205 CAGGACACAGTGGCTTTTGAC 185

RESULT 10
HPV14512/c 271 bp DNA linear VRL 14-SEP-1995
LOCUS HPV14512

DEFINITION Human papillomavirus clone HPV1603 E6 protein (E6) gene, partial cds.
ACCESSION U14512
VERSION U14512.1 GI:984945
KEYWORDS Human papillomavirus
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
REFERENCE 1 (bases 1 to 271)
AUTHORS Heeger, D.G., Galutira, D.F. and Younghusband, B.H.
TITLE Sequence variation in the E6 gene of human papillomavirus type 16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 271)
AUTHORS Galutira, D.F.
TITLE Direct Submission
JOURNAL Submitted (07-SEP-1994) Dante F. Galutira, Memorial University of Newfoundland, Discipline of Pathology, Fac. Medicine, St. John's, Newfoundland, A1B 3V6, Canada
FEATURES
source
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/organism="Human papillomavirus"
/mol_type="genomic DNA"
/strain="HPV16"
/db_xref="taxon:10566"
/clone="HPV1603"
/tissue_type="cervical tissue from invasive carcinoma"
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/gene="E6"
/note="E6"
/protein_id="AAB60566.1"
/db_xref="GI:984946"
/translation="VYDFAFRDLIVYRDGNPYAVCDKCLFKYSKISEYRHYCYSLYG
TTLEQYNKPLCDLLIRCNCKPLCEBEQRHLDKKQRHNIRGR"
85
variation
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/note="T to G transversion from PAL6, GenBank Accession Number K02718, position 310; NCBI gi: 333031"
/replace="t"
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Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAGGACACAGTGGCTTTGAC 21
DB 215 CAGGACACAGTGGCTTTGAC 195
RESULT 11
HPV14513/c 272 bp DNA linear VRL 15-FEB-2001
LOCUS Human papillomavirus clone HPV1607 E6 protein (E6) gene, partial cds.
ACCESSION U14513
VERSION U14513.1 GI:984947
KEYWORDS Human papillomavirus
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
REFERENCE 1 (bases 1 to 271)
AUTHORS Heeger, D.G., Galutira, D.F. and Younghusband, B.H.
TITLE Sequence variation in the E6 gene of human papillomavirus type 16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 271)
AUTHORS Galutira, D.F.
TITLE Direct Submission
JOURNAL Submitted (07-SEP-1994) Dante F. Galutira, Memorial University of

Newfoundland, Discipline of Pathology, Fac. Medicine, St. John's, Newfoundland, A1B 3V6, Canada
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/organism="Human papillomavirus"
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/db_xref="taxon:10566"
/clone="HPV1607"
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/note="E6"
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/db_xref="GI:12831648"
/translation="VYDFAFRDLIVYRDGNPYAVCDKCLFKYSKISEYRHYCYSLYG
TTLEQYNKPLCDLLIRCNCKPLCEBEQRHLDKKQRHNIRGR"
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/note="C to G transversion from PAL6, GenBank Accession Number K02718, position 256; NCBI gi: 333031"
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Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAGGACACAGTGGCTTTGAC 21
DB 215 CAGGACACAGTGGCTTTGAC 195
RESULT 12
HPV14514/c 273 bp DNA linear VRL 15-FEB-2001
LOCUS Human papillomavirus clone HPV1627 E6 protein (E6) gene, partial cds.
ACCESSION U14514
VERSION U14514.1 GI:984949
KEYWORDS Human papillomavirus
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
REFERENCE 1 (bases 1 to 273)
AUTHORS Heeger, D.G., Galutira, D.F. and Younghusband, B.H.
TITLE Sequence variation in the E6 gene of human papillomavirus type 16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 273)
AUTHORS Galutira, D.F.
TITLE Direct Submission
JOURNAL Submitted (07-SEP-1994) Dante F. Galutira, Memorial University of Newfoundland, Discipline of Pathology, Fac. Medicine, St. John's, Newfoundland, A1B 3V6, Canada
FEATURES
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/strain="HPV16"
/db_xref="taxon:10566"
/clone="HPV1627"
/tissue_type="cervical tissue from invasive carcinoma"
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/product="E6 protein"
/replace="t"

variation /db_xref="GI:12831649"
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61
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Number K02718, position 286; NCBI GI: 333031"
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Number K02718, position 289; NCBI GI: 333031"
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110
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/note="C to T transition from PA16, GenBank Accession
Number K02718, position 335; NCBI GI: 333031"
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variation

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CAGGACACAGTGGCTTTTGAC 21
Db 215 CAGGACACAGTGGCTTTTGAC 195

RESULT 13
LOCUS HPV14516 274 bp DNA linear VRL 14-SEP-1995
DEFINITION Human papillomavirus clone HPV1649 E6 protein (E6) gene, partial
cds.
ACCESSION U14516
VERSION U14516.1 GI:384953
KEYWORDS Human papillomavirus
SOURCE Human papillomavirus
ORGANISM Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
unclassified Papillomaviridae.
REFERENCE 1 (bases 1 to 274)
AUTHORS Haeger, D.G., Galutira, D.F. and Younghusband, B.H.
TITLE Sequence variation in the E6 gene of human papillomavirus type 16
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 274)
AUTHORS Galutira, D.F.
TITLE Direct Submission
JOURNAL Submitted (07-SEP-1994) Dante F. Galutira, Memorial University of
Newfoundland, Discipline of Pathology, Fac. Medicine, St. John's,
Newfoundland, A1B 3X6, Canada
FEATURES
source Location/Qualifiers
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/organism="Human papillomavirus"
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/db_xref="taxon:10566"
/clone="HPV1649"
/tissue_type="cervical tissue from invasive carcinoma"
1..274
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/db_xref="GI:984954"
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61
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Number K02718, position 286; NCBI GI: 333031"

variation /replace="t"
64
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Number K02718, position 289; NCBI GI: 333031"
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110
/gene="E6"
/note="C to T transition from PA16, GenBank Accession
Number K02718, position 335; NCBI GI: 333031"
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125
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/note="T to G transversion from PA16, GenBank Accession
Number K02718, position 350; NCBI GI: 333031"
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ORIGIN
Query Match 100.0%; Score 21; DB 10; Length 274;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CAGGACACAGTGGCTTTTGAC 21
Db 215 CAGGACACAGTGGCTTTTGAC 195

RESULT 14
LOCUS AP404704 298 bp DNA linear VRL 09-OCT-2003
DEFINITION Human papillomavirus type 16 isolate HPV166C13 E6 protein (E6)
gene, partial cds.
ACCESSION AP404704
VERSION AP404704.1 GI:15529605
KEYWORDS Human papillomavirus type 16
SOURCE Human papillomavirus type 16
ORGANISM Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Alphapapillomavirus.
REFERENCE 1 (bases 1 to 298)
AUTHORS Wates, K.J., Thompson, C.H., Coscart, Y.E. and Rose, B.R.
TITLE Sequence variation and physical state of human papillomavirus type
16 cervical cancer isolates from Australia and New Caledonia
JOURNAL Int. J. Cancer 97 (6), 868-874 (2002)
REFERENCE 2 (bases 1 to 298)
AUTHORS Wates, K.J., Thompson, C.H., Coscart, Y.E. and Rose, B.R.
TITLE Direct Submission
JOURNAL Submitted (31-OCT-2001) Department of Infectious Diseases,
University of Sydney, Blackburn Building, D06, Off Western Avenue,
Camperdown, Sydney, New South Wales 2006, Australia
FEATURES
source Location/Qualifiers
1..298
/organism="Human papillomavirus type 16"
/mol_type="genomic DNA"
/isolate="HPV166C13"
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/gene="E6"
/gene="E6"
/gene="E6"
/gene="E6"
/codon_start=2
/product="E6 protein"
/protein_id="AA101365.1"
/db_xref="GI:15529606"
/translation="DITLVCVCKQQLRREYVDFPAFRLDIYVRDGNPYAVCDKCL
FYSKISEYRYCYSLYGTLEQQYNKPLCDLIRICNCKKPLCPBEKQRLDKQ"
115
/gene="E6"
/note="T to A transversion from PA16, GenBank Accession
Number K02718, position 286; NCBI GI: 333031"

Qy 1 CAGGACACAGTGGCTTTGAC 21
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Db 266 CAGGACACAGTGGCTTTGAC 246

RESULT 15
AF404692 370 bp DNA linear VRL 09-OCT-2003
LOCUS AF404692/c
DEFINITION Human papillomavirus type 16 isolate HPV16B6CC1 E6 protein (E6) and
E7 protein (E7) genes, partial cds.
ACCESSION AF404692
VERSION AF404692.1 GI:15529569
KEYWORDS
SOURCE Human papillomavirus type 16
ORGANISM Human papillomavirus type 16
VIRUSES; dsDNA viruses, no RNA stage; Papillomaviridae;
Alphapapillomavirus.
REFERENCE
AUTHORS Watts,K.J., Thompson,C.H., Coscart,Y.E. and Rose,B.R.
TITLE Sequence variation and physical state of human papillomavirus type
16 cervical cancer isolates from Australia and New Caledonia
JOURNAL Int. J. Cancer 97 (6), 868-874 (2002)
PUBMED 11857370
REFERENCES
Watts,K.J., Thompson,C.H., Coscart,Y.E. and Rose,B.R.
TITLE Direct Submission
SUBMITTED (31-JUL-2001) Department of Infectious Diseases,
University of Sydney, Blackburn Building, D06, Off Western Avenue,
Camperdown, Sydney, New South Wales 2006, Australia
LOCATION/Qualifiers
1. .370
/organism="Human papillomavirus type 16"
/mol_type="genomic DNA"
/isolate="HPV16B6CC1"
/db_xref="taxon:333760"
<1. .313
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/gene="E6"
/codon_start=2
/product="E6 protein"
/protein_id="AAL01342.1"
/db_xref="GI:15529571"
/translation="IDLCIVRDGDPVAVCDKCLKFYSKISRYHYCVSLYGTLEOOF
NKPCLDLIRICNCQKPLCEBEKQRHLDKQRFNINIGRWTCGMSCCRSRRTREIQ
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316. .>370
/gene="E7"
316. .>370
/gene="E7"
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/codon_start=1
/product="E7 protein"
/protein_id="AAL01341.1"
/db_xref="GI:15529570"
/translation="MHGDTPTLHMYMLDLPB"

ORIGIN
Query Match 100.0%; Score 21; DB 10; Length 370;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGGACACAGTGGCTTTGAC 21
|||||
Db 194 CAGGACACAGTGGCTTTGAC 174

RESULT 16
S51110 421 bp DNA linear VRL 08-MAY-1993
LOCUS S51110/c
DEFINITION Off B6 [human papillomavirus HPV, type 16, head and neck tumor,
Genomic, 421 nt].
ACCESSION S51110
VERSION S51110.1 GI:262061

KEYWORDS
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
VIRUSES; dsDNA viruses, no RNA stage; Papillomaviridae;
unclassified Papillomaviridae.
REFERENCE
AUTHORS Tyau,Y.S., Liu,S.T., Ong,W.R., Chen,M.L., Shu,C.H. and Chang,Y.S.
TITLE Detection of Epstein-Barr virus and human papillomavirus in head
and neck tumors
JOURNAL J. Clin. Microbiol. 31 (1), 53-56 (1993)
PUBMED 8380183
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gisdbg 120826] from the original journal article.
COMMENT PCR primer sequences: 1-21 and 400-421.
FEATURES
source
1. .421
/organism="Human papillomavirus"
/mol_type="genomic DNA"
/db_xref="taxon:10566"
/note="type: 16"
1. .421
/gene="orf E6"

ORIGIN
Query Match 100.0%; Score 21; DB 10; Length 421;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGGACACAGTGGCTTTGAC 21
|||||
Db 338 CAGGACACAGTGGCTTTGAC 318

RESULT 17
AF404695/c 451 bp DNA linear VRL 09-OCT-2003
LOCUS AF404695/c
DEFINITION Human papillomavirus type 16 isolate HPV16B6CC4 E6 protein (E6) and
E7 protein (E7) genes, partial cds.
ACCESSION AF404695
VERSION AF404695.1 GI:15529578
KEYWORDS
SOURCE Human papillomavirus type 16
ORGANISM Human papillomavirus type 16
VIRUSES; dsDNA viruses, no RNA stage; Papillomaviridae;
Alphapapillomavirus.
REFERENCE
AUTHORS Watts,K.J., Thompson,C.H., Coscart,Y.E. and Rose,B.R.
TITLE Sequence variation and physical state of human papillomavirus type
16 cervical cancer isolates from Australia and New Caledonia
JOURNAL Int. J. Cancer 97 (6), 868-874 (2002)
PUBMED 11857370
REFERENCES
Watts,K.J., Thompson,C.H., Coscart,Y.E. and Rose,B.R.
TITLE Direct Submission
SUBMITTED (31-JUL-2001) Department of Infectious Diseases,
University of Sydney, Blackburn Building, D06, Off Western Avenue,
Camperdown, Sydney, New South Wales 2006, Australia
LOCATION/Qualifiers
1. .451
/organism="Human papillomavirus type 16"
/mol_type="genomic DNA"
/isolate="HPV16B6CC4"
/db_xref="taxon:333760"
<1. .395
/gene="E6"
<1. .395
/gene="E6"
/codon_start=3
/product="E6 protein"
/protein_id="AAL01347.1"
/db_xref="GI:15529579"
/translation="TTHDILTECVCKQQLLRREYGFARFDLCIVRDGDPVAVCDK
CLKFYSKISRYHYCVSLYGTLEOOFYNKPLCDLIRICNCQKPLCEBEKQRHLDKQ"

gene RPHNIRGWTGRCMSCRSSRTRRETOL"
398..>451
/gene="E7"
398..>451
/gene="E7"
/codon_start=1
/product="E7 protein"
/protein_id="AL01348.1"
/db_xref="GI:15529580"
/translation="MHGDTPTLHEVWLDLQPE"
ORIGIN

Query Match 100.0%; Score 21; DB 10; Length 451;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGACACAGTGGCTTTTGAC 21
|||||
Db 276 CAGGACACAGTGGCTTTTGAC 256

RESULT 18
AP404696/c 451 bp DNA linear VRL 09-OCT-2003
LOCUS Human papillomavirus type 16 isolate HPV16B6CC5 E6 protein (B6) and
DEFINITION E7 protein (E7) genes, partial cds.
ACCESSION AF404696
VERSION AF404696.1 GI:15529581
KEYWORDS Human papillomavirus type 16
SOURCE Human papillomavirus type 16
ORGANISM Viruses; daDNA viruses, no RNA stage; Papillomaviridae;
Alphapapillomavirus.
1 (bases 1 to 451)
REFERENCE
AUTHORS Watts,K.J., Thompson,C.H., Coscart,Y.E. and Rose,B.R.
TITLE Sequence variation and physical state of human papillomavirus type
JOURNAL 16 cervical cancer isolates from Australia and New Caledonia
PUBMED 11857370
AUTHORS Watts,K.J., Thompson,C.H., Coscart,Y.E. and Rose,B.R.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-2001) Department of Infectious Diseases,
University of Sydney, Blackburn Building, D06, Off Western Avenue,
Camperdown, Sydney, New South Wales 2006, Australia
FEATURES
source 1.451
/organism="Human papillomavirus type 16"
/mol_type="genomic DNA"
/isolate="HPV16B6CC5"
/db_xref="taxon:333760"
<1..395
/gene="B6"
<1..395
/gene="E7"
/codon_start=3
/product="B6 protein"
/protein_id="AL01349.1"
/db_xref="GI:15529582"
/translation="TTHNIIILCCVYCKQQLRREYDPAFRDICTYRRGNPYAVCDK
CKFKYSKISBYRHYCYSVYGTLEQYNKPLCDLLIRCTNCQKPLCPBESKQRLDKKQ
RPHNIRGWTGRCMSCRSSRTRRETOL"
398..>451
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398..>451
/gene="E7"
/codon_start=1
/product="E7 protein"
/protein_id="AL01350.1"
/db_xref="GI:15529583"
/translation="MHGDTPTLHEVWLDLQPE"
ORIGIN

Query Match 100.0%; Score 21; DB 10; Length 451;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGACACAGTGGCTTTTGAC 21
|||||
Db 276 CAGGACACAGTGGCTTTTGAC 256

RESULT 19
AP404699/c 451 bp DNA linear VRL 09-OCT-2003
LOCUS Human papillomavirus type 16 isolate HPV16B6CC8 E6 protein (B6) and
DEFINITION E7 protein (E7) genes, partial cds.
ACCESSION AF404699
VERSION AF404699.1 GI:15529590
KEYWORDS Human papillomavirus type 16
SOURCE Human papillomavirus type 16
ORGANISM Viruses; daDNA viruses, no RNA stage; Papillomaviridae;
Alphapapillomavirus.
1 (bases 1 to 451)
REFERENCE
AUTHORS Watts,K.J., Thompson,C.H., Coscart,Y.E. and Rose,B.R.
TITLE Sequence variation and physical state of human papillomavirus type
JOURNAL 16 cervical cancer isolates from Australia and New Caledonia
PUBMED 11857370
AUTHORS Watts,K.J., Thompson,C.H., Coscart,Y.E. and Rose,B.R.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-2001) Department of Infectious Diseases,
University of Sydney, Blackburn Building, D06, Off Western Avenue,
Camperdown, Sydney, New South Wales 2006, Australia
FEATURES
source 1.451
/organism="Human papillomavirus type 16"
/mol_type="genomic DNA"
/isolate="HPV16B6CC8"
/db_xref="taxon:333760"
<1..395
/gene="B6"
<1..395
/gene="E7"
/codon_start=3
/product="B6 protein"
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/db_xref="GI:15529591"
/translation="TTHNIIILCCVYCKQQLRREYDPAFRDICTYRRGNPYAVCDK
CKFKYSKISBYRHYCYSVYGTLEQYNKPLCDLLIRCTNCQKPLCPBESKQRLDKKQ
RPHNIRGWTGRCMSCRSSRTRRETOL"
398..>451
/gene="E7"
398..>451
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/codon_start=1
/product="E7 protein"
/protein_id="AL01356.1"
/db_xref="GI:15529592"
/translation="MHGDTPTLHEVWLDLHPS"
ORIGIN

Query Match 100.0%; Score 21; DB 10; Length 451;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGACACAGTGGCTTTTGAC 21
|||||
Db 276 CAGGACACAGTGGCTTTTGAC 256

RESULT 20
AP404700/c 451 bp DNA linear VRL 09-OCT-2003
LOCUS

DEFINITION Human papillomavirus type 16 isolate HPV16B6CC9 E6 protein (E6) and
E7 protein (E7) genes, partial cds.
ACCESSION AF404700
VERSION AF404700.1 GI:15529593
KEYWORDS Human papillomavirus type 16
SOURCE Human papillomavirus type 16
ORGANISM Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Alphapapillomavirus.
REFERENCE
AUTHORS 1 (bases 1 to 451)
TITLE Waites,K.J., Thompson,C.H., Cossart,Y.E. and Rose,B.R.
JOURNAL Sequence variation and physical state of human papillomavirus type
PUBMED 16 cervical cancer isolates from Australia and New Caledonia
11857370 Int. J. Cancer 97 (6), 868-874 (2002)
REFERENCE
AUTHORS 2 (bases 1 to 451)
TITLE Waites,K.J., Thompson,C.H., Cossart,Y.E. and Rose,B.R.
JOURNAL Direct Submission
PUBMED Submitted (31-JUL-2001) Department of Infectious Diseases,
REFERENCE University of Sydney, Blackburn Building, D06, Off Western Avenue,
AUTHORS Camperdown, Sydney, New South Wales 2006, Australia
JOURNAL Location/Qualifiers
FEATURES
source
1. .451
/organism="Human papillomavirus type 16"
/mol_type="genomic DNA"
/isolate="HPV16B6CC9"
/db_xref="taxon:333760"
<1. .395
/gene="E6"
/gene="E7"
<1. .395
/codon_start=3
/product="E6 protein"
/protein_id="AA01357.1"
/db_xref="GI:15529594"
/translation="TIDHIIIECYCCKQLRREVDPAFADLCIVYRDGNPYAVCDK
CLKPKYSISRHYCYVGTGLEQYNKPCDLLIRINCQKPLCEPKQRHDKQ
RFINIRGRWTRGRCSCRSSTRRETQL"
398. .>451
/gene="E7"
/gene="E7"
398. .>451
/gene="E7"
/codon_start=1
/product="E7 protein"
/protein_id="AA01358.1"
/db_xref="GI:15529595"
/translation="MHGDTPTLHRYMLDPE"
ORIGIN
Query Match 100.0%; Score 21; DB 10; Length 451;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CQ 1 CAGGACACAGTGGCTTTGAC 21
|||||
Db 276 CAGGACACAGTGGCTTTGAC 256
RESULT 21
AF404701/c 451 bp DNA linear VRL 09-OCT-2003
LOCUS
DEFINITION Human papillomavirus type 16 isolate HPV16B6CC10 E6 protein (E6)
and E7 protein (E7) genes, partial cds.
ACCESSION AF404701
VERSION AF404701.1 GI:15529596
KEYWORDS Human papillomavirus type 16
SOURCE Human papillomavirus type 16
ORGANISM Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Alphapapillomavirus.
REFERENCE
AUTHORS 1 (bases 1 to 451)
TITLE Waites,K.J., Thompson,C.H., Cossart,Y.E. and Rose,B.R.
JOURNAL Sequence variation and physical state of human papillomavirus type

JOURNAL 16 cervical cancer isolates from Australia and New Caledonia
PUBMED Int. J. Cancer 97 (6), 868-874 (2002)
11857370
REFERENCE
AUTHORS 2 (bases 1 to 451)
TITLE Waites,K.J., Thompson,C.H., Cossart,Y.E. and Rose,B.R.
JOURNAL Direct Submission
PUBMED Submitted (31-JUL-2001) Department of Infectious Diseases,
REFERENCE University of Sydney, Blackburn Building, D06, Off Western Avenue,
AUTHORS Camperdown, Sydney, New South Wales 2006, Australia
JOURNAL Location/Qualifiers
FEATURES
source
1. .451
/organism="Human papillomavirus type 16"
/mol_type="genomic DNA"
/isolate="HPV16B6CC10"
/db_xref="taxon:333760"
<1. .395
/gene="E6"
/gene="E7"
<1. .395
/codon_start=3
/product="E6 protein"
/protein_id="AA01359.1"
/db_xref="GI:15529597"
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RFINIRGRWTRGRCSCRSSTRRETQL"
398. .>451
/gene="E7"
/gene="E7"
398. .>451
/gene="E7"
/codon_start=1
/product="E7 protein"
/protein_id="AA01360.1"
/db_xref="GI:15529598"
/translation="MHGDTPTLHRYMLDPE"
ORIGIN
Query Match 100.0%; Score 21; DB 10; Length 451;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CQ 1 CAGGACACAGTGGCTTTGAC 21
|||||
Db 276 CAGGACACAGTGGCTTTGAC 256
RESULT 22
AF404703/c 451 bp DNA linear VRL 09-OCT-2003
LOCUS
DEFINITION Human papillomavirus type 16 isolate HPV16B6CC12 E6 protein (E6)
and E7 protein (E7) genes, partial cds.
ACCESSION AF404703
VERSION AF404703.1 GI:15529602
KEYWORDS Human papillomavirus type 16
SOURCE Human papillomavirus type 16
ORGANISM Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Alphapapillomavirus.
REFERENCE
AUTHORS 1 (bases 1 to 451)
TITLE Waites,K.J., Thompson,C.H., Cossart,Y.E. and Rose,B.R.
JOURNAL Sequence variation and physical state of human papillomavirus type
PUBMED 16 cervical cancer isolates from Australia and New Caledonia
11857370 Int. J. Cancer 97 (6), 868-874 (2002)
REFERENCE
AUTHORS 2 (bases 1 to 451)
TITLE Waites,K.J., Thompson,C.H., Cossart,Y.E. and Rose,B.R.
JOURNAL Direct Submission
PUBMED Submitted (31-JUL-2001) Department of Infectious Diseases,
REFERENCE University of Sydney, Blackburn Building, D06, Off Western Avenue,
AUTHORS Camperdown, Sydney, New South Wales 2006, Australia
JOURNAL Location/Qualifiers
FEATURES
source
1. .451
/organism="Human papillomavirus type 16"

gene /mol_type="genomic DNA"
/isolate="HPV16B6C12"
/db_xref="taxon:333760"
1..395
/gene="E6"
1..395
/gene="E6"
/codon_start=3
/product="E6 protein"
/protein_id="AAL01363.1"
/db_xref="GI:15529603"
/translation="TITNITLCEVYCKQQLLRVYDPAFRDICTYRDNPAVCDK
CNFTSKISEYRHYCYSLVGTLEBQYKPCDLLIRICNCPKLPCKRRLDKKQ
RFHNRGRWTGRMCSCCRSRRRTETOL"
398..>451
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398..>451
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/codon_start=1
/product="E7 protein"
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/db_xref="GI:15529604"
/translation="MHGDTPTLHEVWLIDLOPE"
ORIGIN

Query Match 100.0%; Score 21; DB 10; Length 451;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGACACAGTGGCTTTTGAC 21
|||||
Db 276 CAGGACACAGTGGCTTTTGAC 256

RESULT 23
AR167393/c
LOCUS AR167393 456 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 29 from patent US 6287569.
ACCESSION AR167393
VERSION AR167393.1 GI:117903171
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 456)
AUTHORS Kipps, T.J. and Wu, Y.
TITLE Vaccines with enhanced intracellular processing
JOURNAL Patent: US 6287569-A 29 11-SEP-2001;
FEATURES
source Location/Qualifiers
1..456
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 21; DB 2; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGACACAGTGGCTTTTGAC 21
|||||
Db 337 CAGGACACAGTGGCTTTTGAC 317

RESULT 24
AR177943/c
LOCUS AR177943 456 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 6 from patent US 6313373.
ACCESSION AR177943
VERSION AR177943.1 GI:17920298
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
FEATURES
source Location/Qualifiers
1..456
/organism="unknown"
/mol_type="unassigned DNA"

REFERENCE 1 (bases 1 to 456)
AUTHORS Becker, R.L. and Crish, J.F.
TITLE Tissue specific promoters and transgenic mouse for the screening of
pharmaceuticals
JOURNAL Patent: US 6313373-A 6 06-NOV-2001;
FEATURES
source Location/Qualifiers
1..456
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 21; DB 2; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGACACAGTGGCTTTTGAC 21
|||||
Db 337 CAGGACACAGTGGCTTTTGAC 317

RESULT 25
AF327851/c
LOCUS AF327851 456 bp DNA linear VRL 04-JAN-2001
DEFINITION Human papillomavirus type 16 early transforming protein E6 variant
(E6) gene, complete cds.
ACCESSION AF327851
VERSION AF327851.1 GI:12025467
KEYWORDS
SOURCE Human papillomavirus type 16
Human papillomavirus type 16
Viruses; daDNA viruses, no RNA stage, Papillomaviridae;
Alphapapillomavirus.
1 (bases 1 to 456)
AUTHORS Ma, Z., Qian, D., Ma, J., Lin, R., Ming, W., Zhong, Z., Zhang, Q. and
Zhang, F.
TITLE Cloning and Sequencing of HPV16 E6 gene from Cervical Carcinoma
Biopsies in Xinjiang
JOURNAL Shengwu Huaxue Yu Shengwu Wuli Jinzhan (2001) In press
ACCESSION 2 (bases 1 to 456)
AUTHORS Ma, Z. and Zhang, F.
TITLE Direct Substitution
JOURNAL Submitted (12-DEC-2000) Department of Biology, University of
Xinjiang, 14 Shengli Road, Urumqi, Xinjiang 830046, P.R. China
FEATURES
source Location/Qualifiers
1..456
/organism="Human papillomavirus type 16"
/proviral
/mol_type="genomic DNA"
/strain="Xinjiang"
/specific_host="Homo sapiens"
/db_xref="taxon:333760"
/note="HPV16"
1..456
/gene="E6"
1..456
/gene="E6"
/codon_start=1
/product="early transforming protein E6 variant"
/protein_id="AAG45940.1"
/db_xref="GI:12025468"
/translation="MFQDPERPRKLPQCLTQLTTHIILCEVYCKQQLLRVYD
FAFRDICTYRDNPAVCDKCNFTSKISEYRHYCYSLVGTLEBQYKPCDLLIR
CINCPKLPCKRRLDKKORFHNIRGRWTCMSCCRSRRRTETOL"

ORIGIN

Query Match 100.0%; Score 21; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGACACAGTGGCTTTTGAC 21
|||||
Db 337 CAGGACACAGTGGCTTTTGAC 317

RESULT 26
HPU34107/c 456 bp DNA linear VRL 08-MAR-1996
LOCUS Human papillomavirus type 16, isolate NM 4094, early transforming
DEFINITION protein E6 (E6) gene, complete cds.
ACCESSION U34107
VERSION U34107.1 GI:1098719
KEYWORDS Human papillomavirus
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
REFERENCE 1 (bases 1 to 456)
AUTHORS Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildesheim,A.
and Jenison,S.A.
TITLE Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the
E6, I2, and L1 coding segments
JOURNAL J. Virol. 69 (12), 7743-7753 (1995)
PUBMED 7494284
REFERENCE 2 (bases 1 to 456)
AUTHORS Farmer,A.D.
TITLE Direct Submission
SUBMITTED (16-AUG-1995) Andrew D. Farmer, Los Alamos National
Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
Alamos, NM 87501, USA
LOCATION/Qualifiers
FEATURES
source
1. .456
/organism="Human papillomavirus"
/mol_type="genomic DNA"
/isolate="NM 4094"
/db_xref="taxon:10566"
/note="collected by cervical swab at the University of New
Mexico, New Mexico, United States."
gene
1. .456
/gene="E6"
1. .456
/gene="E6"
/codon_start=1
/product="early transforming protein E6"
/protein_id="AA91654.1"
/db_xref="GI:1098720"
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Qy 1 CAGGACACAGTGGCTTTGAC 21
|||||
Db 337 CAGGACACAGTGGCTTTGAC 317
RESULT 27
HPU34108/c 456 bp DNA linear VRL 08-MAR-1996
LOCUS Human papillomavirus type 16, isolate NM 9999, early transforming
DEFINITION protein E6 (E6) gene, complete cds.
ACCESSION U34108
VERSION U34108.1 GI:1098721
KEYWORDS Human papillomavirus
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
REFERENCE 1 (bases 1 to 456)
AUTHORS Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildesheim,A.
and Jenison,S.A.
TITLE Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the

populations characterized by nucleotide sequence analysis of the
E6, I2, and L1 coding segments
JOURNAL J. Virol. 69 (12), 7743-7753 (1995)
PUBMED 7494284
REFERENCE 2 (bases 1 to 456)
AUTHORS Farmer,A.D.
TITLE Direct Submission
SUBMITTED (16-AUG-1995) Andrew D. Farmer, Los Alamos National
Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
Alamos, NM 87501, USA
LOCATION/Qualifiers
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/db_xref="taxon:10566"
/note="collected by cervical swab at the University of New
Mexico, New Mexico, United States."
gene
1. .456
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1. .456
/gene="E6"
/codon_start=1
/product="early transforming protein E6"
/protein_id="AA91655.1"
/db_xref="GI:1098723"
/translation="MFQDPOBRPKLPHLCTELQTHDITLHICVCKQQLRREYD
FARPLDCTIVRDGNPIAVCDKLFYSKISIRYCYSGVTGTLDEQYKPKPLDLLR
CINQKPLCEBKORHLDKORFNHNGRWGRCMSCRSTRRETOL"
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Qy 1 CAGGACACAGTGGCTTTGAC 21
|||||
Db 337 CAGGACACAGTGGCTTTGAC 317
RESULT 28
HPU34109/c 456 bp DNA linear VRL 08-MAR-1996
LOCUS Human papillomavirus type 16, isolate NM T197, early transforming
DEFINITION protein E6 (E6) gene, complete cds.
ACCESSION U34109
VERSION U34109.1 GI:1098723
KEYWORDS Human papillomavirus
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
REFERENCE 1 (bases 1 to 456)
AUTHORS Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildesheim,A.
and Jenison,S.A.
TITLE Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the
E6, I2, and L1 coding segments
JOURNAL J. Virol. 69 (12), 7743-7753 (1995)
PUBMED 7494284
REFERENCE 2 (bases 1 to 456)
AUTHORS Farmer,A.D.
TITLE Direct Submission
SUBMITTED (16-AUG-1995) Andrew D. Farmer, Los Alamos National
Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
Alamos, NM 87501, USA
LOCATION/Qualifiers
FEATURES
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1. .456
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/db_xref="taxon:10566"
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CDS 1. .456
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/translation="MFODPQERPRKLPOLCTELQTTIHIIIECYCKQOLLRREYD
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ORIGIN
Query Match 100.0%; Score 21; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGACACAGTGCGCTTTTGAC 21
HPJ34110/c 456 bp DNA linear VRL 08-MAR-1996
LOCUS Human papillomavirus type 16, isolate NM T446, early transforming
DEFINITION protein E6 (E6) gene, complete cds.
ACCESSION U34110
VERSION U34110.1 GI:1098725
KEYWORDS Human papillomavirus
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
VIRUSES; dsDNA viruses, no RNA stage; Papillomaviridae;
unclassified Papillomaviridae.
1 (bases 1 to 456)
/organism="Human papillomavirus"
/mol_type="genomic DNA"
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/db_xref="taxon:10566"
/note="collected by cervical swab at the University of New
Mexico, New Mexico, United States."
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/product="early transforming protein E6"
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/db_xref="GI:1098726"
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CINCKPLCEBKQRHLDKKRFHNRGRWGTGCMSCSSSRTRRETOL"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS Human papillomavirus type 16, isolate NM T446, early transforming
DEFINITION protein E6 (E6) gene, complete cds.
ACCESSION U34110
VERSION U34110.1 GI:1098725
KEYWORDS Human papillomavirus
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
VIRUSES; dsDNA viruses, no RNA stage; Papillomaviridae;
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/db_xref="taxon:10566"
/note="collected by cervical swab at the University of New
Mexico, New Mexico, United States."
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/db_xref="GI:1098726"
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CINCKPLCEBKQRHLDKKRFHNRGRWGTGCMSCSSSRTRRETOL"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS Human papillomavirus type 16, isolate NM T446, early transforming
DEFINITION protein E6 (E6) gene, complete cds.
ACCESSION U34110
VERSION U34110.1 GI:1098725
KEYWORDS Human papillomavirus
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
VIRUSES; dsDNA viruses, no RNA stage; Papillomaviridae;
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FARDLCIVRDGNPYAVCDKCLKFSKISRYHCYSYGTTLLEQYKPLCDLLIR
CINCKPLCEBKQRHLDKKRFHNRGRWGTGCMSCSSSRTRRETOL"

QY 1 CAGGACACAGTGCGCTTTTGAC 21
HPJ34110/c 456 bp DNA linear VRL 08-MAR-1996
LOCUS Human papillomavirus type 16, isolate NM T455, early transforming
DEFINITION protein E6 (E6) gene, complete cds.
ACCESSION U34111
VERSION U34111.1 GI:1098727
KEYWORDS Human papillomavirus
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
VIRUSES; dsDNA viruses, no RNA stage; Papillomaviridae;
unclassified Papillomaviridae.
1 (bases 1 to 456)
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/mol_type="genomic DNA"
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/db_xref="taxon:10566"
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CDS 1. .456
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CINCKPLCEBKQRHLDKKRFHNRGRWGTGCMSCSSSRTRRETOL"

ORIGIN
Query Match 100.0%; Score 21; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGACACAGTGCGCTTTTGAC 21
HPJ34110/c 456 bp DNA linear VRL 08-MAR-1996
LOCUS Human papillomavirus type 16, isolate NM T529, early transforming
DEFINITION protein E6 (E6) gene, complete cds.
ACCESSION U34112
VERSION U34112.1 GI:1098729
KEYWORDS Human papillomavirus
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
VIRUSES; dsDNA viruses, no RNA stage; Papillomaviridae;
unclassified Papillomaviridae.
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/note="collected by cervical swab at the University of New
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CDS 1. .456
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/product="early transforming protein E6"
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/db_xref="GI:1098730"
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CINCKPLCEBKQRHLDKKRFHNRGRWGTGCMSCSSSRTRRETOL"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS Human papillomavirus type 16, isolate NM T529, early transforming
DEFINITION protein E6 (E6) gene, complete cds.
ACCESSION U34112
VERSION U34112.1 GI:1098729
KEYWORDS Human papillomavirus
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
VIRUSES; dsDNA viruses, no RNA stage; Papillomaviridae;
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CINCKPLCEBKQRHLDKKRFHNRGRWGTGCMSCSSSRTRRETOL"

unclassified Papillomaviridae.
REFERENCE 1 (bases 1 to 456)
AUTHORS Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildesheim,A.
and Jensen,S.A.
TITLE Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the
E6, E2, and L1 coding segments
J. Virol. 69 (12), 7743-7753 (1995)
JOURNAL 7494284
PUBMED 2 (bases 1 to 456)
REFERENCE Farmer,A.D.
AUTHORS Direct Submission
TITLE Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National
Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
Alamos, NM 87501, USA
JOURNAL Location/Qualifiers
FEATURES
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Mexico, New Mexico, United States."
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Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGGACACAGTGGCTTTGAC 21
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Db 337 CAGGACACAGTGGCTTTGAC 317

RESULT 32
HPV34113/c 456 bp DNA linear VRL 08-MAR-1996
LOCUS Human papillomavirus type 16, isolate OR 0198, early transforming
DEFINITION protein E6 (E6) gene, complete cds.
ACCESSION U34113
VERSION U34113.1 GI:1098731
KEYWORDS Human papillomavirus
SOURCE Human papillomavirus
ORGANISM Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
unclassified Papillomaviridae.
REFERENCE 1 (bases 1 to 456)
AUTHORS Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildesheim,A.
and Jensen,S.A.
TITLE Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the
E6, E2, and L1 coding segments
J. Virol. 69 (12), 7743-7753 (1995)
JOURNAL 7494284
PUBMED 2 (bases 1 to 456)
REFERENCE Farmer,A.D.
AUTHORS Direct Submission
TITLE Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National
Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
Alamos, NM 87501, USA
JOURNAL Location/Qualifiers
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Portland, Oregon, United States."
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CDS 1. .456
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Portland, Oregon, United States."
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Query Match 100.0%; Score 21; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGGACACAGTGGCTTTGAC 21
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Db 337 CAGGACACAGTGGCTTTGAC 317

RESULT 33
HPV34114/c 456 bp DNA linear VRL 08-MAR-1996
LOCUS Human papillomavirus type 16, isolate OR 1905, early transforming
DEFINITION protein E6 (E6) gene, complete cds.
ACCESSION U34114
VERSION U34114.1 GI:1098733
KEYWORDS Human papillomavirus
SOURCE Human papillomavirus
ORGANISM Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
unclassified Papillomaviridae.
REFERENCE 1 (bases 1 to 456)
AUTHORS Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildesheim,A.
and Jensen,S.A.
TITLE Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the
E6, E2, and L1 coding segments
J. Virol. 69 (12), 7743-7753 (1995)
JOURNAL 7494284
PUBMED 2 (bases 1 to 456)
REFERENCE Farmer,A.D.
AUTHORS Direct Submission
TITLE Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National
Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
Alamos, NM 87501, USA
JOURNAL Location/Qualifiers
FEATURES
source 1. .456
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Portland, Oregon, United States."
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ORIGIN
Query Match      100.0%; Score 21; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.3;
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QY
1 CAGACACAGTGGCTTTGAC 21
|||||
337 CAGACACAGTGGCTTTGAC 317

RESULT 34
HPU34115/c      456 bp      DNA      linear      VRL 08-MAR-1996
LOCUS
DEFINITION      Human papillomavirus type 16, isolate OR 2087, early transforming
ACCESSION
VERSION          U34115
KEYWORDS
SOURCE           Human papillomavirus
ORGANISM         Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
REFERENCE
AUTHORS          Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildesheim,A.
and Jenison,S.A.
TITLE            Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the
E6, E2, and L1 coding segments
JOURNAL          J. Virol. 69 (12), 7743-7753 (1995)
PUBMED
REFERENCES       2 (bases 1 to 456)
AUTHORS          Farmer A.D.
TITLE            Direct Submision
SUBMITTED (16-AUG-1995) Andrew D. Farmer, Los Alamos National
Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
Alamos, NM 87501, USA
LOCATION/Qualifiers
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/mol_type="genomic DNA"
/isolate="OR 2087"
/db_xref="taxon:10566"
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Portland, Oregon, United States."
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ORIGIN
Query Match      100.0%; Score 21; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 CAGACACAGTGGCTTTGAC 21
|||||
337 CAGACACAGTGGCTTTGAC 317

RESULT 35
HPU34116/c      456 bp      DNA      linear      VRL 08-MAR-1996
LOCUS
DEFINITION      Human papillomavirus type 16, isolate OR 3136, early transforming
protein E6 (E6) gene, complete cds.
ACCESSION
VERSION          U34116

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VERSION          U34116.1 GI:1098737
KEYWORDS
SOURCE           Human papillomavirus
ORGANISM         Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
REFERENCE
AUTHORS          Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildesheim,A.
and Jenison,S.A.
TITLE            Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the
E6, E2, and L1 coding segments
JOURNAL          J. Virol. 69 (12), 7743-7753 (1995)
PUBMED
REFERENCES       2 (bases 1 to 456)
AUTHORS          Farmer A.D.
TITLE            Direct Submision
SUBMITTED (16-AUG-1995) Andrew D. Farmer, Los Alamos National
Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
Alamos, NM 87501, USA
LOCATION/Qualifiers
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Portland, Oregon, United States."
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Query Match      100.0%; Score 21; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 CAGACACAGTGGCTTTGAC 21
|||||
337 CAGACACAGTGGCTTTGAC 317

RESULT 36
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LOCUS
DEFINITION      Human papillomavirus type 16, isolate OR 3473, early transforming
protein E6 (E6) gene, complete cds.
ACCESSION
VERSION          U34117
KEYWORDS
SOURCE           Human papillomavirus
ORGANISM         Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
REFERENCE
AUTHORS          Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildesheim,A.
and Jenison,S.A.
TITLE            Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the
E6, E2, and L1 coding segments
JOURNAL          J. Virol. 69 (12), 7743-7753 (1995)
PUBMED
REFERENCES       2 (bases 1 to 456)
AUTHORS          Farmer A.D.
TITLE            Direct Submision

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JOURNAL Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los Alamos, NM 87501, USA

FEATURES
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CINQKPLCEBKQRLDKKQRFNIRGWTGRCMSCRSSRTRERQL"

ORIGIN
Query Match 100.0%; Score 21; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.3; Mismatches 0; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGACACAGTGGCTTTGAC 21
|||||
337 CAGGACACAGTGGCTTTGAC 317

Db

RESULT 37
HPJ34118/c 456 bp DNA linear VRL 08-MAR-1996
LOCUS
DEFINITION Human papillomavirus type 16, isolate OR 3759, early transforming protein E6 (E6) gene, complete cds.
VERSION U34118.1 GI:1098741
KEYWORDS Human papillomavirus
SOURCE Human papillomavirus
ORGANISM
Virusess; dsDNA viruses, no RNA stage; Papillomaviridae;
unclassified Papillomaviridae.
1 (bases 1 to 456)
Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildeheim,A.
and Jenison,S.A.
Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the
E6, E2, and L1 coding segments
J. Virol. 69 (12), 7743-7753 (1995)
7494284
2 (bases 1 to 456)
Farmer,A.D.
Direct Submission
Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National
Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
Alamos, NM 87501, USA
location/Qualifiers
1. .456
/organism="Human papillomavirus"
/mol_type="genomic DNA"
/isolate="OR 3759"
/db_xref="taxon:10566"
/note="collected by cervical lavage at Kaiser Permanente,
Portland, Oregon, United States."
1. .456
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1. .456
/gene="E6"
/codon_start=1
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/gene="E6"
/codon_start=1
/product="early transforming protein E6"

CDS

/protein_id="AA91665.1"
/db_xref="GI:1098742"
/translation="MFQDPERPKLPDLCTELQTTIHDIILCEVCCKOQLRREYD
FARFDCIVRDGNPYAVCDKCKAFYSKISEYRYCYSLYGTTLEQYNNPCLDLIR
CINQKPLCEBKQRLDKKQRFNIRGWTGRCMSCRSSRTRERQL"

ORIGIN
Query Match 100.0%; Score 21; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.3; Mismatches 0; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGACACAGTGGCTTTGAC 21
|||||
337 CAGGACACAGTGGCTTTGAC 317

Db

RESULT 38
HPJ34119/c 456 bp DNA linear VRL 08-MAR-1996
LOCUS
DEFINITION Human papillomavirus type 16, isolate OR 4541, early transforming protein E6 (E6) gene, complete cds.
VERSION U34119.1 GI:1098743
KEYWORDS Human papillomavirus
SOURCE Human papillomavirus
ORGANISM
Virusess; dsDNA viruses, no RNA stage; Papillomaviridae;
unclassified Papillomaviridae.
1 (bases 1 to 456)
Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildeheim,A.
and Jenison,S.A.
Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the
E6, E2, and L1 coding segments
J. Virol. 69 (12), 7743-7753 (1995)
7494284
2 (bases 1 to 456)
Farmer,A.D.
Direct Submission
Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National
Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
Alamos, NM 87501, USA
location/Qualifiers
1. .456
/organism="Human papillomavirus"
/mol_type="genomic DNA"
/isolate="OR 4541"
/db_xref="taxon:10566"
/note="collected by cervical lavage at Kaiser Permanente,
Portland, Oregon, United States."
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/gene="E6"
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/gene="E6"
/codon_start=1
/product="early transforming protein E6"
/protein_id="AA91666.1"
/db_xref="GI:1098744"
/translation="MFQDPERPKLPDLCTELQTTIHDIILCEVCCKOQLRREYD
FARFDCIVRDGNPYAVCDKCKAFYSKISEYRYCYSLYGTTLEQYNNPCLDLIR
CINQKPLCEBKQRLDKKQRFNIRGWTGRCMSCRSSRTRERQL"

ORIGIN
Query Match 100.0%; Score 21; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.3; Mismatches 0; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGACACAGTGGCTTTGAC 21
|||||
337 CAGGACACAGTGGCTTTGAC 317

Db

RESULT 39

HPU34120/c 456 bp DNA linear VRL 08-MAR-1996
 LOCUS HPU34121/c
 DEFINITION Human papillomavirus type 16, isolate OR 4716, early transforming protein E6 (E6) gene, complete cds.
 ACCESSION U34120
 VERSION U34120.1 GI:1098745
 KEYWORDS Human papillomavirus
 SOURCE Human papillomavirus
 ORGANISM Human papillomavirus
 REFERENCES
 AUTHORS Yamaoka, T., Wheeler, C.M., Halpern, A.L., Stewart, A.C., Hildesheim, A. and Jenison, S.A.
 TITLE Human papillomavirus type 16 variant lineages in United States populations characterized by nucleotide sequence analysis of the E6, E2, and L1 coding segments
 JOURNAL J. Virol. 69 (12), 7743-7753 (1995)
 PUBMED 7494284
 REFERENCES
 AUTHORS Farmer, A.D.
 TITLE Direct Submission
 JOURNAL Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los Alamos, NM 87501, USA
 FEATURES
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 1..456
 /organism="Human papillomavirus"
 /mol_type="genomic DNA"
 /isolate="OR 4716"
 /db_xref="taxon:10566"
 /note="collected by cervical lavage at Kaiser Permanente, Portland, Oregon, United States."
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 /db_xref="GI:1098746"
 /translation="MFQDPQERPRKLPQCTELQTTIHILICVYCKQQLRREYD FAFRDLCIVRDGNPYAVCDCKLFYSKSEYHVCYSYGLTEQYNNPCLDILLIR CINQKPLCPBEKQRHLDKQRFHNRGWTGRCMCCRSSRTRRETOL"
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 Query Match 100.0%; Score 21; DB 10; Length 456;
 Best Local Similarity 100.0%; Pred. No. 0.3;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 CAGACACAGTGGCTTTGAC 21
 Db 337 CAGACACAGTGGCTTTGAC 317
 RESULT 40
 HPU34121 456 bp DNA linear VRL 08-MAR-1996
 LOCUS HPU34121/c
 DEFINITION Human papillomavirus type 16, isolate OR 4724, early transforming protein E6 (E6) gene, complete cds.
 ACCESSION U34121
 VERSION U34121.1 GI:1098747
 KEYWORDS Human papillomavirus
 SOURCE Human papillomavirus
 ORGANISM Human papillomavirus
 REFERENCES
 AUTHORS Yamaoka, T., Wheeler, C.M., Halpern, A.L., Stewart, A.C., Hildesheim, A. and Jenison, S.A.
 TITLE Human papillomavirus type 16 variant lineages in United States populations characterized by nucleotide sequence analysis of the E6, E2, and L1 coding segments

JOURNAL J. Virol. 69 (12), 7743-7753 (1995)
 PUBMED 7494284
 REFERENCES
 AUTHORS Farmer, A.D.
 TITLE Direct Submission
 JOURNAL Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los Alamos, NM 87501, USA
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 /db_xref="taxon:10566"
 /note="collected by cervical lavage at Kaiser Permanente, Portland, Oregon, United States."
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 /product="early transforming protein E6"
 /protein_id="AA91668.1"
 /db_xref="GI:1098748"
 /translation="MFQDPQERPRKLPQCTELQTTIHILICVYCKQQLRREYD FAFRDLCIVRDGNPYAVCDCKLFYSKSEYHVCYSYGLTEQYNNPCLDILLIR CINQKPLCPBEKQRHLDKQRFHNRGWTGRCMCCRSSRTRRETOL"
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 Query Match 100.0%; Score 21; DB 10; Length 456;
 Best Local Similarity 100.0%; Pred. No. 0.3;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 CAGACACAGTGGCTTTGAC 21
 Db 337 CAGACACAGTGGCTTTGAC 317
 RESULT 41
 HPU34122/c 456 bp DNA linear VRL 08-MAR-1996
 LOCUS HPU34122/c
 DEFINITION Human papillomavirus type 16, isolate OR 4997, early transforming protein E6 (E6) gene, complete cds.
 ACCESSION U34122
 VERSION U34122.1 GI:1098749
 KEYWORDS Human papillomavirus
 SOURCE Human papillomavirus
 ORGANISM Human papillomavirus
 REFERENCES
 AUTHORS Yamaoka, T., Wheeler, C.M., Halpern, A.L., Stewart, A.C., Hildesheim, A. and Jenison, S.A.
 TITLE Human papillomavirus type 16 variant lineages in United States populations characterized by nucleotide sequence analysis of the E6, E2, and L1 coding segments
 JOURNAL J. Virol. 69 (12), 7743-7753 (1995)
 PUBMED 7494284
 REFERENCES
 AUTHORS Farmer, A.D.
 TITLE Direct Submission
 JOURNAL Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los Alamos, NM 87501, USA
 FEATURES
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 1..456
 /organism="Human papillomavirus"
 /mol_type="genomic DNA"
 /isolate="OR 4997"
 /db_xref="taxon:10566"
 /note="collected by cervical lavage at Kaiser Permanente, Portland, Oregon, United States."
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 /gene="E6"
 /codon_start=1
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 /protein_id="AA91669.1"
 /db_xref="GI:1098749"
 /translation="MFQDPQERPRKLPQCTELQTTIHILICVYCKQQLRREYD FAFRDLCIVRDGNPYAVCDCKLFYSKSEYHVCYSYGLTEQYNNPCLDILLIR CINQKPLCPBEKQRHLDKQRFHNRGWTGRCMCCRSSRTRRETOL"
 ORIGIN
 Query Match 100.0%; Score 21; DB 10; Length 456;
 Best Local Similarity 100.0%; Pred. No. 0.3;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 CAGACACAGTGGCTTTGAC 21
 Db 337 CAGACACAGTGGCTTTGAC 317

CDS

/gene="E6"
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/db_xref="GI:1098750"
/translation="MFODPQERPRKLPOLCTELQTTIHILICVCYCKQQLRREYVD
FARFDLCIVRDGNPYAVCDKCKFKYSKISEYHYCYSLYGTLEQYNNPCLDILLR
CINCKQPLCEBEKQRIHDKKQRFHNIRGRWTRGCMSCRSRRTRRETOL"

ORIGIN

Query Match 100.0%; Score 21; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGACACAGTGGCTTTGAC 21
337 CAGGACACAGTGGCTTTGAC 317

RESULT 42
HPU34123/c 456 bp DNA linear VRL 08-MAR-1996
LOCUS Human papillomavirus type 16, isolate OR 5110, early transforming
DEFINITION protein E6 (E6) gene, complete cds.
ACCESSION U34123.1 GI:1098751
VERSION
KEYWORDS
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
VIRUSES; dsDNA viruses, no RNA stage; Papillomaviridae;
unclassified Papillomaviridae.
REFERENCE 1 (bases 1 to 456)
AUTHORS Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildeheim,A.
and Jenison,S.A.
TITLE Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the
E6, E2, and L1 coding segments
J. Virol. 69 (12), 7743-7753 (1995)

JOURNAL
PUBMED 7494284
REFERENCE 2 (bases 1 to 456)
AUTHORS Farmer,A.D.
TITLE Direct Submission
SUBMITTED (16-AUG-1995) Andrew D. Farmer, Los Alamos National
Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
Alamos, NM 87501, USA
LOCATION/Qualifiers
1..456
/organism="Human papillomavirus"
/mol_type="genomic DNA"
/isolate="OR 5110"
/db_xref="taxon:10566"
/note="collected by cervical lavage at Kaiser Permanente,
Portland, Oregon, United States."
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/gene="E6"
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/gene="E6"
/codon_start=1
/product="early transforming protein E6"
/protein_id="AA91670.1"
/db_xref="GI:1098752"
/translation="MFODPQERPRKLPOLCTELQTTIHILICVCYCKQQLRREYVD
FARFDLCIVRDGNPYAVCDKCKFKYSKISEYHYCYSLYGTLEQYNNPCLDILLR
CINCKQPLCEBEKQRIHDKKQRFHNIRGRWTRGCMSCRSRRTRRETOL"

ORIGIN

Query Match 100.0%; Score 21; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGACACAGTGGCTTTGAC 21
1 CAGGACACAGTGGCTTTGAC 21

Db 337 CAGGACACAGTGGCTTTGAC 317

RESULT 43
HPU34124/c 456 bp DNA linear VRL 08-MAR-1996
LOCUS Human papillomavirus type 16, isolate OR 5428, early transforming
DEFINITION protein E6 (E6) gene, complete cds.
ACCESSION U34124.1 GI:1098753
VERSION
KEYWORDS
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
VIRUSES; dsDNA viruses, no RNA stage; Papillomaviridae;
unclassified Papillomaviridae.
REFERENCE 1 (bases 1 to 456)
AUTHORS Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildeheim,A.
and Jenison,S.A.
TITLE Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the
E6, E2, and L1 coding segments
J. Virol. 69 (12), 7743-7753 (1995)

JOURNAL
PUBMED 7494284
REFERENCE 2 (bases 1 to 456)
AUTHORS Farmer,A.D.
TITLE Direct Submission
SUBMITTED (16-AUG-1995) Andrew D. Farmer, Los Alamos National
Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
Alamos, NM 87501, USA
LOCATION/Qualifiers
1..456
/organism="Human papillomavirus"
/mol_type="genomic DNA"
/isolate="OR 5428"
/db_xref="taxon:10566"
/note="collected by cervical lavage at Kaiser Permanente,
Portland, Oregon, United States."
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/db_xref="GI:1098754"
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FARFDLCIVRDGNPYAVCDKCKFKYSKISEYHYCYSLYGTLEQYNNPCLDILLR
CINCKQPLCEBEKQRIHDKKQRFHNIRGRWTRGCMSCRSRRTRRETOL"

ORIGIN

Query Match 100.0%; Score 21; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGACACAGTGGCTTTGAC 21
337 CAGGACACAGTGGCTTTGAC 317

RESULT 44
HPU34125/c 456 bp DNA linear VRL 08-MAR-1996
LOCUS Human papillomavirus type 16, isolate OR 6106, early transforming
DEFINITION protein E6 (E6) gene, complete cds.
ACCESSION U34125.1 GI:1098755
VERSION
KEYWORDS
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
VIRUSES; dsDNA viruses, no RNA stage; Papillomaviridae;
unclassified Papillomaviridae.
REFERENCE 1 (bases 1 to 456)

AUTHORS Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildesheim,A.
and Jenison,S.A.
TITLE Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the
E6, E2, and L1 coding segments
J. Virol. 69 (12), 7743-7753 (1995)
JOURNAL
PUBMED 7494284
REFERENCE 2 (bases 1 to 456)
AUTHORS Farmer A.D.
TITLE Direct Submision
Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National
Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
Alamos, NM 87501, USA
FEATURES
source
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/isolate="OR 6106"
/db_xref="taxon:10566"
/note="collected by cervical lavage at Kaiser Permanente,
Portland, Oregon, United States."
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/gene="E6"
/codon_start=1
/product="early transforming protein E6"
/protein_id="AA91672.1"
/db_xref="GI:1098756"
/translation="MFQDPERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYD
FAFRDLCIVRDGNPYAVCDKCLKFYSKISEYHYCYSLYGTLLBOQYKPKLDDLIR
CINQKPLCPBEKQRLDKQRFHNRGWTGRCMSCSSRRTRRTQ."

Query Match 100.0%; Score 21; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGACACAGTGGCTTTGAC 21
Db 337 CAGGACACAGTGGCTTTGAC 317

RESULT 45
HPV34126/c 456 bp DNA linear VRL 08-MAR-1996
LOCUS Human papillomavirus type 16, isolate OR 6170, early transforming
DEFINITION protein E6 (E6) gene, complete cds.
ACCESSION U34126
VERSION U34126.1 GI:1098757
KEYWORDS
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
VIRUSES; deDNA viruses, no RNA stage; Papillomaviridae;
unclassified Papillomaviridae.
REFERENCE 1 (bases 1 to 456)
AUTHORS Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildesheim,A.
and Jenison,S.A.
TITLE Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the
E6, E2, and L1 coding segments
J. Virol. 69 (12), 7743-7753 (1995)
JOURNAL
PUBMED 7494284
REFERENCE 2 (bases 1 to 456)
AUTHORS Farmer,A.D.
TITLE Direct Submision
Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National
Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
Alamos, NM 87501, USA
FEATURES
source
1..456
/organism="Human papillomavirus"
/mol_type="genomic DNA"
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/db_xref="taxon:10566"
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Portland, Oregon, United States."
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/gene="E6"
/codon_start=1
/product="early transforming protein E6"
/protein_id="AA91674.1"
/db_xref="GI:1098760"
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FAFRDLCIVRDGNPYAVCDKCLKFYSKISEYHYCYSLYGTLLBOQYKPKLDDLIR
CINQKPLCPBEKQRLDKQRFHNRGWTGRCMSCSSRRTRRTQ."

Query Match 100.0%; Score 21; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGACACAGTGGCTTTGAC 21
Db 337 CAGGACACAGTGGCTTTGAC 317

RESULT 46
HPV34127/c 456 bp DNA linear VRL 08-MAR-1996
LOCUS Human papillomavirus type 16, isolate OR 6311, early transforming
DEFINITION protein E6 (E6) gene, complete cds.
ACCESSION U34127
VERSION U34127.1 GI:1098759
KEYWORDS
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
VIRUSES; deDNA viruses, no RNA stage; Papillomaviridae;
unclassified Papillomaviridae.
REFERENCE 1 (bases 1 to 456)
AUTHORS Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildesheim,A.
and Jenison,S.A.
TITLE Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the
E6, E2, and L1 coding segments
J. Virol. 69 (12), 7743-7753 (1995)
JOURNAL
PUBMED 7494284
REFERENCE 2 (bases 1 to 456)
AUTHORS Farmer,A.D.
TITLE Direct Submision
Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National
Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
Alamos, NM 87501, USA
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/mol_type="genomic DNA"
/isolate="OR 6311"
/db_xref="taxon:10566"
/note="collected by cervical lavage at Kaiser Permanente,
Portland, Oregon, United States."
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/codon_start=1
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FAFRDLCIVRDGNPYAVCDKCLKFYSKISEYHYCYSLYGTLLBOQYKPKLDDLIR
CINQKPLCPBEKQRLDKQRFHNRGWTGRCMSCSSRRTRRTQ."

QY 1 CAGGACACAGTGGCTTTGAC 21
Db 337 CAGGACACAGTGGCTTTGAC 317

RESULT 46
HPV34127/c 456 bp DNA linear VRL 08-MAR-1996
LOCUS Human papillomavirus type 16, isolate OR 6311, early transforming
DEFINITION protein E6 (E6) gene, complete cds.
ACCESSION U34127
VERSION U34127.1 GI:1098759
KEYWORDS
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
VIRUSES; deDNA viruses, no RNA stage; Papillomaviridae;
unclassified Papillomaviridae.
REFERENCE 1 (bases 1 to 456)
AUTHORS Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildesheim,A.
and Jenison,S.A.
TITLE Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the
E6, E2, and L1 coding segments
J. Virol. 69 (12), 7743-7753 (1995)
JOURNAL
PUBMED 7494284
REFERENCE 2 (bases 1 to 456)
AUTHORS Farmer,A.D.
TITLE Direct Submision
Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National
Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
Alamos, NM 87501, USA
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/organism="Human papillomavirus"
/mol_type="genomic DNA"
/isolate="OR 6311"
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/note="collected by cervical lavage at Kaiser Permanente,
Portland, Oregon, United States."
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/product="early transforming protein E6"
/protein_id="AA91674.1"
/db_xref="GI:1098760"
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FAFRDLCIVRDGNPYAVCDKCLKFYSKISEYHYCYSLYGTLLBOQYKPKLDDLIR
CINQKPLCPBEKQRLDKQRFHNRGWTGRCMSCSSRRTRRTQ."

Query Match 100.0%; Score 21; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGACACAGTGGCTTTGAC 21
Db 337 CAGGACACAGTGGCTTTGAC 317

RESULT 46
HPV34127/c 456 bp DNA linear VRL 08-MAR-1996
LOCUS Human papillomavirus type 16, isolate OR 6311, early transforming
DEFINITION protein E6 (E6) gene, complete cds.
ACCESSION U34127
VERSION U34127.1 GI:1098759
KEYWORDS
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
VIRUSES; deDNA viruses, no RNA stage; Papillomaviridae;
unclassified Papillomaviridae.
REFERENCE 1 (bases 1 to 456)
AUTHORS Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildesheim,A.
and Jenison,S.A.
TITLE Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the
E6, E2, and L1 coding segments
J. Virol. 69 (12), 7743-7753 (1995)
JOURNAL
PUBMED 7494284
REFERENCE 2 (bases 1 to 456)
AUTHORS Farmer,A.D.
TITLE Direct Submision
Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National
Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
Alamos, NM 87501, USA
FEATURES
source
1..456
/organism="Human papillomavirus"
/mol_type="genomic DNA"
/isolate="OR 6311"
/db_xref="taxon:10566"
/note="collected by cervical lavage at Kaiser Permanente,
Portland, Oregon, United States."
1..456
/gene="E6"
/codon_start=1
/product="early transforming protein E6"
/protein_id="AA91674.1"
/db_xref="GI:1098760"
/translation="MFQDPERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYD
FAFRDLCIVRDGNPYAVCDKCLKFYSKISEYHYCYSLYGTLLBOQYKPKLDDLIR
CINQKPLCPBEKQRLDKQRFHNRGWTGRCMSCSSRRTRRTQ."

Query Match 100.0%; Score 21; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGACACAGTGGCTTTGAC 21
Db 337 CAGGACACAGTGGCTTTGAC 317

RESULT 46
HPV34127/c 456 bp DNA linear VRL 08-MAR-1996
LOCUS Human papillomavirus type 16, isolate OR 6311, early transforming
DEFINITION protein E6 (E6) gene, complete cds.
ACCESSION U34127
VERSION U34127.1 GI:1098759
KEYWORDS
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
VIRUSES; deDNA viruses, no RNA stage; Papillomaviridae;
unclassified Papillomaviridae.
REFERENCE 1 (bases 1 to 456)
AUTHORS Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildesheim,A.
and Jenison,S.A.
TITLE Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the
E6, E2, and L1 coding segments
J. Virol. 69 (12), 7743-7753 (1995)
JOURNAL
PUBMED 7494284
REFERENCE 2 (bases 1 to 456)
AUTHORS Farmer,A.D.
TITLE Direct Submision
Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National
Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
Alamos, NM 87501, USA
FEATURES
source
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/organism="Human papillomavirus"
/mol_type="genomic DNA"
/isolate="OR 6311"
/db_xref="taxon:10566"
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Query Match 100.0%; Score 21; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGGACACAGTGGCTTTTGAC 21
Db 337 CAGGACACAGTGGCTTTTGAC 317

RESULT 47
HPU34128/c 456 bp DNA linear VRL 08-MAR-1996
LOCUS
DEFINITION Human papillomavirus type 16, isolate OR 7145, early transforming protein E6 (E6) gene, complete cds.
ACCESSION U34128
KEYWORDS
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
REFERENCE 1 (bases 1 to 456)
AUTHORS Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildeheim,A. and Jenison,S.A.
TITLE Human papillomavirus type 16 variant lineages in United States populations characterized by nucleotide sequence analysis of the E6, E2, and L1 coding segments
J. Virol. 69 (12), 7743-7753 (1995)

JOURNAL PUBLISHED 7494284
REFERENCE 2 (bases 1 to 456)
AUTHORS Farmer,A.D.
TITLE Direct Submission
JOURNAL Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los Alamos, NM 87501, USA
LOCATION/Qualifiers
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Query Match 100.0%; Score 21; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGGACACAGTGGCTTTTGAC 21
Db 337 CAGGACACAGTGGCTTTTGAC 317

RESULT 48
HPU34129/c 456 bp DNA linear VRL 08-MAR-1996
LOCUS
DEFINITION Human papillomavirus type 16, isolate OR 7574, early transforming protein E6 (E6) gene, complete cds.
ACCESSION U34129
KEYWORDS
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
REFERENCE 1 (bases 1 to 456)
AUTHORS Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildeheim,A. and Jenison,S.A.
TITLE Human papillomavirus type 16 variant lineages in United States populations characterized by nucleotide sequence analysis of the E6, E2, and L1 coding segments
J. Virol. 69 (12), 7743-7753 (1995)

JOURNAL PUBLISHED 7494284
REFERENCE 2 (bases 1 to 456)
AUTHORS Farmer,A.D.
TITLE Direct Submission
JOURNAL Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los Alamos, NM 87501, USA
LOCATION/Qualifiers
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/organism="Human papillomavirus"
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SOURCE Human papillomavirus
ORGANISM Human papillomavirus
REFERENCE 1 (bases 1 to 456)
AUTHORS Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildeheim,A. and Jenison,S.A.
TITLE Human papillomavirus type 16 variant lineages in United States populations characterized by nucleotide sequence analysis of the E6, E2, and L1 coding segments
J. Virol. 69 (12), 7743-7753 (1995)

JOURNAL PUBLISHED 7494284
REFERENCE 2 (bases 1 to 456)
AUTHORS Farmer,A.D.
TITLE Direct Submission
JOURNAL Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los Alamos, NM 87501, USA
LOCATION/Qualifiers
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/organism="Human papillomavirus"
/mol_type="genomic DNA"
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Query Match 100.0%; Score 21; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGGACACAGTGGCTTTTGAC 21
Db 337 CAGGACACAGTGGCTTTTGAC 317

RESULT 49
HPU34130/c 456 bp DNA linear VRL 08-MAR-1996
LOCUS
DEFINITION Human papillomavirus type 16, isolate OR 7587, early transforming protein E6 (E6) gene, complete cds.
ACCESSION U34130
KEYWORDS
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
REFERENCE 1 (bases 1 to 456)
AUTHORS Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildeheim,A. and Jenison,S.A.
TITLE Human papillomavirus type 16 variant lineages in United States populations characterized by nucleotide sequence analysis of the E6, E2, and L1 coding segments
J. Virol. 69 (12), 7743-7753 (1995)

JOURNAL PUBLISHED 7494284
REFERENCE 2 (bases 1 to 456)
AUTHORS Farmer,A.D.
TITLE Direct Submission
JOURNAL Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los Alamos, NM 87501, USA
LOCATION/Qualifiers
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/organism="Human papillomavirus"
/mol_type="genomic DNA"
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/db_xref="taxon:10566"
/note="collected by cervical lavage at Kaiser Permanente, Portland, Oregon, United States."
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/protein_id="AA91677.1"
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FEATURES Alamos, NM 87501, USA
Location/Qualifiers
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Portland, Oregon, United States."
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ORIGIN

Query Match 100.0%; Score 21; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGACACAGTGGCTTTGAC 21
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Db 337 CAGACACAGTGGCTTTGAC 317

RESULT 50
HPV34131/c 456 bp DNA linear VRL 08-MAR-1996
LOCUS Human papillomavirus type 16, isolate OR 7632, early transforming
DEFINITION protein E6 (E6) gene, complete cds.
ACCESSION U34131
VERSION U34131.1 GI:1098767
KEYWORDS
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
unclassified Papillomaviridae.
1 (bases 1 to 456)
Yamada,T., Wheeler,C.M., Halpern,A.L., Stewart,A.C., Hildesheim,A.
and Jensen,S.A.
Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the
E6, E2, and L1 coding segments
J. Virol. 69 (12), 7743-7753 (1995)
7494284
2 (bases 1 to 456)
Farmer,A.D.
Direct Submission
Submitted (16-AUG-1995) Andrew D. Farmer, Los Alamos National
Laboratory, HIV Sequence Database, T-10, Mail Stop K710, Los
Alamos, NM 87501, USA
Location/Qualifiers
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/mol_type="genomic DNA"
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/db_xref="taxon:10566"
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Portland, Oregon, United States."
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/codon_start=1
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/protein_id="AA91678.1"
/db_xref="GI:1098768"

gene
CDS

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CINCKPLCPBEKQRLDKKQRFHNRGHWGRCMSCCRSSRTRETOL"

ORIGIN

Query Match 100.0%; Score 21; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGACACAGTGGCTTTGAC 21
|||||
Db 337 CAGACACAGTGGCTTTGAC 317

Search completed: May 24, 2006, 06:54:50
Job time : 698.284 secs

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2006, 05:46:37 ; Search time 972.624 Seconds
(without alignments)
2103.915 Million cell updates/sec

Title: US-10-601-913-121

Perfect score: 32
Sequence: 1 TTATTATTAAGGCGCGCGGTGCCAAGAAC 32

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

GenEmbl:*
1: gb env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_ay:*
9: gb_un:*
10: gb_vl:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_da:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	32	100.0	32	2	AR349181	AR349181 Sequence	
2	32	100.0	32	2	AR349182	AR349182 Sequence	
3	32	100.0	32	2	AR349183	AR349183 Sequence	
4	32	100.0	32	2	AR349184	AR349184 Sequence	
5	32	100.0	476	2	AR080321	AR080321 Sequence	
6	32	100.0	476	2	AR085249	AR085249 Sequence	
7	32	100.0	477	2	CS113238	CS113238 Sequence	
8	32	100.0	528	10	PAHPV181	X05568 Integrated	
9	32	100.0	817	2	188814	188814 Sequence	
10	32	100.0	837	2	A98759	A98759 Sequence	
11	32	100.0	837	2	BD080320	BD080320 Vaccine.	
12	32	100.0	837	2	BD103169	BD103169 Vaccine.	
13	32	100.0	837	2	AR183581	AR183581 Sequence	
14	32	100.0	837	2	AX020943	AX020943 Sequence	
15	32	100.0	843	10	HPV18491	Y18491 Human papilloma	
16	32	100.0	912	10	PPH18A	M26798 Human papilloma	
17	32	100.0	1000	2	A06328	A06328 HPV18 mRNA	
18	32	100.0	1000	2	A07621	A07621 Amplified sequence	

19	32	100.0	1152	2	A98761	A98761 Sequence 22
20	32	100.0	1152	2	BD080321	BD080321 Vaccine.
21	32	100.0	1152	2	BD103170	BD103170 Vaccine.
22	32	100.0	1152	2	AR183582	AR183582 Sequence
23	32	100.0	1152	2	AX020945	AX020945 Sequence
24	32	100.0	1152	2	BD015779	BD015779 Method fo
25	32	100.0	1188	2	ES4157	ES4157 Method for
26	32	100.0	1188	10	PARHPV6	X04354 Human papil
27	32	100.0	1750	2	A06324	A06324 HPV18 genes
28	32	100.0	1750	10	PAHPV18E	X04773 Human papil
29	32	100.0	3135	10	HDMHIEB	M20325 Human papil
30	32	100.0	5210	2	HPU89349	U89349 Human papil
31	32	100.0	7857	10	CS073239	CS073239 Sequence
32	32	100.0	7857	10	AY262282	AY262282 Human pap
33	32	100.0	7857	10	PAHPV18	X05015 Human papil
34	32	95.0	910	10	HPV45BE67	Y13218 Human papil
35	30.4	95.0	1843	10	PPH45E67A	M38198 Human papil
36	30.4	95.0	7858	10	HPV45	X74479 Human papil
37	30.4	95.0	8039	5	HS242956	AJ242956 Homo sapi
38	24.6	76.9	866	6	MUSRP	M85235 Mus musculu
39	24.2	75.6	1225	5	BC056907	BC056907 Homo sapi
40	24.2	75.6	1300	10	HDMHIEA	M20324 Human papil
41	24	75.0	1095	2	AR084350	AR084350 Sequence
42	24	75.0	1108	2	AR084344	AR084344 Sequence
43	24	75.0	1110	2	AR084343	AR084343 Sequence
44	24	75.0	1313	10	AR084345	AR084345 Sequence
45	24	75.0	3283	2	AR084352	X67150 Human papil
46	24	75.0	3283	10	HPV22461	U22461 Human papil
47	24	75.0	3283	10	HPV22461	Y14591 Viral-cellu
48	24	75.0	4618	10	HSFUSION	M73258 Human cellu
49	24	75.0	6042	10	HDMHPVME18	DO080079 Human pap
50	24	75.0	7822	2	DO080079	DO080079 Human pap
51	24	75.0	7833	2	160253	160253 Sequence 9
52	24	75.0	7833	2	164482	164482 Sequence 9
53	24	75.0	7833	10	PPH139	M62849 Human papil
54	24	75.0	7905	2	CS073246	CS073246 Sequence
55	24	75.0	7905	10	HPV21941	U21941 Human papil
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57	23.8	74.4	778	6	RATRP17	M17422 Rat ribosom
58	23.8	74.4	836	11	BX933673	BX933673 Gallus ga
59	23.8	74.4	836	11	BX935217	BX935217 Gallus ga
60	23.8	74.4	836	11	BX936251	BX936251 Gallus ga
61	23.8	74.4	885	2	AX552259	AX552259 Sequence
62	23.8	74.4	221962	12	AC136580	AC136580 Rattus no
63	23.6	73.8	16099	5	AL589786	AL589786 Human DNA
64	23.6	73.8	161632	12	AC053508	AC053508 Homo sapi
65	23.6	73.8	183118	12	AL355528	AL355528 Homo sapi
66	23.6	73.8	183118	5	AL450108	AL450108 Human DNA
67	23	71.9	30	2	AR077014	AR077014 Sequence
68	23	71.9	30	2	AR099824	AR099824 Sequence
69	23	71.9	30	2	AR142235	AR142235 Sequence
70	23	71.9	30	2	134496	134496 Sequence 5
71	23	71.9	30	2	157331	157331 Sequence 5
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73	23	71.9	7759	10	HPV37488	U37488 Human papil
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77	22.4	70.0	137036	15	AJ698720	AJ698720 Yersinia
78	22.4	70.0	172732	6	AC113039	AC113039 Mus muscu
79	22.4	70.0	174313	12	AC165234	AC165234 Mus muscu
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82	22.2	69.4	207	2	C0715203	C0715203 Sequence
83	22.2	69.4	460	2	C0049241	C0049241 Sequence
84	22.2	69.4	460	2	C0064262	C0064262 Sequence
85	22.2	69.4	460	2	C0091202	C0091202 Sequence
86	22.2	69.4	460	2	C0130040	C0130040 Sequence
87	22.2	69.4	460	2	C0168659	C0168659 Sequence
88	22.2	69.4	460	2	C0197782	C0197782 Sequence
89	22.2	69.4	460	2	C0213224	C0213224 Sequence
90	22.2	69.4	460	2	C0251803	C0251803 Sequence
91	22.2	69.4	460	2	C0288957	C0288957 Sequence

92	22.2	69.4	460	2	CQ325963	Sequence	c 165	22	68.8	51	2	AX803129
93	22.2	69.4	581	2	CS211030	Sequence	c 166	22	68.8	650	2	CQ671722
94	22.2	69.4	581	2	CS214672	Sequence	c 167	22	68.8	13338	12	AC153776
95	22.2	69.4	659	2	AX552261	Sequence	c 168	21.6	67.5	120782	12	AC144505
96	22.2	69.4	741	2	CQ732742	Sequence	c 169	21.4	66.9	7717	10	G77890
97	22.2	69.4	750	2	CQ054321	Sequence	c 170	21.4	66.9	7717	7	AF36129
98	22.2	69.4	750	2	CQ073558	Sequence	c 171	21.4	66.9	180764	12	AC160487
99	22.2	69.4	750	2	CQ104440	Sequence	c 172	21.4	66.9	186611	6	AC119215
100	22.2	69.4	750	2	CQ143159	Sequence	c 173	21.4	66.9	193136	12	AC095585
101	22.2	69.4	750	2	CQ178644	Sequence	c 174	21.4	66.9	220936	12	AC164869
102	22.2	69.4	750	2	CQ020993	Sequence	c 175	21.4	66.9	222448	12	AC161085
103	22.2	69.4	750	2	CQ226340	Sequence	c 176	21.4	66.9	246551	12	AC096478
104	22.2	69.4	750	2	CQ264482	Sequence	c 177	21.4	66.9	249620	6	AC161484
105	22.2	69.4	750	2	CQ301577	Sequence	c 178	21.4	66.9	252524	12	AC114081
106	22.2	69.4	824	2	CQ338792	Sequence	c 179	21.4	66.9	269435	12	AC167349
107	22.2	69.4	845	5	CQ716065	Sequence	c 180	21.4	66.9	269435	12	AC167349
108	22.2	69.4	845	5	AB169738	Macaca fa	c 181	21.2	66.2	123	2	CQ080989
109	22.2	69.4	1023	2	CQ490614	Sequence	c 182	21.2	66.2	123	2	CQ115474
110	22.2	69.4	1023	2	CQ493111	Sequence	c 183	21.2	66.2	123	2	CQ154282
111	22.2	69.4	1023	2	CQ493249	Sequence	c 184	21.2	66.2	123	2	CQ186859
112	22.2	69.4	1023	2	CQ493345	Sequence	c 185	21.2	66.2	123	2	CQ237529
113	22.2	69.4	1023	2	CQ493672	Sequence	c 186	21.2	66.2	123	2	CQ275152
114	22.2	69.4	1023	2	CQ493995	Sequence	c 187	21.2	66.2	123	2	CQ312126
115	22.2	69.4	1023	2	CQ496449	Sequence	c 188	21.2	66.2	123	2	CQ349522
116	22.2	69.4	1030	14	BT021516	Sequence	c 189	21.2	66.2	354	2	CQ734529
117	22.2	69.4	1033	12	AC126748	Sequence	c 190	21.2	66.2	380	2	CQ676372
118	22.2	69.4	1033	12	AC158317	Homo sapi	c 191	21.2	66.2	598	2	CQ071784
119	22.2	69.4	38703	5	AC000031	Homo sapi	c 192	21.2	66.2	598	2	CQ102405
120	22.2	69.4	44422	12	AC146400	Pan trogl	c 193	21.2	66.2	598	2	CQ141332
121	22.2	69.4	99766	12	AL153702	Homo sapi	c 194	21.2	66.2	598	2	CQ176982
122	22.2	69.4	103186	5	AL158218	Human DNA	c 195	21.2	66.2	598	2	CQ224613
123	22.2	69.4	106735	12	AC011381	Homo sapi	c 196	21.2	66.2	598	2	CQ262631
124	22.2	69.4	110000	12	AC106662_1	Continuation (2 of	c 197	21.2	66.2	598	2	CQ299688
125	22.2	69.4	112911	5	AL155310	Continuation (3 of	c 198	21.2	66.2	598	2	CQ336842
126	22.2	69.4	126807	5	HS391022	Human DNA	c 199	21.2	66.2	123169	5	AC008771
127	22.2	69.4	126807	5	HS391022	Human DNA	c 200	21.2	66.2	126052	5	AC018764
128	22.2	69.4	132764	5	AC073842	Homo sapi	c 201	21.2	66.2	130117	5	AC004907
129	22.2	69.4	145294	12	AC009856	Homo sapi	c 202	21.2	66.2	167684	12	AC027303
130	22.2	69.4	146224	5	AC005883	Homo sapi	c 203	21.2	66.2	181226	5	AC012312
131	22.2	69.4	160439	5	AC005345	Homo sapi	c 204	21.2	66.2	184598	5	AL139406
132	22.2	69.4	163332	5	AC004821	Homo sapi	c 205	21.2	66.2	194874	12	AC080090
133	22.2	69.4	164702	2	AX706960	Sequence	c 206	21.2	66.2	246164	12	AC098751
134	22.2	69.4	164702	2	AX707890	Sequence	c 207	21.2	66.2	253402	5	AC008534
135	22.2	69.4	167854	12	AC092483	Homo sapi	c 208	21.2	66.2	263827	12	AC094579
136	22.2	69.4	170819	12	AC092483	Homo sapi	c 209	21.2	66.2	322972	12	AC129853
137	22.2	69.4	172043	12	AC055750	Homo sapi	c 210	21	65.6	22	2	AR349169
138	22.2	69.4	175281	5	AC092859	Homo sapi	c 211	21	65.6	22	2	AR349170
139	22.2	69.4	175281	5	AC092859	Homo sapi	c 212	21	65.6	22	2	AR349171
140	22.2	69.4	175794	5	AC147031	Pan trogl	c 213	21	65.6	22	2	AR349172
141	22.2	69.4	179583	12	AC011931	Homo sapi	c 214	21	65.6	420	2	CQ471329
142	22.2	69.4	179583	12	AC078994	Homo sapi	c 215	21	65.6	55677	12	AC154949
143	22.2	69.4	182256	5	AC005058	Homo sapi	c 216	21	65.6	110000	4	AP008207
144	22.2	69.4	183155	5	AC073021	Homo sapi	c 217	21	65.6	151630	12	AC169467
145	22.2	69.4	188167	12	AC068983	Homo sapi	c 218	21	65.6	171849	12	AC175179
146	22.2	69.4	189863	12	AC027463	Homo sapi	c 219	21	65.6	181997	12	AC165359
147	22.2	69.4	193986	12	AC130783	Pan trogl	c 220	21	65.6	182709	12	AC148374
148	22.2	69.4	197252	12	AC170498	Bos tauri	c 221	21	65.6	188707	12	AC162039
149	22.2	69.4	197360	5	AC117401	Homo sapi	c 222	21	65.6	190659	12	AC170342
150	22.2	69.4	200536	5	AL156093	Human DNA	c 223	21	65.6	191022	4	AP003431
151	22.2	69.4	208310	12	AC166382	Bos tauri	c 224	21	65.6	222962	12	AC160677
152	22.2	69.4	213601	12	AC165037	Bos tauri	c 225	21	65.6	230115	12	AC095927
153	22.2	69.4	224862	12	AC125660	Rattus no	c 226	21	65.6	237025	12	AC149690
154	22.2	69.4	229155	5	AC018755	Homo sapi	c 227	20.8	65.0	757	6	MUSRPL7R
155	22.2	69.4	237165	6	AC167216	Bos tauri	c 228	20.8	65.0	899	6	BC096452
156	22.2	69.4	237532	12	AC094950	Rattus no	c 229	20.8	65.0	906	6	BC025909
157	22.2	69.4	240792	12	AC130623	Rattus no	c 230	20.8	65.0	915	6	BC051261
158	22.2	69.4	247475	12	AC008247	Homo sapi	c 231	20.8	65.0	962	6	BC086786
159	22.2	69.4	251835	12	AC157033	Bos tauri	c 232	20.8	65.0	1867	5	HS080579
160	22.2	69.4	258216	12	AC156331	Bos tauri	c 233	20.8	65.0	2455	11	XL063920
161	22.2	69.4	275862	12	AC112376	Rattus no	c 234	20.8	65.0	2639	11	BC045089
162	22.2	69.4	284106	12	AC166087	Bos tauri	c 235	20.8	65.0	3112	11	XL063919
163	22.2	68.8	51	2	DD178844	METHOD FO	c 236	20.8	65.0	3418	6	MUSRPL7A
164	22.2	68.8	51	2	AX802744	Sequence	c 237	20.8	65.0	7871	10	AB027021

238	20.8	65.0	7904	10	AF293961	AF293961 Human pap	311	20.6	64.4	471	2	C0696169	C0696169 Sequence
239	20.8	65.0	75296	5	AC110795	AC110795 Homo sapi	312	20.6	64.4	473	2	C0679633	C0679633 Sequence
240	20.8	65.0	83518	12	AC117971	AC117971 Bos tauri	313	20.6	64.4	479	2	C0687119	C0687119 Sequence
241	20.8	65.0	153292	5	AL513318	AL513318 Human DNA	314	20.6	64.4	490	2	C0711883	C0711883 Sequence
242	20.8	65.0	160008	6	AC158217	AC158217 Mus muscu	315	20.6	64.4	492	2	AX360681	AX360681 Sequence
243	20.8	65.0	161949	6	CT485613	CT485613 Mouse DNA	316	20.6	64.4	498	2	C0712880	C0712880 Sequence
244	20.8	65.0	169321	6	AC107725	AC107725 Mus muscu	317	20.6	64.4	500	2	C0712891	C0712891 Sequence
245	20.8	65.0	171102	12	CT476835	CT476835 Homo sapi	318	20.6	64.4	513	2	C0670105	C0670105 Sequence
246	20.8	65.0	171864	12	AC016248	AC016248 Homo sapi	319	20.6	64.4	514	2	C0672486	C0672486 Sequence
247	20.8	65.0	174615	12	AC021249	AC021249 Homo sapi	320	20.6	64.4	548	2	C0832487	C0832487 Sequence
248	20.8	65.0	176870	6	AL844583	AL844583 Mouse DNA	321	20.6	64.4	556	2	C0671702	C0671702 Sequence
249	20.8	65.0	184674	12	AC102557	AC102557 Mus muscu	322	20.6	64.4	567	2	C0669223	C0669223 Sequence
250	20.8	65.0	185440	12	AC015499	AC015499 Homo sapi	323	20.6	64.4	572	2	C0673737	C0673737 Sequence
251	20.8	65.0	189335	6	AC112945	AC112945 Mus muscu	324	20.6	64.4	584	2	C0700469	C0700469 Sequence
252	20.8	65.0	190466	6	AC163446	AC163446 Mus muscu	325	20.6	64.4	591	2	C0832470	C0832470 Sequence
253	20.8	65.0	201383	6	AC162442	AC162442 Mus muscu	326	20.6	64.4	593	2	C0669667	C0669667 Sequence
254	20.8	65.0	202155	6	AC113269	AC113269 Mus muscu	327	20.6	64.4	596	7	BV250070	BV250070 S234P6364
255	20.8	65.0	216945	12	AC156619	AC156619 Mus muscu	328	20.6	64.4	605	2	C0671503	C0671503 Sequence
256	20.8	65.0	218283	12	AC079476	AC079476 Mus muscu	329	20.6	64.4	607	2	C0701376	C0701376 Sequence
257	20.8	65.0	218908	12	AC163174	AC163174 Bos tauri	330	20.6	64.4	614	2	C0671277	C0671277 Sequence
258	20.8	65.0	228645	6	AL450397	AL450397 Mouse DNA	331	20.6	64.4	747	5	CR456773	CR456773 Homo sapi
259	20.8	65.0	231119	12	AC113521	AC113521 Mus muscu	332	20.6	64.4	747	8	AY892427	AY892427 Synthetic
260	20.8	65.0	237247	6	AC099934	AC099934 Mus muscu	333	20.6	64.4	810	2	AR380730	AR380730 Sequence
261	20.8	65.0	243689	12	AC095265	AC095265 Rattus no	334	20.6	64.4	818	2	C0721654	C0721654 Sequence
262	20.8	65.0	249835	12	AC135200	AC135200 Rattus no	335	20.6	64.4	825	5	HSRPL7	HSRPL7
263	20.8	65.0	249835	12	AC135200	AC135200 Rattus no	336	20.6	64.4	825	5	HSRBRPL7A	HSRBRPL7A
264	20.8	65.0	249835	12	AC098753	AC098753 Rattus no	337	20.6	64.4	827	5	EC071671	EC071671 Homo sapi
265	20.8	65.0	258038	12	AC016018	AC016018 Mus muscu	338	20.6	64.4	830	5	BC087837	BC087837 Homo sapi
266	20.8	65.0	258226	12	AC167453	AC167453 Bos tauri	339	20.6	64.4	831	5	BC071895	BC071895 Homo sapi
267	20.8	65.0	259263	12	AC166522	AC166522 Bos tauri	340	20.6	64.4	833	5	CS162870	CS162870 Sequence
268	20.8	65.0	260162	12	AC127763	AC127763 Rattus no	341	20.6	64.4	838	2	BC006095	BC006095 Homo sapi
269	20.8	65.0	318115	12	AC098550	AC098550 Rattus no	342	20.6	64.4	838	5	BC071894	BC071894 Homo sapi
270	20.8	64.4	102	2	AX322263	AX322263 Sequence	343	20.6	64.4	839	5	HSRBRPL7B	HSRBRPL7B
271	20.6	64.4	102	2	AX523086	AX523086 Sequence	344	20.6	64.4	861	5	BC009599	BC009599 Homo sapi
272	20.6	64.4	126	2	C0734682	C0734682 Sequence	345	20.6	64.4	866	5	BC0481861	BC0481861 Sequence
273	20.6	64.4	205	5	BC070215	BC070215 Homo sapi	346	20.6	64.4	882	2	CS071093	CS071093 Sequence
274	20.6	64.4	211	2	C0701109	C0701109 Sequence	347	20.6	64.4	892	5	BC008850	BC008850 Homo sapi
275	20.6	64.4	225	2	C0662414	C0662414 Sequence	348	20.6	64.4	1365	2	AR448326	AR448326 Sequence
276	20.6	64.4	265	2	AX985386	AX985386 Sequence	349	20.6	64.4	1383	2	BD268056	BD268056 Therapeut
277	20.6	64.4	265	2	BD120245	BD120245 EST and e	350	20.6	64.4	1383	2	115237	115237 Sequence 3
278	20.6	64.4	265	2	AR424692	AR424692 Sequence	351	20.6	64.4	1447	5	BC106056	BC106056 Homo sapi
279	20.6	64.4	279	2	C0736273	C0736273 Sequence	352	20.6	64.4	1841	5	HUMRPL7X	HUMRPL7X
280	20.6	64.4	295	2	C0689212	C0689212 Sequence	353	20.6	64.4	2216	2	CS071093	CS071093 Sequence
281	20.6	64.4	316	2	C0680657	C0680657 Sequence	354	20.6	64.4	2339	2	AR448325	AR448325 Sequence
282	20.6	64.4	329	2	C0671400	C0671400 Sequence	355	20.6	64.4	23401	5	AC099061	AC099061 Homo sapi
283	20.6	64.4	343	2	C0670851	C0670851 Sequence	356	20.6	64.4	86829	5	AC011382	AC011382 Homo sapi
284	20.6	64.4	356	2	C0667011	C0667011 Sequence	357	20.6	64.4	102008	12	AC016552	AC016552 Homo sapi
285	20.6	64.4	372	2	C0706324	C0706324 Sequence	358	20.6	64.4	107381	12	AC115093	AC115093 Homo sapi
286	20.6	64.4	372	2	C0678383	C0678383 Sequence	359	20.6	64.4	110000	5	AB128049_17	AB128049_17
287	20.6	64.4	375	2	C0677902	C0677902 Sequence	360	20.6	64.4	110000	5	HS107	HS107
288	20.6	64.4	383	2	C0480497	C0480497 Sequence	361	20.6	64.4	115932	2	AF286885	AF286885 Homo sapi
289	20.6	64.4	386	2	C0664882	C0664882 Sequence	362	20.6	64.4	121265	12	AF286885	AF286885 Homo sapi
290	20.6	64.4	387	2	C0712454	C0712454 Sequence	363	20.6	64.4	127836	5	AC092828	AC092828 Homo sapi
291	20.6	64.4	400	2	C0664183	C0664183 Sequence	364	20.6	64.4	129109	5	AL390239	AL390239 Human DNA
292	20.6	64.4	400	2	C0676176	C0676176 Sequence	365	20.6	64.4	129592	12	AC170060	AC170060 Callicebu
293	20.6	64.4	406	2	AX360574	AX360574 Sequence	366	20.6	64.4	135213	5	AC111149	AC111149 Homo sapi
294	20.6	64.4	415	2	C0662299	C0662299 Sequence	367	20.6	64.4	13969	5	AL357552	AL357552 Human DNA
295	20.6	64.4	419	2	C0685720	C0685720 Sequence	368	20.6	64.4	147098	5	AC008651	AC008651 Homo sapi
296	20.6	64.4	439	2	C0472692	C0472692 Sequence	369	20.6	64.4	150124	12	AC148886	AC148886 Ocolemur
297	20.6	64.4	439	2	C0673749	C0673749 Sequence	370	20.6	64.4	152747	5	AL359260	AL359260 Human DNA
298	20.6	64.4	440	2	C0707670	C0707670 Sequence	371	20.6	64.4	157090	12	AC144497	AC144497 Takifugu
299	20.6	64.4	441	2	C0698538	C0698538 Sequence	372	20.6	64.4	161795	12	AC060832	AC060832 Homo sapi
300	20.6	64.4	443	2	CQ707833	CQ707833 Sequence	373	20.6	64.4	167036	12	AC188855	AC188855 Ocolemur
301	20.6	64.4	444	2	CQ679348	CQ679348 Sequence	374	20.6	64.4	170048	12	AC025240	AC025240 Homo sapi
302	20.6	64.4	452	2	CQ503001	CQ503001 Sequence	375	20.6	64.4	174346	5	AC108173	AC108173 Homo sapi
303	20.6	64.4	452	2	CQ511852	CQ511852 Sequence	376	20.6	64.4	174766	5	AC148659	AC148659 Macaca mu
304	20.6	64.4	454	2	C0682304	C0682304 Sequence	377	20.6	64.4	175150	12	AC136657	AC136657 Rattus no
305	20.6	64.4	462	2	C0692098	C0692098 Sequence	378	20.6	64.4	175710	12	AC116652	AC116652 Rattus no
306	20.6	64.4	464	2	C0685059	C0685059 Sequence	379	20.6	64.4	176063	12	AC119777	AC119777 Rattus no
307	20.6	64.4	464	2	CQ711448	CQ711448 Sequence	380	20.6	64.4	181948	12	AC169003	AC169003 Callicebu
308	20.6	64.4	466	2	CQ694492	CQ694492 Sequence	381	20.6	64.4	186516	6	AC122499	AC122499 Mus muscu
309	20.6	64.4	469	2	CQ691352	CQ691352 Sequence	382	20.6	64.4	191318	12	AC020670	AC020670 Homo sapi
310	20.6	64.4	471	2	CQ679552	CQ679552 Sequence	383	20.6	64.4	197103	5	AL590036	AL590036 Human DNA

C 384	20.6	64.4	203261	12	AC021464	Homo sapi	457	20	62.5	237138	12	AC166759	Bos tauru
385	20.6	64.4	222701	12	AC174851	Colobus g	458	20	62.5	237428	12	AC127053	Rattus no
386	20.6	64.4	224611	12	AC174629	Colobus g	459	20	62.5	245384	12	AC127053	Rattus no
387	20.6	64.4	237624	12	AC113662	AC081499 Homo sapi	460	19.8	61.9	470	2	CO713366	Sequence
388	20.6	64.4	24525	5	AC008499	AC008499 Homo sapi	461	19.8	61.9	566	1	AY596585	Pagrus ma
C 389	20.6	64.4	247917	12	AC095906	AC095906 Rattus no	462	19.8	61.9	756	2	BD216963	Novel hum
C 390	20.6	64.4	252132	12	AC095221	AC095221 Rattus no	463	19.8	61.9	756	2	AR770553	Sequence
C 391	20.6	64.4	252630	12	AC112099	AC112099 Rattus no	464	19.8	61.9	768	7	BV669265	Sequence
C 392	20.6	64.4	256245	12	AC096122	AC096122 Rattus no	465	19.8	61.9	4065	15	AJ628731	Rickettsi
C 393	20.6	64.4	257652	12	AC106597	AC106597 Rattus no	466	19.8	61.9	4734	15	RSP582615	Rickettsi
C 394	20.6	64.4	272658	12	AC131544	AC131544 Rattus no	467	19.8	61.9	4734	15	RSP582615	Rickettsi
C 395	20.6	64.4	294286	12	AC137391	AC137391 Rattus no	468	19.8	61.9	4735	15	RSP582615	Rickettsi
C 396	20.6	64.4	29784	12	AC097020	AC097020 Rattus no	469	19.8	61.9	51049	12	AC155140	Bos tauru
C 397	20.6	63.7	348986	15	BX572093	BX572093 Prochiloto	470	19.8	61.9	53045	6	AL844890	Mus muscu
C 398	20.4	63.7	1648	4	AB072566	AB072566 Drosoph	471	19.8	61.9	57594	12	AC104552	Mus muscu
C 399	20.4	63.7	1708	4	AY096115	AY096115 Drosoph	472	19.8	61.9	82485	14	AC149769	Bos tauru
C 400	20.4	63.7	2595	2	AX653293	AX653293 Sequence	473	19.8	61.9	84982	5	AY589041	Sequence
C 401	20.4	63.7	56154	12	AC079961	AC079961 Homo sapi	474	19.8	61.9	86763	12	AC16406	Sequence
C 402	20.4	63.7	110000	4	AE017342_03	Continuation (4 of	475	19.8	61.9	110000	15	CR93197_06	Continuation (7 of
C 403	20.4	63.7	110000	4	AE017342_04	Continuation (5 of	476	19.8	61.9	110000	15	CR93197_06	Continuation (7 of
C 404	20.4	63.7	110000	4	AP008207_328	Continuation (329	477	19.8	61.9	124269	12	AC152482	Sequence
C 405	20.4	63.7	120924	12	AC151492	AC151492 Sorex ara	478	19.8	61.9	125967	11	AC174721	Sequence
C 406	20.4	63.7	134736	12	AC151493	AC151493 Sorex ara	479	19.8	61.9	126474	5	HS181N1	Human DNA
C 407	20.4	63.7	148978	5	HSAB9612	AB009612 Homo sapi	480	19.8	61.9	136436	12	AC152155	Sequence
C 408	20.4	63.7	149000	5	AC127540	AC127540 Homo sapi	481	19.8	61.9	147811	11	CR847546	Sequence
C 409	20.4	63.7	155633	4	AP003344	AP003344 Oryza sat	482	19.8	61.9	150884	11	BX005161	Sequence
C 410	20.4	63.7	158939	12	AC102266	AC102266 Mus muscu	483	19.8	61.9	154727	12	AC152368	Sequence
C 411	20.4	63.7	158950	5	AL391425	AL391425 Human DNA	484	19.8	61.9	156042	12	AC013614	Sequence
C 412	20.4	63.7	152276	11	CR388052	CR388052 Zebrafish	485	19.8	61.9	158311	12	AC013614	Sequence
C 413	20.4	63.7	153421	12	AC012664	AC012664 Homo sapi	486	19.8	61.9	158311	12	AL669892	Sequence
C 414	20.4	63.7	155777	6	AL807741	AL807741 Mouse DNA	487	19.8	61.9	158979	6	AL669892	Sequence
C 415	20.4	63.7	165857	12	BX601643	BX601643 Zebrafish	488	19.8	61.9	152278	12	AC104697	Sequence
C 416	20.4	63.7	169931	5	AC005822	AC005822 Homo sapi	489	19.8	61.9	165535	6	CR932808	Sequence
C 417	20.4	63.7	176435	12	AC149874	AC149874 Xenopus t	490	19.8	61.9	165535	6	CR932808	Sequence
C 418	20.4	63.7	186710	12	AC178132	AC178132 Strongylo	491	19.8	61.9	178072	6	AC131791	Sequence
C 419	20.4	63.7	197709	5	AC073641	AC073641 Homo sapi	492	19.8	61.9	180252	12	AL844538	Sequence
C 420	20.4	63.7	19819	12	AC161639	AC161639 Bos tauru	493	19.8	61.9	181794	5	AC145186	Sequence
C 421	20.4	63.7	210085	12	AC012460	AC012460 Homo sapi	494	19.8	61.9	182023	12	AC055869	Sequence
C 422	20.4	63.7	211027	12	AC134724	AC134724 Rattus no	495	19.8	61.9	189246	12	AC177713	Sequence
C 423	20.4	63.7	212486	6	AC153562	AC153562 Mus muscu	496	19.8	61.9	191954	12	AC159845	Sequence
C 424	20.4	63.7	213586	6	AC174220	AC174220 Bos tauru	497	19.8	61.9	192944	12	AC146902	Sequence
C 425	20.4	63.7	220679	12	AL928658	AL928658 Mouse DNA	498	19.8	61.9	196206	5	AC012368	Sequence
C 426	20.4	63.7	233339	12	AC094194	AC094194 Rattus no	499	19.8	61.9	199027	12	AC137061	Sequence
C 427	20.4	63.7	237003	12	AC172758	AC172758 Bos tauru	500	19.8	61.9	203840	5	AP001007	Sequence
C 428	20.4	63.7	253322	12	AC110626	AC110626 Rattus no	501	19.8	61.9	204132	12	AC150925	Sequence
C 429	20.4	63.7	254812	12	AC107123	AC107123 Rattus no	502	19.8	61.9	217470	12	AC150925	Sequence
C 430	20.4	63.7	261576	12	AC127398	AC127398 Rattus no	503	19.8	61.9	220157	12	AC166843	Sequence
C 431	20.4	63.7	273967	12	AC160690	AC160690 Bos tauru	504	19.8	61.9	230158	12	AC159988	Sequence
C 432	20.4	63.7	285280	12	AC156819	AC156819 Bos tauru	505	19.8	61.9	235516	12	AC163072	Sequence
C 433	20.4	63.7	285280	12	AC156819	AC156819 Bos tauru	506	19.8	61.9	241161	12	AC164734	Sequence
C 434	20.4	63.1	285280	5	HSPA26E5	Z79234 H.sapiens f	507	19.8	61.9	241237	12	AC156960	Sequence
C 435	20.2	63.1	96202	5	AL138824	AL138824 Human DNA	508	19.8	61.9	242359	6	AC158534	Sequence
C 436	20.2	63.1	197835	12	AC169043	AC169043 Bos tauru	509	19.8	61.9	245606	12	AC149739	Sequence
C 437	20	62.5	20	2	DD178685	DD178685 METHOD FO	510	19.8	61.9	249008	6	AC124672	Sequence
C 438	20	62.5	20	2	AX802585	AX802585 Sequence	511	19.8	61.9	256207	12	AC164767	Sequence
C 439	20	62.5	20	2	AX803128	AX803128 Sequence	512	19.8	61.9	259807	12	AC154977	Sequence
C 440	20	62.5	20	2	AX803304	AX803304 Sequence	513	19.8	61.9	301192	12	AC154975	Sequence
C 441	20	62.5	27	2	AR142040	AR142040 Sequence	514	19.6	61.3	451	2	AX393741	Sequence
C 442	20	62.5	27	2	IS59907	IS59907 Sequence 34	515	19.6	61.3	452	2	CO682243	Sequence
C 443	20	62.5	27	2	IS59907	IS59907 Sequence 34	516	19.6	61.3	459	2	CO681579	Sequence
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C 447	20	62.5	27	2	IS59907	IS59907 Sequence 34	520	19.6	61.3	459	2	CO681579	Sequence
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C 449	20	62.5	27	2	IS59907	IS59907 Sequence 34	522	19.6	61.3	459	2	CO681579	Sequence
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C 452	20	62.5	27	2	IS59907	IS59907 Sequence 34	525	19.6	61.3	459	2	CO681579	Sequence
C 453	20	62.5	27	2	IS59907	IS59907 Sequence 34	526	19.6	61.3	459	2	CO681579	Sequence
C 454	20	62.5	27	2	IS59907	IS59907 Sequence 34	527	19.6	61.3	459	2	CO681579	Sequence
C 455	20	62.5	27	2	IS59907	IS59907 Sequence 34	528	19.6	61.3	459	2	CO681579	Sequence
C 456	20	62.5	27	2	IS59907	IS59907 Sequence 34	529	19.6	61.3	459	2	CO681579	Sequence

c 968 19 59.4 110000 15 BA000004.40 Continuation (41 o
c 969 19 59.4 110000 15 BA000039.24 Continuation (25 o
c 970 19 59.4 110000 15 CP000026.22 Continuation (23 o
c 971 19 59.4 110000 15 CP000026_23 Continuation (24 o
c 972 19 59.4 119956 12 AC154939 AC154939 Loxodonta
c 973 19 59.4 121963 5 AL162397 AL162397 Human DNA
c 974 19 59.4 133226 12 AL512364 AL512364 Homo sapi
c 975 19 59.4 139687 5 AL590993 AL590993 Human DNA
c 976 19 59.4 143717 12 AC069245 AC069245 Homo sapi
c 977 19 59.4 143969 5 AL357552 AL357552 Human DNA
c 978 19 59.4 147007 12 AC157471 AC157471 Rhinoph
c 979 19 59.4 148654 5 AL683813 AL683813 Human DNA
c 980 19 59.4 153650 5 AC022296 AC022296 Homo sapi
c 981 19 59.4 153927 12 AC155985 AC155985 Xenopus t
c 982 19 59.4 153953 6 AC153577 AC153577 Mus muscu
c 983 19 59.4 154258 12 AC079049 AC079049 Homo sapi
c 984 19 59.4 159862 12 AC160582 AC160582 Ateles
c 985 19 59.4 160066 12 AC027295 AC027295 Homo sapi
c 986 19 59.4 160314 12 AC090661 AC078815 Homo sapi
c 987 19 59.4 163475 5 AC078815 AC078815 Homo sapi
c 988 19 59.4 165206 12 AC068488 AC068488 Homo sapi
c 989 19 59.4 165237 2 AX232505 AX232505 Sequence
c 990 19 59.4 166305 12 AC160585 AC160585 Ateles
c 991 19 59.4 166866 11 BX005238 BX005238 Zebrafish
c 992 19 59.4 166980 12 AC092907 AC092907 Homo sapi
c 993 19 59.4 167865 5 AC087446 AC087446 Homo sapi
c 994 19 59.4 168344 6 AC126028 AC126028 Mus muscu
c 995 19 59.4 169362 12 AL136440 AL136440 Homo sapi
c 996 19 59.4 169669 5 AL157777 AL157777 Human DNA
c 997 19 59.4 171135 5 AC093895 AC093895 Homo sapi
c 998 19 59.4 172731 12 AC020623 AC020623 Homo sapi
c 999 19 59.4 174583 6 AC124685 AC124685 Mus muscu
1000 19 59.4 175064 5 AC074277 AC074277 Homo sapi

ALIGNMENTS

RESULT 1
AR349181 32 bp DNA linear PAT 17-AUG-2003
LOCUS AR349181 Sequence 121 from patent US 6583278.
ACCESSION AR349181
VERSION AR349181.1 GI:33749886
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 32)
AUTHORS Carter,N.M.
TITLE Nucleic acid probes complementary to human papilloma virus nucleic acid
JOURNAL Patent: US 6583278-A 121 24-JUN-2003;
FEATURES Gen-Probe Incorporated; San Diego, CA
source Location/Qualifiers
1..32
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 32; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTATTAATAGGTCCTGCGTGCAGAAACC 32
|||||
Db 1 TTATTAATAGGTCCTGCGTGCAGAAACC 32

RESULT 2
AR349182/c 32 bp DNA linear PAT 17-AUG-2003
LOCUS AR349182 Sequence 122 from patent US 6583278.
DEFINITION

ACCESSION AR349182
VERSION AR349182.1 GI:33749887
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 32)
AUTHORS Carter,N.M.
TITLE Nucleic acid probes complementary to human papilloma virus nucleic acid
JOURNAL Patent: US 6583278-A 122 24-JUN-2003;
FEATURES Gen-Probe Incorporated; San Diego, CA
source Location/Qualifiers
1..32
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 32; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTATTAATAGGTCCTGCGTGCAGAAACC 32
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Db 32 TTATTAATAGGTCCTGCGTGCAGAAACC 1

RESULT 3
AR349183 32 bp DNA linear PAT 17-AUG-2003
LOCUS AR349183 Sequence 123 from patent US 6583278.
ACCESSION AR349183
VERSION AR349183.1 GI:33749888
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 32)
AUTHORS Carter,N.M.
TITLE Nucleic acid probes complementary to human papilloma virus nucleic acid
JOURNAL Patent: US 6583278-A 123 24-JUN-2003;
FEATURES Gen-Probe Incorporated; San Diego, CA
source Location/Qualifiers
1..32
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 32; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTATTAATAGGTCCTGCGTGCAGAAACC 32
|||||
Db 1 TTATTAATAGGTCCTGCGTGCAGAAACC 32

RESULT 4
AR349184/c 32 bp DNA linear PAT 17-AUG-2003
LOCUS AR349184 Sequence 124 from patent US 6583278.
ACCESSION AR349184
VERSION AR349184.1 GI:33749889
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 32)
AUTHORS Carter,N.M.
TITLE Nucleic acid probes complementary to human papilloma virus nucleic acid
JOURNAL Patent: US 6583278-A 124 24-JUN-2003;

ORIGIN
Query Match 100.0%; Score 32; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Gen-Probe Incorporated, San Diego, CA

FEATURES
source
1. .32
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 32; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTATTATAAGTGCTCGCGTCCAGAAACC 32
32 TTATTATAAGTGCTCGCGTCCAGAAACC 1

Db 32 TTATTATAAGTGCTCGCGTCCAGAAACC 1

RESULT 5
AR080321 476 bp DNA linear PAT 31-AUG-2000
LOCUS Sequence 16 from patent US 5968761.
DEFINITION AR080321
ACCESSION AR080321 GI:10007056
VERSION AR080321.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 476)
AUTHORS Rolfe,M., Chiu,M.,Isabel., Cottarel,G., Berlin,V., Damagnez,V. and Draetta,G.
TITLE Ubiquitin conjugating enzymes
JOURNAL Patent: US 5968761-A 16 19-OCT-1999;
FEATURES location/Qualifiers
source 1. .476
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 32; DB 2; Length 476;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTATTATAAGTGCTCGCGTCCAGAAACC 32
301 TTATTATAAGTGCTCGCGTCCAGAAACC 332

Db 301 TTATTATAAGTGCTCGCGTCCAGAAACC 332

RESULT 6
AR085249 476 bp DNA linear PAT 01-SEP-2000
LOCUS Sequence 9 from patent US 5981699.
DEFINITION AR085249
ACCESSION AR085249 GI:10012019
VERSION AR085249.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 476)
AUTHORS Draetta,G., Rolfe,M. and Eckstein,J.W.
TITLE Human ubiquitin conjugating enzyme
JOURNAL Patent: US 5981699-A 9 09-NOV-1999;
FEATURES location/Qualifiers
source 1. .476
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 32; DB 2; Length 476;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTATTATAAGTGCTCGCGTCCAGAAACC 32
301 TTATTATAAGTGCTCGCGTCCAGAAACC 332

Db 301 TTATTATAAGTGCTCGCGTCCAGAAACC 332

RESULT 7
CS113238 477 bp DNA linear PAT 24-JUN-2005
LOCUS Sequence 15 from Patent WO2005051431.
DEFINITION CS113238
ACCESSION CS113238
VERSION CS113238.1 GI:68224783
KEYWORDS
SOURCE Human papillomavirus - 18
ORGANISM Human papillomavirus - 18
REFERENCE 1
AUTHORS Milner,A.J.
TITLE Colloidal delivery system for biological therapeutic agents
JOURNAL Patent: WO 2005051431-A 15 09-JUN-2005;
FEATURES location/Qualifiers
source 1. .477
/organism="Human papillomavirus - 18"
/mol_type="unassigned DNA"
/db_xref="taxon:337042"

ORIGIN
Query Match 100.0%; Score 32; DB 2; Length 477;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTATTATAAGTGCTCGCGTCCAGAAACC 32
301 TTATTATAAGTGCTCGCGTCCAGAAACC 332

Db 301 TTATTATAAGTGCTCGCGTCCAGAAACC 332

RESULT 8
PAHPV181 528 bp DNA linear VRL 06-JUL-1989
LOCUS Integrated HPV-18 E6/E7 ORF with DNaseI-hypersensitive site.
DEFINITION X05568
ACCESSION X05568 GI:60880
VERSION X05568.1
KEYWORDS DNase I hypersensitive site; E6 gene; E7 gene; enhancer-like sequence; inverted repeat.
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
REFERENCE 1 (bases 1 to 528)
AUTHORS Lazo,P.A.
TITLE Structure, DNaseI hypersensitivity and expression of integrated papilloma virus in the genome of HeLa cells
JOURNAL Eur. J. Biochem. 165 (2), 393-401 (1987)
COMMENT 2439332
numbering refers to the Xba site in E6 ORF
Data kindly reviewed (12.2.88) by Lazo P. A.
FEATURES location/Qualifiers
source 1. .528
/organism="Human papillomavirus"
/mol_type="genomic DNA"
/db_xref="taxon:10566"
/cell_line="HeLa"
18. .24
/note="enhancer-like sequence 1"
21. .28
/note="inverted repeat A"
complement (34. .42)
/note="enhancer-like sequence 2"
38. .42
/note="inverted repeat B"
46. .53
/note="enhancer-like sequence 3"
77. .81
/note="inverted repeat B"
90. .97

misc_feature /note="imp.inverted repeat A'"
139..145
/note="enhancer-like sequence 4"
misc_feature 164..171
/note="enhancer-like sequence 5"
misc_feature 250..257
/note="enhancer-like sequence 6"
misc_feature 296..303
/note="enhancer-like sequence 7"
misc_feature 435..442
/note="enhancer-like sequence 8"
misc_feature 445..452
/note="enhancer-like sequence 9"
misc_feature complement(453..460)
/note="enhancer-like sequence 10"
misc_feature complement(460..466)
/note="enhancer-like sequence 11"
misc_feature complement(470..477)
/note="enhancer-like sequence 12"

ORIGIN

Query Match 100.0%; Score 32; DB 10; Length 528;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTATTATAAGTGCTGCGGTGCCAGAAACC 32
85 TTATTATAAGTGCTGCGGTGCCAGAAACC 116

RESULT 9
188814 LOCUS 817 bp DNA linear PAT 10-AUG-1998
DEFINITION Sequence 11 from patent US 5719054.
ACCESSION 188814
VERSION 188814.1 GI:3408754
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 817)
AUTHORS Bourneil,M.E., Ingilis,S.C. and Munro,A.J.
TITLE Recombinant virus vectors encoding human papillomavirus proteins
JOURNAL Patent: US 5719054-A 11 17-FEB-1998;
FEATURES
source 1..817
/organism="Unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 32; DB 2; Length 817;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTATTATAAGTGCTGCGGTGCCAGAAACC 32
306 TTATTATAAGTGCTGCGGTGCCAGAAACC 337

RESULT 10
A98759 LOCUS 837 bp DNA linear PAT 26-JAN-2000
DEFINITION Sequence 20 from Patent WO9910375.
ACCESSION A98759
VERSION A98759.1 GI:6781783
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 837)
AUTHORS Lombardo-Bencheikh,A. and Bruck,C.
TITLE VACCINE
JOURNAL Patent: WO 9910375-A 20 04-MAR-1999;

FEATURES
source 1..837
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 100.0%; Score 32; DB 2; Length 837;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTATTATAAGTGCTGCGGTGCCAGAAACC 32
634 TTATTATAAGTGCTGCGGTGCCAGAAACC 665

RESULT 11
BD080320 LOCUS 837 bp DNA linear PAT 27-AUG-2002
DEFINITION Vaccine.
ACCESSION BD080320
VERSION BD080320.1 GI:22625923
KEYWORDS JP 2001513986-A/10.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 837)
Bruck,C., Silva,T.C., Delisse,A.M.E.F., Gerard,C.M.G. and
Bencheikh,A.L.
Vaccine
Patent: JP 2001513986-A 10 11-SEP-2001;
SMITHKLINE BEECHAM BIOLOGICALS SA
OS Homo sapiens (human)
PN JP 2001513986-A/10
PD 11-SEP-2001
PF 17-AUG-1998 JP 2000507701
PR 22-AUG-1997 GB 9717953.5
PI CLAUDINE BRUCK,TERESA CABEZON SILVA,ANNE MARIE EVA FERNANDE
PI DELISSE,
PI CATHERINE MARIE GHISLAINE GERARD,ANGELA LOMBARDO BENCHEIKH PC
C12N15/09,A61K9/107,A61K39/12,A61K39/145,A61K39/39,A61P35/00, PC
A61P37/00,
PC C07K14/025,C07K19/00,C12N1/15,C12N1/19,C12N1/21,C12N5/10, PC
C12P21/02,
PC C12N15/00,C12N5/00
CC Vaccine
FH Key
FT source 1..837
Location/Qualifiers
/organism="Homo sapiens (human)".
1..837
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 32; DB 2; Length 837;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTATTATAAGTGCTGCGGTGCCAGAAACC 32
634 TTATTATAAGTGCTGCGGTGCCAGAAACC 665

RESULT 12
BD103169 LOCUS 837 bp DNA linear PAT 27-AUG-2002
DEFINITION Vaccine.
ACCESSION BD103169

VERSION BD103169.1 GI:22648743
KEYWORDS JP 2001527091-A/10.
SOURCE unidentified
ORGANISM unidentified
REFERENCE unclassified sequences.
AUTHORS 1 (bases 1 to 837)
TITLE Dalemans, W.L.J. and Gerard, C.M.G.
JOURNAL Vaccine
PATENT: JP 2001527091-A 10 25-DEC-2001;
SMITHKLINE BEECHAM BIOLOGICALS SA
COMMENT OS Unidentified
PN JP 2001527091-A/10
PD 25-DEC-2001
PF 18-DEC-1998 JP 2000526542
PR 24-DEC-1997 GB 9727262.9
PI WILFRIED L.J DALEMAN, CATHERINE MARIE GHISLAINE GERARD PC
COTK14/025, A61K39/00, A61K39/12, A61K39/385, A61P35/00, C07K19/00, PC
C12N15/09,
PC C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC Vaccine
FH Key
FT source
FEATURES
source 1. .837 Location/Qualifiers
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match 100.0%; Score 32; DB 2; Length 837;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTATTATTAAGTGCTGCGGTGCCAGAAACC 32
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634 TTATTATTAAGTGCTGCGGTGCCAGAAACC 665

Db 634 TTATTATTAAGTGCTGCGGTGCCAGAAACC 665

RESULT 13
AR183581 837 bp DNA linear PAT 20-APR-2002
LOCUS
DEFINITION Sequence 20 from patent US 6342224.
ACCESSION AR183581
VERSION AR183581.1 GI:20227550
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 837)
AUTHORS Bruck, C., Silva, T., Gabezon, F., Bernarde Delisse, A.-M., Eva, G., Ghislaine Gerard, C., Marve, A. and Lombardo-Bencheikh, A.
TITLE Recombinant papillomavirus vaccine and method for production and treatment
JOURNAL Patent: US 6342224-A 20 29-JAN-2002;
FEATURES
source 1. .837 Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 32; DB 2; Length 837;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTATTATTAAGTGCTGCGGTGCCAGAAACC 32
|||||
634 TTATTATTAAGTGCTGCGGTGCCAGAAACC 665

Db 634 TTATTATTAAGTGCTGCGGTGCCAGAAACC 665

RESULT 14

AX020943
LOCUS AX020943 837 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 20 from Patent WO9333866.
ACCESSION AX020943
VERSION AX020943.1 GI:10044609
KEYWORDS
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
REFERENCE 1 (bases 1 to 837)
AUTHORS Dalemans, W.L. and Gerard, C.M.
TITLE Vaccine
JOURNAL Patent: WO 9333868-A 20 08-JUL-1999;
DALEMAN WILFRIED L.J (BE); SMITHKLINE BEECHAM BIOLOG (BE); GERARD CATHERINE MARIE GHISLAINE (BE)
FEATURES
source 1. .837 Location/Qualifiers
/organism="Human papillomavirus"
/mol_type="unassigned DNA"
/db_xref="taxon:10566"

ORIGIN
Query Match 100.0%; Score 32; DB 2; Length 837;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTATTATTAAGTGCTGCGGTGCCAGAAACC 32
|||||
634 TTATTATTAAGTGCTGCGGTGCCAGAAACC 665

Db 634 TTATTATTAAGTGCTGCGGTGCCAGAAACC 665

RESULT 15
HPY18491 843 bp DNA linear VRL 18-AUG-1999
LOCUS
DEFINITION Human papillomavirus type 18 E6 and E7 genes.
ACCESSION Y18491
VERSION Y18491.1 GI:5748503
KEYWORDS E6 gene; E6 protein; E7 gene; E7 protein.
SOURCE Human papillomavirus type 18
ORGANISM Human papillomavirus type 18
REFERENCE 1 (bases 1 to 843)
AUTHORS Laaseri, M., Gul'ko, L., Vinokurova, S., Kisseleva, N., Veiko, V. and Kisselev, F.
TITLE Cloning of E6 and E7 Genes of Human Papilloma Virus Type 18 and Transformation Potential of E7 Gene and its Mutants
JOURNAL Virus Genes 182, 139-149 (1999)
REFERENCE 2 (bases 1 to 843)
AUTHORS Veiko, V.P.
TITLE Direct Submision
JOURNAL Submitted (02-DEC-1998) V.P. Veiko, Institute of Genetics and Selection of Industrial Microorganisms, 1st Dorozhny proezd, 1, Moscow 113545, RUSSIA
FEATURES
source 1. .843 Location/Qualifiers
/organism="Human papillomavirus type 18"
/mol_type="genomic DNA"
/db_xref="taxon:333761"
40..516
/gene="E6"
40..516
/gene="E6"
40..516
/gene="E6"
/codon_start=1
/product="E6 protein"
/protein_id="CA853096.1"
/db_xref="GI:5748504"
/db_xref="GOA:Q9QNP8"
/db_xref="UniProtKB/TREMBL:Q9QNP8"
/translation="MAFSDPTRPYPLPDLCTELNLSLDDIEITCYCTVLELTV
FERAFKDLFVYRDSIPLHACHKCIDPYSHIRELRHSDSVYGDTEKLTNTGYNLL
IRCIKCKPLNPAKELRLHNEKRFRFKIAGHYRGQCHSCCNRAQERLQRRRETV"

gene 525..842
/gene="E7"
CDS 525..842
/gene="E7"
/codon_start=1
/product="E7 protein"
/protein_id="CA53097.1"
/db_xref="GI:5748505"
/db_xref="UniProtKB/TREMBL:Q90NP7"
/translation="MHGPKATLQDYLHLPEPONEIPVDLLCHEQLSDSEBNDIDGV
NHQHLPARAEPRHTMLCMCKCKEARIKLVVSSADDLRAFOQLPLNTLSFVCPWCA
SQO"

ORIGIN

Query Match 100.0%; Score 32; DB 10; Length 843;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTATTATAAGTGCCTGCGGTCGCGAACC 32
|||||
340 TTATTATAAGTGCCTGCGGTCGCGAACC 371

RESULT 16
PPH18A 912 bp DNA linear VRL 02-AUG-1993
LOCUS Human papillomavirus type 18 encoding envelope proteins E6 and E7,
DEFINITION complete cds., and envelope protein E1, 5' end.
ACCESSION M26798.1 GI:333043
VERSION E1 protein; E6 gene; E7 gene; envelope-associated protein.
KEYWORDS Human papillomavirus
SOURCE Human papillomavirus
ORGANISM Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
unclassified Papillomaviridae.
REFERENCE 1 (bases 1 to 912)
Schneider-Geddicke, A. and Schwarz, E.
Different human cervical carcinoma cell lines show similar
transcription patterns of human papillomavirus type 18 early genes
EMBO J. 5 (9), 2285-2292 (1986)

JOURNAL
3023067
Original source text: Human papillomavirus type 18, cDNA to mRNA,
from human cervical carcinoma HeLa, C4-1 and SW756 cell lines.
COMMENT
PUBMED
FEATURES
source
1..912
/organism="Human papillomavirus"
/mol_type="genomic DNA"
/db_xref="taxon:10566"
12..488
/note="ORF E6"
/codon_start=1
/protein_id="AAA46946.1"
/db_xref="GI:333044"
/translation="MARFDPTRRPYKLPDLCTELSTLSODIITCVYCKTVLETV
FERAPDLFVYVRDIPHAACHKICIDFYRIELRYSDSYDITLTKLNTGLNYML
IRCLRCQKPLNPAEKRLHNEKRFRFNIAGHYRGQCHSCNRRORLORRRTQV"
497..814
/note="ORF E7"
/codon_start=1
/protein_id="AAA46947.1"
/db_xref="GI:333045"
/translation="MHGPKATLQDYLHLPEPONEIPVDLLCHEQLSDSEBNDIDGV
NHQHLPARAEPRHTMLCMCKCKEARIKLVVSSADDLRAFOQLPLNTLSFVCPWCA
SQO"

CDS
821..>912
/note="ORF E1"
/codon_start=1
/protein_id="AAA46948.1"
/db_xref="GI:333046"
/translation="MADPBGTDGEGTGCNGMFVVOAIVDKKTGDV"

ORIGIN

Query Match 100.0%; Score 32; DB 10; Length 912;

Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTATTATAAGTGCCTGCGGTCGCGAACC 32
|||||
312 TTATTATAAGTGCCTGCGGTCGCGAACC 343

RESULT 17
A06328
LOCUS Hpv18 mRNA for E6, E7 and E1.
DEFINITION A06328
ACCESSION A06328.1 GI:413673
VERSION E1 gene; E6 gene; E7 gene.
KEYWORDS Human papillomavirus type 18
SOURCE Human papillomavirus type 18
ORGANISM Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Alphapapillomavirus.
REFERENCE 1 (bases 1 to 1000)
Oltersdorf, T., Roewer, W., Schneider-Geddicke, A., Seedorf, K.,
Duerst, M. and Schwarz, E.
Expression products of human papilloma virus type 18, antibodies
specific for these proteins, and diagnostic reagents containing
these antibodies or the corresponding DNA
Patent: EP 0256321-A 5 24-FEB-1988;
BEHRINGWERKE Aktiengesellschaft

JOURNAL
location/Qualifiers
1..1000
/organism="Human papillomavirus type 18"
/mol_type="unassigned RNA"
/db_xref="taxon:333761"
100..576
/codon_start=1
/product="E6"
/protein_id="CAA00542.1"
/db_xref="GI:413674"
/db_xref="GOA:P06788"
/db_xref="UniProtKB/Swiss-Prot:P06788"
/translation="MARFDPTRRPYKLPDLCTELSTLSODIITCVYCKTVLETV
FERAPDLFVYVRDIPHAACHKICIDFYRIELRYSDSYDITLTKLNTGLNYML
IRCLRCQKPLNPAEKRLHNEKRFRFNIAGHYRGQCHSCNRRORLORRRTQV"
585..902
/codon_start=1
/product="E7"
/protein_id="CAA00543.1"
/db_xref="GI:413675"
/db_xref="GOA:P06788"
/db_xref="UniProtKB/Swiss-Prot:P06788"
/translation="MHGPKATLQDYLHLPEPONEIPVDLLCHEQLSDSEBNDIDGV
NHQHLPARAEPRHTMLCMCKCKEARIKLVVSSADDLRAFOQLPLNTLSFVCPWCA
SQO"

CDS
909..>1000
/codon_start=1
/product="E1"
/protein_id="CAA00544.1"
/db_xref="GI:413676"
/translation="MADPBGTDGEGTGCNGMFVVOAIVDKKTGDV"

ORIGIN

Query Match 100.0%; Score 32; DB 2; Length 1000;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTATTATAAGTGCCTGCGGTCGCGAACC 32
|||||
400 TTATTATAAGTGCCTGCGGTCGCGAACC 431

RESULT 18
A07621
LOCUS Amplified spliced mRNA for HPV 18.
DEFINITION A07621 1000 bp RNA linear PAT 22-JUN-1993

ACCESSION A07621
VERSION A07621.1 GI:413119
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
OTHER SEQUENCES; artificial sequences.
REFERENCE 1 (bases 1 to 1000)
AUTHORS Cerutti, P., Whitcomb, J., Zijlstra, J. and De Villiers, E.M.
TITLE Detection of human papillomavirus DNA in cervix smears
JOURNAL BJRHINGWERKE Aktengesellschaft
FEATURES
source 1. 1000
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 100.0%; Score 32; DB 2; Length 1000;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTATTAATAAGTGCTGCGGTGCCAGAAACC 32
Db 405 TTATTAATAAGTGCTGCGGTGCCAGAAACC 436
RESULT 19
LOCUS A98761 1152 bp DNA linear PAT 26-JAN-2000
DEFINITION Sequence 22 from Patent WO910375.
ACCESSION A98761
VERSION A98761.1 GI:6781784
KEYWORDS
SOURCE unidentified
ORGANISM unclassified sequences.
REFERENCE 1 (bases 1 to 1152)
AUTHORS Lombardo-Bencheikh, A. and Bruck, C.
TITLE VACCINE
JOURNAL LOMBARDO BENCHEIKH ANGELA (BR); SMITHKLINE BEECHAM BIOLOG (BR)
FEATURES
source 1. 1152
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 100.0%; Score 32; DB 2; Length 1152;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTATTAATAAGTGCTGCGGTGCCAGAAACC 32
Db 634 TTATTAATAAGTGCTGCGGTGCCAGAAACC 665
RESULT 20
LOCUS BD080321 1152 bp DNA linear PAT 27-AUG-2002
DEFINITION Vaccine.
ACCESSION BD080321
VERSION BD080321.1 GI:22625924
KEYWORDS JP 2001513986-A/11.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 1152)
AUTHORS Bruck, C., Silva, T.C., Delisse, A.M.B.F., Gerard, C.M.G. and Bencheikh, A.L.

TITLE Vaccine
JOURNAL Patent: JP 2001513986-A 11 11-SEP-2001;
SMITHKLINE BEECHAM BIOLOGICALS SA
COMMENT OS Homo sapiens (human)
PN JP 2001513986-A/11
PD 11-SEP-2001
PF 17-AUG-1998 JP 2000507701
PR 22-AUG-1997 GB 9717953.5
PI CLAUDINE BRUCK, TERESA CABEZON SILVA, ANNE MARIE EVA FERNANDE
PI DELISSE,
PI CATHERINE MARIE GHISLAINE GERARD, ANGELA LOMBARDO BENCHEIKH PC
C12N15/09, A61K39/107, A61K39/12, A61K39/145, A61K39/39, A61P35/00, PC
A61P37/00,
PC C07K14/025, C07K19/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, PC
C12P21/02,
PC C12N15/00, C12N5/00
CC Vaccine
CC Key
FH Key
FT source 1. 1152
Location/Qualifiers
/organism="Homo sapiens (human)".
FEATURES
source 1. 1152
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 100.0%; Score 32; DB 2; Length 1152;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTATTAATAAGTGCTGCGGTGCCAGAAACC 32
Db 634 TTATTAATAAGTGCTGCGGTGCCAGAAACC 665
RESULT 21
LOCUS BD103170 1152 bp DNA linear PAT 27-AUG-2002
DEFINITION Vaccine.
ACCESSION BD103170
VERSION BD103170.1 GI:22648744
KEYWORDS JP 2001527091-A/11.
SOURCE unidentified
ORGANISM unclassified sequences.
REFERENCE 1 (bases 1 to 1152)
AUTHORS Dalemans, W.L.J. and Gerard, C.M.G.
TITLE VACCINE
JOURNAL Patent: JP 2001527091-A 11 25-DEC-2001;
SMITHKLINE BEECHAM BIOLOGICALS SA
COMMENT OS Unidentified
PN JP 2001527091-A/11
PD 25-DEC-2001
PF 18-DEC-1998 JP 2000526542
PR 24-DEC-1997 GB 9727262.9
PI WILFRIED L J DALEMANS, CATHERINE MARIE GHISLAINE GERARD PC
C07K14/025, A61K39/00, A61K39/12, A61K39/385, A61P35/00, C07K19/00, PC
C12N15/09,
PC C12N15/00
CC Strandedness: Single;
CC Topology: linear;
CC Vaccine
FH Key
FT source 1. 1152
Location/Qualifiers
/organism="unidentified".
FEATURES
source 1. 1152
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
ORIGIN

Query Match 100.0%; Score 32; DB 2; Length 1152;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTATTATAAGTGCGCTGCGGTCCAGAAACC 32
Db 634 TTATTATAAGTGCGCTGCGGTCCAGAAACC 665

RESULT 22
LOCUS AR183582 1152 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 22 from patent US 6342224.
ACCESSION AR183582
VERSION AR183582.1 GI:20227551
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1152)
AUTHORS Bruck,C., Silva,T,Cabezon., Fernando Dellesse,A.-M.Eva., Ghislaine Gerard,C.Marie. and Lombardo-Benchikh,A.
TITLE Recombinant papillomavirus vaccine and method for production and treatment
JOURNAL Patent: US 6342224-A 22 29-JAN-2002;
FEATURES
source Location/Qualifiers
1..1152
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 32; DB 2; Length 1152;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTATTATAAGTGCGCTGCGGTCCAGAAACC 32
Db 634 TTATTATAAGTGCGCTGCGGTCCAGAAACC 665

RESULT 23
LOCUS AX020945 1152 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 22 from Patent WO9333868.
ACCESSION AX020945
VERSION AX020945.1 GI:10044610
KEYWORDS Human papillomavirus
SOURCE Human papillomavirus
ORGANISM Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
REFERENCE 1
AUTHORS Dalemans,W.L. and Gerard,C.M.
TITLE Vaccine
JOURNAL Patent: WO 9333868-A 22 08-JUL-1999;
DALEMANS WILFRIED L J (BE); SMITHKLINE BEECHAM BIOLOG (BE); GERARD CATHERINE MARIE GHISLAIN (BE)
FEATURES
source Location/Qualifiers
1..1152
/organism="Human papillomavirus"
/mol_type="unassigned DNA"
/db_xref="taxon:10566"

ORIGIN
Query Match 100.0%; Score 32; DB 2; Length 1152;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTATTATAAGTGCGCTGCGGTCCAGAAACC 32
Db 634 TTATTATAAGTGCGCTGCGGTCCAGAAACC 665

RESULT 24
LOCUS BD015779 1188 bp DNA linear PAT 27-AUG-2002
DEFINITION Method for detecting human carcinogenic papilloma virus.
ACCESSION BD015779
VERSION BD015779.1 GI:22556916
KEYWORDS JP 2001197894-A/1.
SOURCE Papillomaviridae
ORGANISM Viruses; dsDNA viruses, no RNA stage.
REFERENCE 1 (bases 1 to 1188)
AUTHORS Morris,B.J. and Nightingale,B.
TITLE Method for detecting human carcinogenic papilloma virus
JOURNAL Patent: JP 2001197894-A 1 24-JUL-2001;
COMMENT BIOSEARCH INTERNATIONAL PTY LTD
OS Papillomavirus
PN JP 2001197894-A/1
PD 24-JUL-2001 JP 2000379281
PF 13-DEC-2000 JP 2000379281
PR 26-FEB-1987 AU P10559
PI BRYAN JAMES MORRIS, BRYAN NIGHTINGALE
PC C12N15/09,C12Q1/42,C12Q1/68,C12Q1/70//C12Q1/42,C12R1:01), PC
(C12Q1/42,C12R1:93), (C12Q1/68,C12R1:01), (C12Q1/68,C12R1:93), PC
(C12Q1/70,C12R1:93), (C12Q1/70,C12R1:01), C12N15/00 CC Method for
detecting human carcinogenic papilloma virus FH Key
Location/Qualifiers
FT source 1..1188
/organism="Papillomavirus".

FEATURES
source Location/Qualifiers
1..1188
/organism="Papillomaviridae"
/mol_type="genomic DNA"
/db_xref="taxon:151340"

ORIGIN

Query Match 100.0%; Score 32; DB 2; Length 1188;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTATTATAAGTGCGCTGCGGTCCAGAAACC 32
Db 610 TTATTATAAGTGCGCTGCGGTCCAGAAACC 641

RESULT 25
LOCUS E54157 1188 bp DNA linear PAT 31-JAN-2002
DEFINITION Method for detecting human carcinogenic papilloma virus HPV18.
ACCESSION E54157
VERSION E54157.1 GI:18628305
KEYWORDS JP 2000189200-A/1.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 1188)
AUTHORS James,M.B. and Bryan,N.
TITLE Method for detecting human carcinogenic papilloma virus HPV18
JOURNAL Patent: JP 2000189200-A 1 11-JUL-2000;
COMMENT BIOSEARCH INTERNATIONAL PTI LTD
OS Papilloma virus
PN JP 2000189200-A/1
PD 11-JUL-2000 JP 2000043673
PF 21-FEB-2000 JP 2000043673
PR 26-FEB-1987 AU P10559
PI MAURICE BRYAN JAMES, NIGHTINGALE BRYAN
PC C12Q1/68,C12N15/09,C12Q1/70//C12Q1/70,C12R1:91) CC
FT Key Location/Qualifiers
FT source 1..1188
/organism="Papilloma virus".

FEATURES

source Location/Qualifiers
1..1188
/organism="unidentified"
/mol_type="genomic DNA"

ORIGIN /db_xref="taxon:32644"

Query Match 100.0%; Score 32; DB 2; Length 1188;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTATTATAAGTGCCTGCGTCCAGAAACC 32
|||||
Db 610 TTATTATAAGTGCCTGCGTCCAGAAACC 641

RESULT 26
PARHPV6 1188 bp DNA linear VRL 12-SEP-1993
LOCUS Human papilloma virus (HPV-18) E6 ORF.
X04354
ACCESSION X04354.1 GI:60995
VERSION transforming capacity; unidentified reading frame.
KEYWORDS Human papillomavirus
SOURCE Human papillomavirus
ORGANISM
VIRUSES; dsDNA viruses, no RNA stage; Papillomaviridae;
unclassified Papillomaviridae.
1 (bases 1 to 1188)
Matishefski, G., Banks, L., Wu-Liao, J., Spence, P., Pim, D. and Crawford, L.
The expression of human papillomavirus type 18 E6 protein in bacteria and the production of anti-E6 antibodies
J. Gen. Virol. 67 (Pt 9), 1909-1916 (1986)
3018129

FEATURES
source location/Qualifiers
1..1188
/organism="Human papillomavirus"
/mol_type="genomic DNA"
/strain="type 18"
/db_xref="taxon:10566"
/tissue type="cervical carcinoma"
310..786
/note="unnamed protein product; E6 ORF (aa 1-158)"
/codon_start=1
/protein_id="CA27879.1"
/db_xref="GI:60996"
/db_xref="GOA:P06463"
/translation="MARFEDPTRRPYKLPDLCELNLSODIETTCYCKTVLETEV
FERAFKDLFVYRDSIPHAACHKCIDPYSIRLEIRHYSDSVDTLEKLTNTGLYNL
IRCLRCOKPLNPAEKJLHNEKRRFNHIAHYRGQCHSCCNRAQERLQRRRETQV"

ORIGIN

Query Match 100.0%; Score 32; DB 10; Length 1188;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTATTATAAGTGCCTGCGTCCAGAAACC 32
|||||
Db 610 TTATTATAAGTGCCTGCGTCCAGAAACC 641

RESULT 27
A06324 1750 bp DNA linear PAT 23-JUL-1993
LOCUS Hpv18 genes for E6, E7, and E1.
A06324.1 GI:413669
VERSION E1 gene; E6 gene; E7 gene.
KEYWORDS Human papillomavirus type 18
SOURCE Human papillomavirus type 18
ORGANISM
VIRUSES; dsDNA viruses, no RNA stage; Papillomaviridae;
alpha papillomavirus.
1 (bases 1 to 1750)
Oltersdorf, T., Roewekamp, W., Schneider-Gaedcke, A., Seedorf, K.,
Duerst, M. and Schwarz, E.
Expression products of human papilloma virus type 18, antibodies

JOURNAL specific for these proteins, and diagnostic reagents containing these antibodies or the corresponding DNA
Patent: EP 0256321-A 1 24-FEB-1988;
BEHRINGWERKE Aktiengesellschaft
Location/Qualifiers
1..1750
/organism="Human papillomavirus type 18"
/mol_type="unassigned DNA"
/db_xref="taxon:333761"
118..594
/codon_start=1
/product="E6"
/protein_id="CAA00539.1"
/db_xref="GI:413670"
/db_xref="GOA:P06463"
/db_xref="UniProtKB/Swiss-Prot:P06463"
/translation="MARFEDPTRRPYKLPDLCELNLSODIETTCYCKTVLETEV
FERAFKDLFVYRDSIPHAACHKCIDPYSIRLEIRHYSDSVDTLEKLTNTGLYNL
IRCLRCOKPLNPAEKJLHNEKRRFNHIAHYRGQCHSCCNRAQERLQRRRETQV"
603..920

CDS
/codon_start=1
/product="E7"
/protein_id="CAA00540.1"
/db_xref="GI:413671"
/db_xref="GOA:P06788"
/db_xref="UniProtKB/Swiss-Prot:P06788"
/translation="MHGPKATLDIVLHLEPQNBIFPDLLCHEQLSPSEBNDIDGV
NHQHLPRRREPQRHTMLCMCKCEARIELVESSADLRAFOQLFNTLSPVCPWCA
SQQ"
927..1750
/codon_start=1
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/protein_id="CAA00541.1"
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/db_xref="GOA:Q84181"
/db_xref="UniProtKB/TrEMBL:Q84181"
/translation="MADPEGTDEGTGNGMFPYQAIIVDKKTGDIISDDEENATDNG
SDMVDPIQGTGFCBOALETTALFHAQSVHNDADVLHVLKRFAGSGSTENSPIGSR
LEVDTLSRPLQGISLNSGCKAKRRLFTISDGYGSEVRAIOIQTTHGSHGAVC
SGGSTALINDGTGNNSSVDGTSNENIENVAPQCTIAQKDLKRNNOGAMLAIV
KDTYGSFIDLVNPFKSDKTYCTDWVTAJFGVNPITABGFKTLIQPILYAHIOCL"

ORIGIN

Query Match 100.0%; Score 32; DB 2; Length 1750;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTATTATAAGTGCCTGCGTCCAGAAACC 32
|||||
Db 418 TTATTATAAGTGCCTGCGTCCAGAAACC 449

RESULT 28
PARHPV18 1750 bp DNA linear VRL 12-SEP-1993
LOCUS Human papilloma virus type 18 (HPV 18) DNA for early region with proteins E6, E7, E1.
X04773
ACCESSION X04773.1 GI:60876
VERSION unidentified reading frame.
KEYWORDS Human papillomavirus
SOURCE Human papillomavirus
ORGANISM
VIRUSES; dsDNA viruses, no RNA stage; Papillomaviridae;
unclassified Papillomaviridae.
1 (bases 1 to 1750)
Seedorf, K., Oltersdorf, T., Krammer, G. and Roewekamp, W.
Identification of early proteins of the human papilloma viruses
type 16 (HPV 16) and type 18 (HPV 18) in cervical carcinoma cells
EMBO J. 6 (1), 139-144 (1987)
3034571
Data kindly reviewed (31-OCT-1987) by SEEDORF K.
Location/Qualifiers
1..1750

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/organism="Human papillomavirus"
/mol_type="genomic DNA"
/db_xref="taxon:10566"
39..43
/feature="TATA box"
86..90
/feature="TATA box"
118..594
/feature="TATA box"
/codon_start=1
/feature="unnamed protein product; E6 protein (AA 1-158)"
/protein_id="CAA28466.1"
/db_xref="GI:60877"
/db_xref="GOA:P06463"
/db_xref="UniProtKB/Swiss-Prot:P06463"
/translation="MARFEDPTRRPYKLPDLCTELNTSLQDIEITCYVCKTVELTEV
FEAFKDLFVYVRDSIIPHACHKCIDFYRSIRLRHYSDSVGDTEKLTNTGLVNL
IRCLRQCKPLNPAEKRLHNEKRRFPHNIAGHYGQCHSCNRRARORLORRRTQV"
603..920
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ORIGIN
Query Match 100.0%; Score 32; DB 10; Length 1750;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTATTATAAGTGCTGCGTCCAGAAACC 32
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Db 418 TTATTATAAGTGCTGCGTCCAGAAACC 449

RESULT 29
HIMHELB 3135 bp mRNA linear VRL 06-DEC-1999
DEFINITION Human papillomavirus type 18 proteins E6 and E7 mRNA, complete
ACCESSION M20325
VERSION M20325.1 GI:183936
KEYWORDS protein E1; protein E6; protein E7.
SOURCE Human papillomavirus type 18
ORGANISM Human papillomavirus type 18
REFERENCE 1 (bases 1 to 3135)
AUTHORS Inagaki,Y., Tanukawa,Y., Takebe,N., Nawa,H., Nakanishi,S.,
Terada,H. and Sugimura,T.
TITLES Nucleotide sequences of cDNAs for human papillomavirus type 18
transcripts in HeLa cells
JOURNAL J. Virol. 62 (5), 1640-1646 (1988)
PUBMED 2833614
COMMENT The integrated viral sequence starts at position 1.
FEATURES
source 1..2393
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FEAFKDLFVYVRDSIIPHACHKCIDFYRSIRLRHYSDSVGDTEKLTNTGLVNL
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ORIGIN
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QY 1 TTATTATAAGTGCTGCGTCCAGAAACC 32
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Db 301 TTATTATAAGTGCTGCGTCCAGAAACC 332

RESULT 30
HP089349 5210 bp DNA linear VRL 02-DEC-1999
LOCUS HP089349
DEFINITION Human papillomavirus type 18 variant, partial sequence.
ACCESSION U89349
VERSION U89349.1 GI:2052453
KEYWORDS Human papillomavirus type 18
SOURCE Human papillomavirus type 18
ORGANISM Human papillomavirus type 18
REFERENCE 1 (bases 2216 to 2355; 2538 to 3127)
AUTHORS Schneider-Gedicks,A. and Schwarz,E.
TITLES Different human cervical carcinoma cell lines show similar
transcription patterns of human papillomavirus type 18 early genes
JOURNAL EMBO J. 5 (9), 2285-2292 (1986)
PUBMED 3023067
REFERENCE 2 (bases 1 to 5210)
AUTHORS Cole,S.T. and Dancos,O.
TITLES Nucleotide sequence and comparative analysis of the human
```

papillomavirus type 18 genome. Phylogeny of papillomaviruses and repeated structure of the E6 and E7 gene products
J. Mol. Biol. 193 (4), 599-608 (1987)

JOURNAL
PUBMED
3039146
3 (bases 1246 to 4619)
Inagaki, Y., Tsunokawa, Y., Takebe, N., Nawa, H., Nakanishi, S., Terada, M. and Sugimura, T.
Nucleotide sequences of cDNAs for human papillomavirus type 18 transcripts in HeLa cells
J. Virol. 62 (5), 1640-1646 (1988)

JOURNAL
PUBMED
2833614
4 (bases 1750 to 2070)
Ong, C.K., Chan, S.Y., Campo, M.S., Fujinaga, K., Mayromara-Nazos, P., Labropoulou, V., Pfister, H., Tay, S.K., ter Meulen, J., Villa, L.L. and Bernard, H.-U.
Evolution of human papillomavirus type 18: an ancient phylogenetic root in Africa and intratype diversity reflect coevolution with human ethnic groups
J. Virol. 67 (11), 6424-6431 (1993)

JOURNAL
PUBMED
8411344
5 (bases 1 to 5210)
Weisener, J.D.
Nucleotide sequences and further characterization of human papillomavirus DNA present in the Caski, SiHa and HeLa cervical carcinoma cell lines
J. Gen. Virol. 80 (Pt 7), 1725-1733 (1999)

JOURNAL
PUBMED
10423141
6 (bases 1 to 5210)
Weisener, J.D.
Direct Submission
Submitted (10-FEB-1997) VEB, Centers for Disease Control and Prevention, 1600 Clifton Road NE, Atlanta, GA 30333, USA
Location/Qualifiers
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140
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1935
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FEATURES
source

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Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTATTAATAAGTGCGCTGCGGTCAGAAACC 32
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Db 2527 TTATTAATAAGTGCGCTGCGGTCAGAAACC 2558
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RESULT 31
CS073239 7857 bp DNA linear PAT 05-MAY-2005
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1
Chau, M.F., Bisgaard-Franzen, K., Lin, J., Rasmussen, O.F., Wang, Z., Lusk, J., Lindberg, M. and Yeast, S.
Methods and compositions for the diagnosis of cancer
Patent: WO 2005033333-A2 14-APR-2005;
Dakocytomation Denmark A/S (DK)
Location/Qualifiers
1. 7857
/organism="Homo sapiens"
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FEATURES
source

ORIGIN
Query Match 100.0%; Score 32; DB 2; Length 7857;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTATTAATAAGTGCGCTGCGGTCAGAAACC 32
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Db 405 TTATTAATAAGTGCGCTGCGGTCAGAAACC 436
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[illegible]

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AFSDSISLEVPQGTGVANAVFGPTSGTHQYERIPLQTFASGCTGSEPLISVPLPV
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ORIGIN
Query Match 100.0%; Score 32; DB 10; Length 7857;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTATTATAAGTGCTGCGGTCCAGAAACC 32
Db 405 TTATTATAAGTGCTGCGGTCCAGAAACC 436

RESULT 34
HPV45E67 910 bp DNA linear VRL 20-MAY-1997
LOCUS Human papillomavirus type 45, E6 and E7 genes.
DEFINITION
ACCESSION Y13218.1 GI:2113839
VERSION Y13218.1 GI:2113839
KEYWORDS E6 gene; E7 gene.
SOURCE Human papillomavirus type 45
ORGANISM Human papillomavirus type 45
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Alphapapillomavirus.
REFERENCE 1
Saxtre-Garau,X., Favre,M., Couturier,J. and Orth,G.
Distinct patterns of alteration of myc genes associated with
integration of HPV16 or HPV45 DNA in two genital tumors
J. Gen. Virol.
2 (bases 1 to 910)
Favre,M.
Direct Submission
Submitted (09-MAY-1997) M. Favre, Institut Pasteur, Virology, 25
Rue du Dr Roux, 75015-Paris, FRANCE
location/Qualifiers
1..910
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FEATURES
source
gene
CDS
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Query Match 95.0%; Score 30.4; DB 10; Length 910;
Best Local Similarity 96.9%; Pred. No. 0.015;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTATTATAAGTGCTGCGGTCCAGAAACC 32
Db 402 TTATTATAAGTGCTGCGGTCCAGAAACC 433

RESULT 35
PPH45E67A 1843 bp DNA linear VRL 02-AUG-1993
LOCUS Human papillomavirus type 45 E6 and E7 genes, complete cds.
DEFINITION
ACCESSION M38198
VERSION M38198.1 GI:333059
KEYWORDS
SOURCE Human papillomavirus
ORGANISM Human papillomavirus
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
unclassified Papillomaviridae.
REFERENCE 1
Kaplan,U.B. and Burk,R.D.
Evolution of the papillomaviruses
Unpublished (1990)
Original source text: Human papillomavirus (type 45) DNA.
Draft entry and computer-readable sequence for [1] kindly submitted
by U.B.Kaplan, 27-AUG-1990.
Lederle Laboratories
60B-317
Pearl River, NY 10965.
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FEATURES
source
gene
CDS
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ORIGIN

Query Match 95.0%; Score 30.4; DB 10; Length 1843;
Best Local Similarity 96.9%; Pred. No. 0.014;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTATTAATAGTGCTGCGGTCGACGAAACC 32
Db 1323 TTGTATAAGTGCTGCGGTCGACGAAACC 1354

RESULT 36
HPV45 7858 bp DNA linear VRL 18-Apr-2005
LOCUS Human papillomavirus type 45 genomic DNA.
DEFINITION X74479.1 GI:397022
ACCESSION E1 gene; E2 gene; E4 gene; E6 gene; E7 gene; early protein; L1
VERSION K74479.1
KEYWORDS Human papillomavirus type 45
SOURCE Human papillomavirus type 45
ORGANISM Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
REFERENCE 1 (bases 1 to 7858)
AUTHORS Delius,H. and Hofmann,B.
TITLE Primer-directed sequencing of human papillomavirus types
JOURNAL Curr. Top. Microbiol. Immunol. 186, 13-31 (1994)
PUBMED 8205838
REFERENCE 2 (bases 1 to 7858)
AUTHORS Delius,H.
TITLE Direct Submision
JOURNAL Submitted (06-AUG-1993) H. Delius, Deutsches
Krebsforschungszentrum, Abteilung ATV, Im Neuenheimer Feld 506, W
6900 Heidelberg, FRG

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VHSYOSGGSDSNAENVDPHCSITELKELQANKKAAVLAFKDIYGLSFVDLVN
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TKYALMDATHTCTWYEDNMRNALDGNPISIRKKHPLQLKCPILTSTNIDPAD
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YMGVYIKGSDTTYVQFKSECKGNSNWEYQGNVLDQNSMSTHDDPTASQ
IVQLOHASTSTPKNASVGTPEPHIQTATKPRQGLCTVQHGKRVATNPLCCS
TSNNKRRKVCSGNTTPIILKGDKNLSKLRRLRKADHYSEISSYTHWTGCKNKG
ILTVYNSGEQRTFLDVVTIPNSVQISVGWYMTI"

gene 4236..5627
/gene="L2"
4236..5627
/gene="L2"
/codon_start=1
/product="late protein"
/protein_id="CA52577.1"
/db_xref="GI:397028"
/db_xref="GOA:P36761"
/db_xref="InterPro:IPR000784"
/translation="MYSRRARRRRASATDLRYTCKQSGCPDPVINKVEGTLADKI
LWSSIGIFGIGIGISGGGRTGVPILGGRSNVVDVGPTRPPVIVIPGPTDS
ITVLVEDSSVYASGAVPTPTGSGREITSSGTTTTPAVDITTPVDSVSSSTFNP
AFSDPEITIEPQGEVSQNLFEPTPSGSHGYEILPQTPASSGSGTEPSSITPLPV
RRVGRGLYSRAGQVRSVSTQPLTHPSLSLVTDNPAVEPLDTLSEPTSNVPSDF
MDIIRLRLPALSSRGTVRFSRLGQRAIMTRGSKQGGVHFYHDISPIAAEIEIL
QPLISATNDSDLFDVYADFPFPASTPTSTHKSFYPKSLTWPSTASSYSNVTVL
TSAMDVPIYTGPDIIILPSHTPMWPSPTNASTTYYIGHGTYVYLMFWYYPKCKK
RIYPPFADGRVA"

gene 5350..7149
/gene="L1"
5350..7149
/gene="L1"
/codon_start=1
/product="late protein"
/protein_id="CA52578.1"
/db_xref="GI:397029"
/db_xref="GOA:P36741"
/db_xref="InterPro:IPR002210"
/db_xref="InterPro:IPR008975"
/db_xref="UniProtKB/Swiss-Prot:P36741"
/translation="MAHNTIYGHGIIIFLEKNVVPFLQMALMRPSDSTVYLPPEV
ARVSTDDVYSRTSIFYHAGSSRLTVGNVEYFVVPVPGAGNKAQVPPVSAVQKRVFV
ALPDPNPKFGLDSTIYNPETORLVMACVGMEIGRGPLGIGLGHGHPYXNLDTESAH
AATAVITQDVADVNDVYKOTQCLICIGVAIIEHNAKGLTCKPAQLOPDCPLLEK
NTIIEGDWVDVGYGAMDFETLQDTKCEVPLDLCQSIKCKPYLQNSADPYGSMFC

Query Match 95.0%; Score 30.4; DB 5; Length 8039;
 Best Local Similarity 96.9%; Pred. No. 0.012;
 Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTATTAAATAGGTCCTGCGGTGCCAGAAACC 32
 |||
 Db 6428 TTGTTAAATAGGTCCTGCGGTGCCAGAAACC 6459

RESULT 38
 MUSRP 886 bp mRNA linear ROD 27-APR-1993
 LOCUS Mus musculus ribosomal protein mRNA, complete cds.
 M55235 M38426
 VERSION M55235.1 GI:200769
 KEYWORDS ribosomal protein.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 886)
 Zheng, Y.-M., Su, P., Wang, J.-X., Basu, A., Bhat, K.S., Carter, R. and Avadhani, N.G.
 Immunochemical and structural similarity between a mouse cytochrome oxidase subunit and ribosomal protein- L7
 Unpublished (1991)
 COMMENT Original source text: Mus musculus (strain Swiss) cDNA to mRNA.
 FEATURES location/Qualifiers
 source 1..886
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="Swiss"
 /db_xref="taxon:10090"
 1..886
 /gene="ribosomal protein"
 11..823
 /gene="ribosomal protein"
 /codon_start=1
 /product="ribosomal protein"
 /protein_id="AA040064.1"
 /db_xref="GI:200770"
 /translation="MEAVPEKKKQVATVPGTLKKKVPAMAKNSKKVPAVETKKKR
 RNPAELKRLRKKKAKTAKYAKRKLIYEKAKHYEYQMTETIRMAKAKN
 PYPAPBKLAFAVIRIRGINSPPRYKYLQLRKQIPNGTFVAKASIMLAIVDP
 YIANGYPLNSVNEILYKRGKINKRIATDLSLARSIGKGIICMEDLHEIYT
 VGRKFEKANNFLMPFKLSSPRGKKKKTTFVEGDAGNREDQINRLIRRMN"
 886
 /gene="ribosomal protein"

polya_site
 886
 /gene="ribosomal protein"

ORIGIN
 Query Match 76.9%; Score 24.6; DB 6; Length 886;
 Best Local Similarity 87.1%; Pred. No. 6.7;
 Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 TATTAAATAGGTCCTGCGGTGCCAGAAACC 32
 |||
 Db 97 TAAGAAAAAGGTCCTGCGGTGCCAGAAACC 127

RESULT 39
 BC056907 1225 bp mRNA linear PRI 08-OCT-2003
 LOCUS Homo sapiens cDNA clone MGC:51514 IMAGE:5122136, complete cds.
 BC056907
 ACCESSION BC056907.1 GI:34784913
 VERSION BC056907.1 GI:34784913
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 1225)

AUTHORS
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
 Altschul, S.P., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
 Scapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
 Scheetz, T.E., Brownstein, M.J., Ustiel, T.B., Tothiyuki, S.,
 Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
 Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
 McKernan, K.D., Malek, U.A., Gunaratne, P.H., Richards, S.,
 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.U., Hu, Y., S.W.,
 Vallaloo, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
 Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,
 Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,
 Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D.,
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smalins, D.E.,
 Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

TITLE
 JOURNAL PUBLISHED
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 Submitted (25-AUG-2003) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: gcgabs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LULNL)
 DNA Sequencing by: Genome Sequence Center,
 BC Cancer Agency, Vancouver, BC, Canada
 info@cgsc.bc.ca
 Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butlerfield,
 Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
 Leticia Hsiao, Martin Krzywinski, Reta Kutische, Oliver Lee, Soo
 Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
 Nee, Pawan Pandoh, Anna-Lisa Prabhu, Parvaneh Saeei, Jacqueline
 Schein, Duane Smalins, Michael Smith, Lorraine Spence, Jeff Stott,
 Michael Thorne, Miranda Tsai, Natasja van den Bosch, Jill Vardy,
 George Yang, Scott Zuyderduyn, Marco Marra.

FEATURES
 source
 1..1225
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="MGC:51514 IMAGE:5122136"
 /issue_type="Cervix, carcinoma"
 /clone_id="NIH MGC_12"
 /lab_host="DH10B"
 /note="vector: pCMV-SPORT6"
 282..599
 /codon_start=1
 /product="Unknown (protein for MGC:51514)"
 /protein_id="AA056907.1"
 /db_xref="GI:34784914"
 /translation="MNGPKATLQDIVLHLEPQNEIPVPLICHEQLSPRENDRIDCV
 NQGLPAPRAEPQPHMLCMCKCKBARIKLVESASDDLAAPOLPLNTLSPVCPMCA
 SQQ"
 282..587
 /note="E7; Region: E7 protein, Early protein"

ORIGIN /db_xref="CDD:pfam00527"

Query Match 75.6%; Score 24.2; DB 5; Length 1225;
Best Local Similarity 89.7%; Pred. No. 9.8;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TTATAAGGTGCTCGGTGCCAGAAACC 32
|||||
Db 100 TTACAGAGGTGCTCGGTGCCAGAAACC 128

RESULT 40
LOCUS HUMHELA 1300 bp mRNA linear VRL 06-DEC-1999
DEFINITION Human papillomavirus type 18 proteins E6 and E7 mRNA, complete
ACCESSION M20324.1 GI:183933
VERSION M20324.1 GI:183933
KEYWORDS Protein E6; protein E7.
SOURCE Human papillomavirus type 18
ORGANISM Human papillomavirus type 18
VIRUSES/dedDNA viruses, no RNA stage; Papillomaviridae;
Alphapapillomavirus.
1 (bases 1 to 1300)
Inagaki,Y., Tsunokawa,Y., Takebe,N., Nawa,H., Nakanishi,S.,
Terada,M. and Sugimura,T.
Nucleotide sequences of cDNAs for human papillomavirus type 18
transcripts in HeLa cells
J. VIROL. 62 (5), 1640-1646 (1988)
2833614

COMMENT The integrated viral sequence starts at position 1.
FEATURES
source
1..724
/organism="Human papillomavirus type 18"
/mol_type="mRNA"
/db_xref="taxon:333761"
/map="841 bp upstream from Bali site"
/clone="20"
/cell_line="HeLa; SKG-[I,II]"
/focus
725..1300
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
82..255
/codon_start=1
/product="protein E6"
/protein_id="AA09512.1"
/db_xref="GI:306834"
/translation="MARFDPTRRPYKLPDLCTELNTSLQDIEITCVYCKTVLRETV
PVPETVESRKT"
385..702
/codon_start=1
/product="protein E7"
/protein_id="AA09513.1"
/db_xref="GI:306835"
/translation="MHGPKATLQDIVLHLEPONEIPVDLLCHQLSDSEENDEIDGV
MHOHLPARARAPRHTMLCMCCRCARITKLVYSSADDLAPQDLPLNTLSFVCPWCA
SQO"

ORIGIN

Query Match 75.6%; Score 24.2; DB 10; Length 1300;
Best Local Similarity 89.7%; Pred. No. 9.8;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TTATAAGGTGCTCGGTGCCAGAAACC 32
|||||
Db 203 TTACAGAGGTGCTCGGTGCCAGAAACC 231

RESULT 41
LOCUS AR084350 1109 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 12 from patent US 5981173.
ACCESSION AR084350
VERSION AR084350.1 GI:10011121
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 1095)
AUTHORS Orth,G., Beaudenon,S. and Longuet,M.
Genital human papillomavirus type 68a (HPV-68a), related to the
potentially oncogenic HPV-39
Patent: US 5981173-A 12 09-NOV-1999;
JOURNAL Location/Qualifiers
1..1095
source
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 75.0%; Score 24; DB 2; Length 1095;
Best Local Similarity 84.4%; Pred. No. 12;
Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TTATTATAAGGTGCTCGGTGCCAGAAACC 32
|||||
Db 580 TTATTGATTAAGGTGATGAGTTGCTGGAACC 611

RESULT 42
LOCUS AR084344 1108 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 6 from patent US 5981173.
ACCESSION AR084344
VERSION AR084344.1 GI:10011115
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 1108)
AUTHORS Orth,G., Beaudenon,S. and Longuet,M.
Genital human papillomavirus type 68a (HPV-68a), related to the
potentially oncogenic HPV-39
Patent: US 5981173-A 6 09-NOV-1999;
JOURNAL Location/Qualifiers
1..1108
source
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 75.0%; Score 24; DB 2; Length 1108;
Best Local Similarity 84.4%; Pred. No. 12;
Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TTATTATAAGGTGCTCGGTGCCAGAAACC 32
|||||
Db 593 TTATTGATTAAGGTGATGAGTTGCTGGAACC 624

RESULT 43
LOCUS AR084343 1110 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 5 from patent US 5981173.
ACCESSION AR084343
VERSION AR084343.1 GI:10011114
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 1110)
AUTHORS Orth,G., Beaudenon,S. and Longuet,M.
Genital human papillomavirus type 68a (HPV-68a), related to the
potentially oncogenic HPV-39
Patent: US 5981173-A 5 09-NOV-1999;
JOURNAL

FEATURES
source
Location/Qualifiers
1. 1110
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 75.0%; Score 24; DB 2; Length 1110;
Best Local Similarity 84.4%; Pred. No. 12;
Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TTATTATAAGTGCCTGCGGTGCCAGAAACC 32
594 TTATCATTAAGTGCATGATGTTGCTGAAACC 625

RESULT 44
LOCUS AR084345 1110 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 7 from patent US 5981173.
ACCESSION AR084345
VERSION AR084345.1 GI:10011116
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1110)
AUTHORS Orth,G., Beaudenon,S. and Longuet,M.
TITLE Genital human papillomavirus type 68a (HPV-68a), related to the
JOURNAL Potentially oncogenic HPV-39
FEATURES Location/Qualifiers
1. 1110
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 75.0%; Score 24; DB 2; Length 1110;
Best Local Similarity 84.4%; Pred. No. 12;
Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TTATTATAAGTGCCTGCGGTGCCAGAAACC 32
596 TTATCATTAAGTGCATGATGTTGCTGAAACC 627

RESULT 45
LOCUS HPV66 1313 bp DNA linear VRL 02-JUN-1996
DEFINITION Human Papilloma Virus E6 gene for transforming protein.
ACCESSION X67160
VERSION X67160.1 GI:1197491
KEYWORDS E6 gene; transforming gene.
SOURCE Human papillomavirus type 68
ORGANISM Human papillomavirus type 68
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Alphapapillomavirus.
REFERENCE 1 (bases 1 to 1313)
AUTHORS Longuet,M., Beaudenon,S. and Orth,G.
TITLE Two novel genital human papillomavirus (HPV) types, HPV68 and
JOURNAL HPV70, related to the potentially oncogenic HPV39
FEATURES J. Clin. Microbiol. 34 (3), 738-744 (1996)
PUBMED 8904450
REFERENCE 2 (bases 1 to 1313)
AUTHORS Longuet,M.
TITLE Direct Submission
JOURNAL Submitted (03-JUL-1992) M. Longuet, Institut Pasteur, Laboratoire
des Papillomavirus, 25 Rue du Dr Roux, 75024 Paris Cedex 15, FRANCE
FEATURES 1. 1313
Location/Qualifiers
/organism="Human papillomavirus type 68"
/mol_type="genomic DNA"
/db_xref="taxon:45240"
/cell_line="intraepithelial neoplasia"

gene 280..1095
/gene="E6"
CDS 280..756
/gene="E6"
/codon_start=1
/product="transforming protein"
/protein_id="CAA47632.1"
/db_xref="GI:1197493"
/db_xref="GOA:P54667"
/db_xref="UniProtKB/Swiss-Prot:P54668"
/translation="MALFNPERPYLPDLCTLDLTDLTLDVTCHEQLDSDDEINPEPH
YEPASFDLCVVRDGVFPACOSCIKRYAIRIERYSESVATLTETINTKLYNL
IRMGSLKPLCPAEKJLHLLTKRLHKLIAGNFTGQCHWCSTSKEDRRRIROETQV"
763..1095
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/db_xref="GI:1197493"
/db_xref="GOA:P54668"
/db_xref="UniProtKB/Swiss-Prot:P54668"
/translation="MGPKPTVDEIYELCPYNEIQPVLDVYCHEQLDSDDEINPEPH
AVNHQHLIARDEQRRRIQCLCKCNFALDLVEASRDNLKTLQQLFMDSLNFCV
PWCATETQ"

ORIGIN
Query Match 75.0%; Score 24; DB 10; Length 1313;
Best Local Similarity 84.4%; Pred. No. 12;
Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TTATTATAAGTGCCTGCGGTGCCAGAAACC 32
580 TTATTGATTAAGTGCATGATGTTGCTGAAACC 611

RESULT 46
LOCUS AR084352 3283 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 14 from patent US 5981173.
ACCESSION AR084352
VERSION AR084352.1 GI:10011123
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3283)
AUTHORS Orth,G., Beaudenon,S. and Longuet,M.
TITLE Genital human papillomavirus type 68a (HPV-68a), related to the
JOURNAL Potentially oncogenic HPV-39
FEATURES Patent: US 5981173-A 14 09-NOV-1999;
Location/Qualifiers
1. 3283
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 75.0%; Score 24; DB 2; Length 3283;
Best Local Similarity 84.4%; Pred. No. 11;
Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TTATTATAAGTGCCTGCGGTGCCAGAAACC 32
2754 TTATCATTAAGTGCATGATGTTGCTGAAACC 2785

RESULT 47
LOCUS HPU22461 3283 bp DNA linear VRL 31-MAY-1996
DEFINITION Human papillomavirus type 70 E6 protein (E6), E7 protein (E7), and
ACCESSION U22461
VERSION U22461.1 GI:1345087
KEYWORDS

SOURCE	Human papillomavirus type 70
ORGANISM	Human papillomavirus type 70 viruses; deDNA viruses, no RNA stage; Papillomaviridae; Alphapapillomavirus.
REFERENCE	1 (bases 1 to 3283)
AUTHORS	Longuet, M., Beaudenon, S. and Orth, G.
TITLE	Two novel genital human papillomavirus (HPV) types, HPV68 and HPV70, related to the potentially oncogenic HPV39
JOURNAL	J. Clin. Microbiol. 34 (3), 738-744 (1996)
PUBMED	8904450
AUTHORS	2 (bases 1 to 3283)
TITLE	Longuet, M.
JOURNAL	Direct Submission
PUBMED	Submitted (13-MAR-1995)
AUTHORS	Michelle Longuet, Laboratoire des Papillomavirus, Unite INSERM 190, Institut Pasteur, 25 rue du Dr Roux, Paris 75015, France
FEATURES	Location/Qualifiers
source	1..3283
gene	/organism="Human papillomavirus type 70"
CDS	/mol_type="genomic DNA"
gene	/db_xref="taxon:39457"
CDS	26..1546
gene	/gene="L1"
CDS	26..1546
gene	/note="putative major capsid protein"
CDS	/codon_start=1
gene	/product="L1 protein"
CDS	/protein_id="AAC54879.1"
gene	/db_xref="GI:1345088"
CDS	/translation="MALNRSSDNTVYLPPEPSAVKAVNTDDYVTRTGYYVAGTSRLTLTVGHVYFRVAVNGRKHPIKVAAYQVRFVSLDPNPKFGI,PDPSLYNPDIQRLVMAQIGVIGRGQPLGVGSGHPLNRLADTVRFNSHSFSAVSTODSRDVSVDYKOTLCIIGVPMHSGHMAKAKACTTVOOGDCPLLELVNTAIEODMIDTGYGAMDFTTIPSELYEVPIDGOSVCKYPDYLOMSADYGDMSFPLRKEOLFARHFNMGGVNVPITISELYIKGDIIDRRPGCTHYVSPSSWSQGLKRNKYVTHKQGHNGICMNOGLITVVYDTRSTNFTLSACTRTRALPAVYSPTRKRSYRHYBYDLOFTFOLCTITLADMAVITHYMPALIDNNINIGVTPPPSALVDTRYVLOSAIAACQAKAPTEKDDPYDLKFMNVVLDKRFSTELDQFPLGRKFLVLGVARRRPTIGPRKRPASAKSSSSASHKRRKRVSK"
TATA_signal	2419..2425
gene	/note="putative"
CDS	2454..2930
gene	/gene="E6"
CDS	2454..2930
gene	/gene="E6"
CDS	/note="putative transforming protein"
gene	/codon_start=1
CDS	/product="E6 protein"
gene	/protein_id="AAC54880.1"
CDS	/db_xref="GI:1345089"
gene	/translation="MARPNPAERPYKLPDLCALDDTLTDITDCAVCTQLQDTEVYEFPSLAFIYRNGEPYAAQCCKIKPAKVRLEIRHYSNSYVATLTSINTKLYDLSIRCSCKPLCPAPKALRHVNTKRRFHQIAGSYTGQCBHCSWTNSREDRIRIRFQV"
gene	2939..3268
CDS	/gene="E7"
gene	2939..3268
gene	/gene="E7"
CDS	/note="putative transforming protein"
gene	/codon_start=1
CDS	/product="E7 protein"
gene	/protein_id="AAC54881.1"
CDS	/db_xref="GI:1345090"
gene	/translation="MAGRPFLQETIVADLYPYNEIQPYDVLYCHQQLSESDNETEPDPHVVNQOQQLARREPORHKTIQCMCKCKNTTLTALVEASQENLRSLDLEFETLSVFCVWCASGTO"
ORIGIN	
Query Match	75.0% Score 24; DB 10; Length 3283;
Best Local Similarity	84.4%; Pred. No. 11;
Matches	27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
1	TTATTAAATAGTGCCTGCGGTGCGCAAGAAC
32	TTATTAAATAGTGCCTGCGGTGCGCAAGAAC

RESULT 48	DB	2754	TTATCATTAAGGTGCATGATGTCCTAAACC	2785
DEFINITION	HSFUSION	4618 bp	mRNA	linear
LOCUS	Viral-cellular fusion mRNA with Human Papillomavirus type 68 E6 and E7 genes, and Homo sapiens APM-1 gene.			VRL 18-APR-2005
ACCESSION	Y14591	GI:3005941		
VERSION	APM-1 gene; E6 gene; E7 gene; fusion.			
KEYWORDS	Human papillomavirus type 68			
SOURCE	Human papillomavirus type 68			
ORGANISM	Viruses; dsDNA viruses, no RNA stage; Papillomaviridae; Alphapapillomavirus			
REFERENCE	1 (bases 1 to 4618)			
AUTHORS	Reuter,S., Delius,H., Kahn,T., Hofmann,B., zur Hausen,H. and Schwartz,B.			
TITLE	Characterization of a novel human papillomavirus DNA in the cervical carcinoma cell line ME180			
JOURNAL	J. Virol. 65 (10), 5564-5568 (1991)			
PUBMED	1716694			
REFERENCE	2			
AUTHORS	Reuter,S., Bartelmann,M., Vogt,M., Geisen,C., Napieraki,I., Kahn,T., Delius,H., Lichter,P., Wetz,S., Korn,B. and Schwartz,B.			
TITLE	APM-1, a novel human gene, identified by aberrant co-transcription with papillomavirus oncogenes in a cervical carcinoma cell line, encodes a BTR/POZ-zinc finger protein with growth inhibitory activity			
JOURNAL	EMBO J. 17 (1), 215-222 (1998)			
PUBMED	9427755			
REFERENCE	3			
AUTHORS	Delius,H.			
TITLE	Direct Submission			
JOURNAL	Submitted (13-AUG-1997) H. Delius, Deutsches Krebsforschungszentrum, Angewandte Tumorstrologie, Im Neuenheimer Feld 242, D-69120 Heidelberg, FRG			
REMARK	Revised by author 18-DEC-97			
COMMENT	Related sequence M73258.			
FEATURES	Location/Qualifiers			
source	1..839			
	/organism="Human papillomavirus type 68"			
	/mol_type="mRNA"			
	/db_xref="taxon:45240"			
	/focus			
source	840..4618			
	/organism="Homo sapiens"			
	/mol_type="mRNA"			
	/db_xref="taxon:9606"			
	/chromosome="18"			
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ORIGIN

Query Match 75.0%; Score 24; DB 10; Length 4618;
Best Local Similarity 84.4%; Pred. No. 11;
Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TTATTAATAGGTCGCGTCCGACGAAAC 32
Db 301 TTATCAATAGTGCAATGTGTGCTGAAC 332

RESULT 49

HMMHPVME18 6042 bp DNA linear VRL 30-NOV-1999
DEFINITION Human cellular DNA/Human papillomavirus proviral DNA.
ACCESSION M73258.1 GI:184383
VERSION M73258.1
KEYWORDS proviral gene.
SOURCE Human papillomavirus
ORGANISM Human papillomavirus

Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
unclassified Papillomaviridae.
1 (bases 1 to 6042)

REFERENCE
AUTHORS Reuter,S., Dellus,H., Kahn,T., Hofmann,B., zur Hausen,H. and
Schwarz,E.
TITLE Characterization of a novel human papillomavirus DNA in the
JOURNAL J. Virol. 65 (10), 5564-5568 (1991)
PUBMED 1716694

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ORIGIN

Query Match 75.0%; Score 24; DB 10; Length 6042;
Best Local Similarity 84.4%; Pred. No. 10;
Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TTATTAATAGGTCGCGTCCGACGAAAC 32
Db 4246 TTATCAATAGTGCAATGTGTGCTGAAC 4277

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DEFINITION Human papillomavirus type 68a, complete genome.
ACCESSION DQ080079
VERSION DQ080079.1 GI:71726685
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SOURCE
ORGANISM Human papillomavirus type 68a (HPV68a)
Human papillomavirus type 68a
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Alphapapillomavirus.
1 (bases 1 to 7822)
Narechania, A., Chen, Z., Desalle, R. and Burk, R.D.
Phylogenetic incongruence among Oncogenic Genital Alpha Human
Papillomaviruses
J. Virol. 79 (24), 15503-15510 (2005)
JOURNAL
PUBMED 16306621
2 (bases 1 to 7822)
Chen, Z. and Burk, R.D.
Direct Submission
REFERENCES
Submitted (31-MAY-2005) Microbiology and Immunology, Albert
Einstein College of Medicine of Yeshiva University, 1300 Morris
Park Ave., Ullmann Room 515, Bronx, NY 10461, USA
JOURNAL
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ORIGIN

Query Match 75.0%; Score 24; DB 10; Length 7822;
Best Local Similarity 84.4%; Pred. No. 10;
Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Cy 1 TTATTATAGTGCCTGCGCTCCAGAAAC 32
Db 301 TTATTGATTAAGTGATGATGCTCGAAACC 332

Search completed: May 24, 2006, 06:51:31
Job time : 1059.62 secs

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2006, 05:34:58 ; Search time 300.037 Seconds
(without alignments)
650.664 Million cell updates/sec

Title: US-10-601-913-1

Perfect score: 28
Sequence: 1 GACATTATTGTTATGTTGATGAGAC 28

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000.

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

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2: geneseqn1990s:*
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4: geneseqn2001as:*
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15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	28	100.0	28	2	AAT72414 Human pap
4	28	100.0	28	2	AAT72401 Human pap
5	28	100.0	452	14	ADK26909 Human pap
6	28	100.0	477	10	ADK26907 Human pap
7	28	100.0	477	10	ADK26908 Human pap
8	28	100.0	477	10	ADK26908 Human pap
9	28	100.0	519	2	AAT72441 Human pap
10	28	100.0	519	2	AAT72441 Human pap
11	28	100.0	519	2	AAT72441 Human pap
12	28	100.0	712	1	AAAG1600 Partial n
13	28	100.0	768	13	ADR47004 Human pap
14	28	100.0	768	15	ADR47004 Human pap
15	28	100.0	776	2	AAH14663 E6/E7 reg
16	28	100.0	779	2	AAH14663 E6/E7 reg
17	28	100.0	790	2	AAH14663 E6/E7 reg
18	28	100.0	801	2	AAH14663 E6/E7 reg

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21	28	100.0	822	2	AAH14663 E6/E7 reg
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43	28	100.0	1173	2	AAH14663 E6/E7 reg
44	28	100.0	1173	2	AAH14663 E6/E7 reg
45	28	100.0	1173	2	AAH14663 E6/E7 reg
46	28	100.0	1173	2	AAH14663 E6/E7 reg
47	28	100.0	1173	2	AAH14663 E6/E7 reg
48	28	100.0	1173	2	AAH14663 E6/E7 reg
49	28	100.0	1173	2	AAH14663 E6/E7 reg
50	28	100.0	1173	2	AAH14663 E6/E7 reg
51	28	100.0	1173	2	AAH14663 E6/E7 reg
52	28	100.0	1173	2	AAH14663 E6/E7 reg
53	28	100.0	1173	2	AAH14663 E6/E7 reg
54	28	100.0	1173	2	AAH14663 E6/E7 reg
55	28	100.0	1173	2	AAH14663 E6/E7 reg
56	28	100.0	1173	2	AAH14663 E6/E7 reg
57	28	100.0	1173	2	AAH14663 E6/E7 reg
58	28	100.0	1173	2	AAH14663 E6/E7 reg
59	28	100.0	1173	2	AAH14663 E6/E7 reg
60	28	100.0	1173	2	AAH14663 E6/E7 reg
61	28	100.0	1173	2	AAH14663 E6/E7 reg
62	28	100.0	1173	2	AAH14663 E6/E7 reg
63	28	100.0	1173	2	AAH14663 E6/E7 reg
64	28	100.0	1173	2	AAH14663 E6/E7 reg
65	28	100.0	1173	2	AAH14663 E6/E7 reg
66	28	100.0	1173	2	AAH14663 E6/E7 reg
67	28	100.0	1173	2	AAH14663 E6/E7 reg
68	28	100.0	1173	2	AAH14663 E6/E7 reg
69	28	100.0	1173	2	AAH14663 E6/E7 reg
70	28	100.0	1173	2	AAH14663 E6/E7 reg
71	28	100.0	1173	2	AAH14663 E6/E7 reg
72	28	100.0	1173	2	AAH14663 E6/E7 reg
73	28	100.0	1173	2	AAH14663 E6/E7 reg
74	28	100.0	1173	2	AAH14663 E6/E7 reg
75	28	100.0	1173	2	AAH14663 E6/E7 reg
76	28	100.0	1173	2	AAH14663 E6/E7 reg
77	28	100.0	1173	2	AAH14663 E6/E7 reg
78	28	100.0	1173	2	AAH14663 E6/E7 reg
79	28	100.0	1173	2	AAH14663 E6/E7 reg
80	28	100.0	1173	2	AAH14663 E6/E7 reg
81	28	100.0	1173	2	AAH14663 E6/E7 reg
82	28	100.0	1173	2	AAH14663 E6/E7 reg
83	28	100.0	1173	2	AAH14663 E6/E7 reg
84	28	100.0	1173	2	AAH14663 E6/E7 reg
85	28	100.0	1173	2	AAH14663 E6/E7 reg
86	28	100.0	1173	2	AAH14663 E6/E7 reg
87	28	100.0	1173	2	AAH14663 E6/E7 reg
88	28	100.0	1173	2	AAH14663 E6/E7 reg
89	28	100.0	1173	2	AAH14663 E6/E7 reg
90	28	100.0	1173	2	AAH14663 E6/E7 reg
91	28	100.0	1173	2	AAH14663 E6/E7 reg

92	19	67.9	665	6	ABQ26632	Abq26632 Oligonuc1	165	18.2	65.0	6696	4	AB115548	Ab115548 Drosophi1
C 93	19	67.9	665	6	ABQ26633	Abq26633 Oligonuc1	166	18.2	65.0	5250	6	AB133202	Ab133202 Human imm
C 94	19	67.9	1509	4	AAH00681	Aah00681 Cytophaga	167	18.2	65.0	5449	6	AB133641	Ab133641 Human imm
95	19	67.9	1981	10	ADB87400	Adb87400 Transgene	168	18.2	65.0	6680	13	ADBS9857	Adbs9857 Oligonuc1
96	19	67.9	1981	12	ADJ35209	Adj35209 Human str	169	18.2	65.0	6680	13	ADBS9857	Adbs9857 Oligonuc1
97	19	67.9	1981	12	ADL96827	Adl96827 Strablizin	170	18.2	65.0	6692	4	AAS46609	Aas46609 Human imm
C 98	19	67.9	1981	15	AEF41563	Aef41563 Nucleic a	171	18.2	65.0	7456	6	AB133931	Ab133931 Human imm
C 99	19	67.9	4305	8	ACA52686	Aca52686 Prokaryot	172	18.2	65.0	7456	6	AB192293	Ab192293 Human che
C 100	19	67.9	6092	6	AAK833020	Aak833020 Human imm	173	18.2	65.0	9524	6	ABK39994	Abk39994 Human imm
C 101	19	67.9	10697	5	AAK83607	Aak83607 Human imm	174	18.2	65.0	9524	6	ABK32839	Abk32839 Human imm
C 102	19	67.9	10697	5	ABA21005	Aba21005 Human ner	175	18.2	65.0	15698	6	AB134141	Ab134141 Human imm
C 103	19	67.9	14633	4	AAK83608	Aak83608 Human imm	176	18.2	65.0	26241	5	ABA16222	Aba16222 Human ner
C 104	19	67.9	14633	4	ABA21006	Aba21006 Human ner	177	18.2	65.0	45862	8	ABX93110	Abx93110 Genomic D
C 105	18.8	67.1	3780	13	ADBS89381	Adbs89381 Oligonuc1	C 178	18.2	65.0	72215	4	AAK86832	AAK86832 Human imm
C 106	18.8	67.1	3780	13	ADBS89655	Adbs89655 Oligonuc1	C 179	18.2	65.0	79256	13	ABD33177	ABD33177 Murine ca
C 107	18.8	67.1	110000	6	ABA92787	Contribution (4 of	C 180	18.2	65.0	105499	13	ABD33280	ABD33280 Human can
C 108	18.6	66.4	216	14	ACL58824	Contribution (4 of	C 181	18.2	65.0	110000	12	ADK16049	ADK16049 1
C 109	18.6	66.4	826	6	ABST72854	Abst72854 Human gen	C 182	18.2	65.0	110000	13	ABD32594	ABD32594 0
C 110	18.6	66.4	1110	6	ABST92849	Abst92849 Stephyloc	C 183	18.2	65.0	145985	12	ADQ97164	ADQ97164 Ane05091
C 111	18.6	66.4	1110	13	ADBS03046	Adbs03046 Stephyloc	C 184	18.2	65.0	157184	14	ABE05091	ABE05091 Ane05091
C 112	18.6	66.4	2402	4	ABL03061	Ab103061 Drosophi1	C 185	18.2	65.0	212231	11	ACN44598	ACN44598 Ane05091
C 113	18.6	66.4	4258	4	ABL25102	Ab125102 Drosophi1	C 186	18.2	65.0	326633	14	ABED18562	ABED18562 Ane05091
C 114	18.6	66.4	7931	6	ABK83664	Abk83664 DNA trans	C 187	18.2	65.0	30	AAZ07818	AAZ07818 HPV 16 B6	
C 115	18.6	66.4	7931	6	ABM77463	Abm77463 Human flb	C 188	18.2	65.0	30	ADZ64768	ADZ64768 HPV 16 B6	
C 116	18.6	66.4	10189	6	AB134160	Ab134160 Human imm	C 189	18.2	65.0	321	3	AAAC46339	AAAC46339 Ane05091
C 117	18.6	66.4	15333	4	ABL03060	Ab103060 Drosophi1	C 190	18.2	65.0	441	8	ABX52884	ABX52884 Ane05091
C 118	18.6	66.4	15333	4	ABL03060	Ab103060 Drosophi1	C 191	18.2	65.0	447	3	ABC43354	ABC43354 Ane05091
C 119	18.6	66.4	93390	10	ADD773350	Add773350 Glutamine	C 192	18.2	65.0	447	6	ABE12688	ABE12688 Ane05091
C 120	18.6	66.4	188267	14	ADZ13837	Adz13837 Human can	C 193	18.2	65.0	541	10	ADC76717	ADC76717 Ane0

C 822	17	60.7	32236	4	AAK91250	Adg41590 Human res
C 823	17	60.7	32548	4	ABL29482	Adl97364 Human res
C 824	17	60.7	36119	13	ABD33605	Adi68667 Human ova
C 825	17	60.7	45960	11	ACN44372	Adi55029 Human ova
C 826	17	60.7	48674	11	ACN44400	Adi174497 Human ova
C 827	17	60.7	74849	11	ACN44932	Adi168125 Human ova
C 828	17	60.7	90401	12	ADQ97515	Adi46993 Human inf
C 829	17	60.7	91278	13	ABD33289	Adi40266 Human ova
C 830	17	60.7	91278	14	ADL13338	Adi10266 Human ova
C 831	17	60.7	95394	13	ADY87742	Adi18693 Human adu
C 832	17	60.7	95394	13	ADY87895	Adi94374 Gene #872
C 833	17	60.7	100610	12	ADQ97608	Adi9507 Human ova
C 834	17	60.7	101954	13	ABD33574	Adi15847 Human ova
C 835	17	60.7	106556	12	ABE01466	Adi2506 Human kid
C 836	17	60.7	108057	14	ADQ97858	Adi41360 RNA elev
C 837	17	60.7	110000	6	ABQ74954_5	Adi26368 Rice abio
C 838	17	60.7	110000	6	ABE55320_2	Adi16071 Probe #47
C 839	17	60.7	110000	6	ABX08336_13	Abes29756 Human liv
C 840	17	60.7	110000	6	ABA90521_06	Abes04687 Human gen
C 841	17	60.7	110000	6	ABO67196_0	Aak3050 Human cdn
C 842	17	60.7	110000	6	ABO69245_24	Adi129477 3' end of
C 843	17	60.7	110000	6	ABR03041_27	Adi39724 Human ova
C 844	17	60.7	110000	10	ADF77343_15	Adi68314 Human gen
C 845	17	60.7	110000	10	ACF67367_45	Abq18690 Oligonuc1
C 846	17	60.7	110000	10	ACF65388_02	Abq18691 Oligonuc1
C 847	17	60.7	110000	10	ACF65388_03	Adi13360 Solid tum
C 848	17	60.7	110000	10	ACF42745_2	Abes5327 Human pro
C 849	17	60.7	110000	12	ADZ3585_13	Abes5327 Human pro
C 850	17	60.7	110000	12	ADN97989_13	Adi1131 Rice abio
C 851	17	60.7	110000	12	ADN97989_13	Aah12010 Human cdn
C 852	17	60.7	110000	12	ADN97989_13	Aac4827 Arabidops
C 853	17	60.7	110000	12	ADN97989_13	Abq18414 Oligonuc1
C 854	17	60.7	110000	12	ADN97989_13	Abq18415 Oligonuc1
C 855	17	60.7	110000	13	ADY81204_13	Abq33108 Arabidops
C 856	17	60.7	110000	14	ADZ1365_2	Abes6149 Plant DNA
C 857	17	60.7	110000	14	ADZ1365_2	Aec84114 Shrimp ES
C 858	17	60.7	110000	14	AE61160_0	Adi57249 Human CYP
C 859	17	60.7	110000	14	AE61160_0	Abk9505 Human CYP
C 860	17	60.7	110000	14	AE61160_0	Abk9505 Human CYP
C 861	17	60.7	110000	14	AE61160_0	Abk9505 Human CYP
C 862	17	60.7	110000	14	AE61160_0	Adi57249 Human CYP
C 863	17	60.7	110000	14	AE61160_0	Adi57249 Human CYP
C 864	17	60.7	110000	14	AE61160_0	Adi57249 Human CYP
C 865	17	60.7	110000	14	AE61160_0	Adi57249 Human CYP
C 866	17	60.7	110000	14	AE61160_0	Adi57249 Human CYP
C 867	17	60.7	110000	14	AE61160_0	Adi57249 Human CYP
C 868	17	60.7	110000	14	AE61160_0	Adi57249 Human CYP
C 869	17	60.7	110000	14	AE61160_0	Adi57249 Human CYP
C 870	17	60.7	110000	14	AE61160_0	Adi57249 Human CYP
C 871	17	60.7	110000	14	AE61160_0	Adi57249 Human CYP
C 872	17	60.7	110000	14	AE61160_0	Adi57249 Human CYP
C 873	17	60.7	110000	14	AE61160_0	Adi57249 Human CYP
C 874	17	60.7	110000	14	AE61160_0	Adi57249 Human CYP
C 875	17	60.7	110000	14	AE61160_0	Adi57249 Human CYP
C 876	17	60.7	110000	14	AE61160_0	Adi57249 Human CYP
C 877	17	60.7	110000	14	AE61160_0	Adi57249 Human CYP
C 878	17	60.7	110000	14	AE61160_0	Adi57249 Human CYP
C 879	17	60.7	110000	14	AE61160_0	Adi57249 Human CYP
C 880	17	60.7	110000	14	AE61160_0	Adi57249 Human CYP
C 881	17	60.7	110000	14	AE61160_0	Adi57249 Human CYP
C 882	17	60.7	110000	14	AE61160_0	Adi57249 Human CYP
C 883	17	60.7	110000	14	AE61160_0	Adi57249 Human CYP
C 884	17	60.7	110000	14	AE61160_0	Adi57249 Human CYP
C 885	17	60.7	110000	14	AE61160_0	Adi57249 Human CYP
C 886	17	60.7	110000	14	AE61160_0	Adi57249 Human CYP
C 887	17	60.7	110000	14	AE61160_0	Adi57249 Human CYP
C 888	17	60.7	110000	14	AE61160_0	Adi57249 Human CYP
C 889	17	60.7	110000	14	AE61160_0	Adi57249 Human CYP
C 890	17	60.7	110000	14	AE61160_0	Adi57249 Human CYP
C 891	17	60.7	110000	14	AE61160_0	Adi57249 Human CYP
C 892	17	60.7	110000	14	AE61160_0	Adi57249 Human CYP
C 893	17	60.7	110000	14	AE61160_0	Adi57249 Human CYP
C 894	17	60.7	110000	14	AE61160_0	Adi57249 Human CYP

CC are small DNA viruses and HPV Types 16 and 18 are associated with genital
CC cancers. HPV PCR primers can amplify HPV Type 16 and/or 18 nucleic acid
CC in a sample. HPV Type 16 and/or 18 can be detected by adding a probe and
CC detecting probe: target duplex formation; target nucleic acid is
CC optionally amplified. Type 16 or 18 can be specifically detected by
CC amplifying nucleic acids with at least one specifically claimed PCR
CC primer. For Type 18 detection, a helper probe may be used.
CC Oligonucleotides can distinguish target sequences from phylogenetically
CC close HPV Types 16 and 18 whilst available detection sera react with
CC antigens of all papillomaviruses

CC
XX
SQ Sequence 28 BP; 12 A; 6 C; 2 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACATTATTGTTATAGTTGTATGGAAC 28
Db 28 GACATTATTGTTATAGTTGTATGGAAC 1

RESULT 3
AAT72414/c
ID AAT72414 standard; RNA; 28 BP.
XX
XX AAT72414;
XX
XX 09-FEB-1998 (first entry)
XX
XX Human Papillomavirus Type 16 PCR primer.
XX
XX Human Papillomavirus; probe; target region; genital cancer; HPV;
XX cervical smear; PCR primer; ss.
XX
XX Synthetic.
XX OS Human papillomavirus.
XX
XX EP774518-A2.
XX
XX 21-MAY-1997.
XX
XX 15-NOV-1996; 96EP-00308264.
XX
XX 15-NOV-1995; 95US-0006854P.
XX
XX (GENP-) GEN-PROBE INC.
XX
XX Gordon P, Brentano ST, Carter NM, Hammond PW;
XX
XX WPI, 1997-274349/25.
XX
XX Probes for detection of Human Papillomavirus Type 16 and Type 18 - can
XX distinguish between Type 16 and 18, associated with genital cancers.
XX
XX Claim 23; Page 34; 70pp; English.

CC Novel hybridisation assay probes have been developed comprising an
CC oligonucleotide which will hybridise under selected conditions to Human
CC Papillomavirus (HPV) Type 16 and/or 18 (but not Types 6, 11, 31, 33, 35,
CC 39, 45, 51, 52, or 58) target nucleic acids to form detectable target;
CC probe duplex. The present sequence represents a specifically claimed HPV
CC PCR primer (amplification oligonucleotide). Oligonucleotides are useful
CC to detect HPV Type 16 and/or 18 in samples e.g. cervical smears, body
CC fluid, and distinguish these from other HPV variants. Papillomaviruses
CC are small DNA viruses and HPV Types 16 and 18 are associated with genital
CC cancers. HPV PCR primers can amplify HPV Type 16 and/or 18 nucleic acid
CC in a sample. HPV Type 16 and/or 18 can be detected by adding a probe and
CC detecting probe: target duplex formation; target nucleic acid is
CC optionally amplified. Type 16 or 18 can be specifically detected by
CC amplifying nucleic acids with at least one specifically claimed PCR
CC primer. For Type 18 detection, a helper probe may be used.
CC Oligonucleotides can distinguish target sequences from phylogenetically

CC close HPV Types 16 and 18 whilst available detection sera react with
CC antigens of all papillomaviruses

CC
XX
SQ Sequence 28 BP; 12 A; 6 C; 2 G; 8 T; 8 U; 0 Other;

Query Match 100.0%; Score 28; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACATTATTGTTATAGTTGTATGGAAC 28
Db 28 GACATTATTGTTATAGTTGTATGGAAC 1

RESULT 4
AAT72401
ID AAT72401 standard; DNA; 28 BP.
XX
XX AAT72401;
XX
XX 09-FEB-1998 (first entry)
XX
XX Human Papillomavirus Type 16 probe.
XX
XX Human Papillomavirus; probe; target region; genital cancer; HPV;
XX cervical smear; ss.
XX
XX Synthetic.
XX OS Human papillomavirus.
XX
XX EP774518-A2.
XX
XX 21-MAY-1997.
XX
XX 15-NOV-1996; 96EP-00308264.
XX
XX 15-NOV-1995; 95US-0006854P.
XX
XX (GENP-) GEN-PROBE INC.
XX
XX Gordon P, Brentano ST, Carter NM, Hammond PW;
XX
XX WPI, 1997-274349/25.
XX
XX Probes for detection of Human Papillomavirus Type 16 and Type 18 - can
XX distinguish between Type 16 and 18, associated with genital cancers.
XX
XX Claim 22; Page 33; 70pp; English.

CC Novel hybridisation assay probes have been developed comprising an
CC oligonucleotide which will hybridise under selected conditions to Human
CC Papillomavirus (HPV) Type 16 and/or 18 (but not Types 6, 11, 31, 33, 35,
CC 39, 45, 51, 52, or 58) target nucleic acids to form detectable target;
CC probe duplex. The present sequence represents a specifically claimed HPV
CC PCR primer (amplification oligonucleotide). Oligonucleotides are useful
CC to detect HPV Type 16 and/or 18 in samples e.g. cervical smears, body
CC fluid, and distinguish these from other HPV variants. Papillomaviruses
CC are small DNA viruses and HPV Types 16 and 18 are associated with genital
CC cancers. HPV PCR primers can
CC amplify HPV Type 16 and/or 18 nucleic acid in a sample. HPV Type 16
CC and/or 18 can be detected by adding a probe and detecting probe: target
CC duplex formation; target nucleic acid is optionally amplified. Type 16 or
CC 18 can be specifically detected by amplifying nucleic acids with at least
CC one specifically claimed PCR primer. For Type 18 detection, a helper
CC probe may be used. Oligonucleotides can distinguish target sequences from
CC phylogenetically close HPV Types 16 and 18 whilst available detection
CC sera react with antigens of all papillomaviruses

CC
XX
SQ Sequence 28 BP; 8 A; 2 C; 6 G; 12 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1 GACATTATGTTATAGTTGTATGGAAC 28
        |||||||
FY      1 GACATTATGTTATAGTTGTATGGAAC 28

Db

RESULT 5
ADXX26909
ID      ADXX26909 standard; DNA; 452 BP.
XX
AC      ADXX26909;
XX
DT      05-MAY-2005 (first entry)
XX
DB      Human papillomavirus type 16 E6 delta151 mutant DNA.
XX
KV      cell culture; immortalization; gynecology and obstetrics; Andrology;
XX      cancer; neoplasm; mutant; ds.
XX
OS      Human papillomavirus type 16.
XX      Synthetic.
XX
FH      Key      Location/Qualifiers
FT      misc_difference 3..4
FT      /*tag= a
FT      /note= "Wild-type bases 4-25 have been removed"
FT      misc_difference 449..450
FT      /*tag= b
FT      /note= "Wild-type bases 472-474 have been removed"
XX
PN      JP2005046117-A.
XX
PD      24-FEB-2005.
XX
PF      31-JUL-2003; 2003JP-00283911.
XX
PR      31-JUL-2003; 2003JP-00283911.
XX
PA      (UYKA-) UNIV KANAZAMA TLO YG.
XX      (KOKU-) KOKURITSU GAN CENT SOCHO.
XX
DR      WPI; 2005-175815/19.
XX
XX      The invention relates to a novel immortalized endometrial glandular
XX      epithelial cell strain in which an exogenous immortalizing gene is
XX      introduced and the properties of the cell line as non-cancer typical
XX      glandular epithelial cells, are maintained. The cell line of the
XX      invention may be useful for research of reproduction, particularly for
XX      analyzing the adhesion of the fertilized egg during implantation, of
XX      analyzing the effect of steroid hormones, analyzing the mechanism of
XX      multistep canceration of the inner glandular epithelial membrane by
XX      genetic engineering of the cell line which is otherwise non-cancerous,
XX      and analyzing the effect of carcinogenic substances on the cell line. The
XX      cell line maintains the properties of normal somatic cells and the
XX      properties of endometrial glandular epithelial cells. The current
XX      sequence is that of the Human papillomavirus type 16 E6 delta151 mutant
XX      DNA of the invention.
XX
SQ      Sequence 452 BP; 156 A; 70 C; 98 G; 128 T; 0 U; 0 Other;
Query Match      100.0%; Score 28; DB 14; Length 452;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GACATTATGTTATAGTTGTATGGAAC 28
|||||
GACATTATGTTATAGTTGTATGGAAC 256

```

RESULT 6	
ADP09607	
ID	ADP09607 standard; cDNA; 477 BP.
XX	
AC	ADP09607;
XX	
DT	12-FEB-2004 (first entry)
XX	
DE	Human papillomavirus 16 E6 cDNA SEQ ID NO:108.
XX	
KW	human; protein-protein interaction; virucide; cytostatic; vaccine;
XX	
XX	human; papilloma virus; HPV; cancer; ss; gene.
OS	Human papillomavirus.
PN	MO2003068940-A2.
XX	
PD	21-AUG-2003.
XX	
PF	14-FEB-2003; 2003WO-US004594.
XX	
PR	14-FEB-2002; 2002US-035691P.
XX	
PA	(CURA-) CURAGEN CORP.
XX	
PA	(HOFF) HOFFMANN LA ROCHE INC.
XX	
PI	Jackson A, Ooi CE, Lewin DA, Cuthill S;
XX	
DR	WPI; 2003-689668/65.
XX	
DR	P-PSDB; ADP09515.
XX	
PT	New purified complex comprising a first polypeptide and a second
XX	
PT	polypeptide, useful for identifying agents for treating/preventing a
XX	
PT	condition involving altered level of the complex e.g. human papilloma
XX	
PT	virus infection, or cancer.
XX	
PS	Example 3; SEQ ID NO 108; 156pp; English.
XX	
CC	The invention relates to a novel purified complex comprising a first
XX	
CC	polypeptide and a second polypeptide, where the polypeptides comprise
XX	
CC	defined amino acid sequences listed in the specification, and where the
XX	
CC	first polypeptide binds to the second polypeptide. A complex of the
XX	
CC	invention has virucide and cytostatic activity, and may have a use as a
XX	
CC	vaccine. The complex is useful for identifying agents for treating or
XX	
CC	preventing a conditions involving altered level of the complex, e.g.
XX	
CC	human papilloma virus (HPV) infection, or cancer. The compositions,
XX	
CC	antibodies, vectors and methods are useful for treating such diseases.
XX	
CC	The sequences shown in ADP09584-ADP09697 represent cDNA's of the
XX	
CC	invention.
XX	
SEQ	Sequence 477 BP; 167 A; 76 C; 103 G; 131 T; 0 U; 0 Other;
XX	
Query Match	100.0%; Score 28; DB 10; Length 477;
Best Local Similarity	100.0%; Pred. No. 0.41;
Matches 28; Conservative	0; Mismatches 0; Indels 0; Gaps 0.
QY	1 GACATTATTGTTAGTTGATGGAAAC 28
DB	251 GACATTATTGTTAGTTGATGGAAAC 278
RESULT 7	
AA154430	
ID	AA154430 standard; DNA; 477 BP.
XX	
AC	AA154430;
XX	
DT	03-APR-2003 (first entry)
XX	
DE	E6 siRNA sequence.
XX	

KM	Vitrinide; cytostatic; anti-HIV; dermatological; small interfering RNA;
KM	selective post-translational silencing; siRNA; oncogene; genital wart;
KM	human papilloma virus; HPV gene; cancer; human cervical cancer; HIV;
KM	smallpox; flu; common cold; cervical cancer; penile cancer;
KM	malignant squamous cell carcinoma; verruca vulgaris; gene therapy; de.
XX	
OS	Human papilloma virus.
XX	
PN	WO2003008573-A2.
PD	
XX	
PD	30-JAN-2003.
PE	
XX	
PR	17-JUL-2002; 2002WO-GB003300.
XX	
PR	17-JUL-2001; 2001GB-00017358.
PR	14-JAN-2002; 2002GB-0000688.
PR	17-JUN-2002; 2002GB-00013855.
XX	
PA	(MILNER) MILNER A J.
P1	
PI	Milner AJ;
DR	
XX	
WPI:	2003-221850/21.
XX	
PT	Selective post-transcriptional silencing of an exogenous viral gene (e.g.
PT	human papilloma virus (HPV) E6), for treating e.g. cancer, comprises
PT	using a small interfering RNA (siRNA) construct homologous to an mRNA of
PT	the gene.
PS	
XX	
Disclosure:	Fig 1A; 44pp; English.
XX	
CC	The invention relates to a novel method for selective post-translational
CC	silencing in a mammalian cell of the expression of an exogenous gene of
CC	viral origin. The method comprises introducing into the cell a small
CC	interfering RNA (siRNA) construct that is homologous to a part of the
CC	mRNA sequence of the gene. The method is useful for the selective post-
CC	transcriptional silencing of an exogenous gene of viral origin (e.g. an
CC	oncogene or human papilloma virus (HPV) gene) in a mammalian cell. The
CC	method or the siRNA is particularly useful for treating cancer, human
CC	cervical cancer, human immunodeficiency virus (HIV), smallpox, flu,
CC	common cold, or a disease caused by a HPV (e.g. genital warts, cervical
CC	cancer, penile cancer, malignant squamous cell carcinomas or verruca
CC	vulgaris). An siRNA construct or vector is useful for use as a medicament
CC	for the diseases mentioned. The polynucleotide sequence of the invention
CC	can be used to treat disorders by gene therapy. This polynucleotide
CC	sequence represents the DNA of the E6 siRNA sequence of the invention
CC	
SQ	Sequence 477 BP; 167 A; 76 C; 103 G; 131 T; 0 U; 0 Other;
XX	
Query Match	100.0%; Score 28; DB 10; Length 477;
Best Local Similarity	100.0%; Pred. No. 0.41;
Matches	28; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Dy	1 GACATTATTTAGTATTGTATGGAC 28 251 GACATTATTTAGTATTGTATGGAC 278
Db	
RESULT 8	
ID	ADX26908
AD	ADX26908 standard; DNA; 477 BP.
XX	
AC	ADX26908;
XX	
DT	05-MAY-2005 (first entry)
XX	
DE	Human papillomavirus type 16 E6 wild-type gene.
XX	
KM	cell culture; immortalization; Gynecology and obstetrics; Andrology;
KM	cancer; neoplasia; ds.
XX	
DS	Human papillomavirus type 16.
XX	

PX		JF0205046117-A.
PD	24-FEB-2005.	
PF	31-JUL-2003; 2003JP-00283911.	
PR	31-JUL-2003; 2003JP-00283911.	
PA	(UYKA-) UNIV KANAZAWA TLO YG. (KOKU-) KOKURITSU GAN CENT SOCHO.	
DR	WPI; 2005-175815/19.	
PT	Immortalized endometrial glandular epithelial cell strain containing exogenous immortalizing gene and maintains properties of non-cancer cell and typical glandular epithelial cells, useful in field of research of reproduction.	
PS	Claim 4; SEQ ID NO 3; 22pp; Japanese.	
CC	The invention relates to a novel immortalized endometrial glandular epithelial cell strain in which an exogenous immortalizing gene is introduced and the properties of the cell line as non-cancer typical glandular epithelial cells, are maintained. The cell line of the invention may be useful for research of reproduction, particularly for analyzing the adhesion of the fertilized egg during implantation, analyzing the effect of steroid hormones, analyzing the mechanism of multistep cancerization of the inner glandular epithelial membrane by genetic engineering of the cell line which is otherwise non-carcinogenic and analyzing the effect of carcinogenic substances on the cell line. The cell line maintains the properties of normal somatic cells and the properties of endometrial glandular epithelial cells. The current sequence is that of the Human papillomavirus type 16 E6 wild-type gene of the invention.	
SQ	Sequence 477 BP; 167 A; 76 C; 103 G; 131 T; 0 U; 0 Other; Query Match 100.0%; Score 28; DB 14; Length 477; Best Local Similarity 100.0%; Pred.No. 0.41;	
Dt	MATCHES 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
OY	1 GACATTATGTATTAGTTGGTAGTGAAC 28 	
Db	251 GACATTATGTATTAGTTGGTAGTGAAAC 278	
RSTRT 9		
AATJ1834		
ID	AATJ1834 standard; DNA; 519 BP.	
XX	AATJ1834;	
AC		
DT	27-AUG-2003 (revised)	
DT	11-JAN-1997 (first entry)	
DE	Human papilloma virus E6/E7 protein variant.	
KM	Human papilloma virus; E6; E7; deletion mutant; HPV; immune response;	
KW	humoral immune response; cellular immune response; vaccine; ss.	
OS	Human papillomavirine.	
FH	Key	
FT	CDS	Location/Qualifiers
FT	/tag= a	1..519
FT	/product= "E6/E7 fusion protein (deletion mutant)."	109..111
FT	/tag= b	
FT	/transl_except= TAC encodes Ile	115..117
FT	/tag= c	
FT	/transl_except= AAA encodes Cys	118..120
FT	misc_feature	

FT	/tag= d	
FT	/transl_except= CCG encodes Gln	
FT	121. .123	
FT	/tag= e	
FT	/transl_except= TTG encodes Lys	
FT	124. .126	
FT	/tag= f	
FT	/transl_except= TGT encodes Pro	
FT	127. .129	
FT	/tag= g	
FT	/transl_except= GAT encodes Tyr	
FT	130. .132	
FT	/tag= h	
FT	/transl_except= TTG encodes Asn	
FT	133. .135	
FT	/tag= i	
FT	/transl_except= TTA encodes Lys	
FT	136. .138	
FT	/tag= j	
FT	/transl_except= ATT encodes Pro	
FT	139. .141	
FT	/tag= k	
FT	/transl_except= AGG encodes Leu	
FT	142. .144	
FT	/tag= l	
FT	/transl_except= TGT encodes Cys	
FT	145. .147	
FT	/tag= m	
FT	/transl_except= ATT encodes Asp	
FT	148. .150	
FT	/tag= n	
FT	/transl_except= AAC encodes Leu	
FT	151. .153	
FT	/tag= o	
FT	/transl_except= TGT encodes Leu	
FT	154. .156	
FT	/tag= p	
FT	/transl_except= CAA encodes Ile	
FT	157. .159	
FT	/tag= q	
FT	/transl_except= AAG encodes Arg	
FT	160. .162	
FT	/tag= r	
FT	/transl_except= CCA encodes Cys	
XX		
XX	MO9619496-A1.	
XX		
XX	27-JUN-1996.	
XX		
XX	20-DEC-1995;	95WO-AU000868.
XX		
XX	20-DEC-1994;	94AU-00000157.
XX		
XX	(CSLC-) CSL LTD.	
XX	(UYOU) UNIV QUEENSLAND.	
XX		
XX	Edwards SJ, Cox J, Webb EA, Frazer I;	
XX		
XX	WPI, 1996-309518/31.	
XX	P-PSDB, AAR97562.	
XX		
PT	Vaccine variants of human papilloma virus antigens - contain variants of	
PT	E6 and/or E7 protein, pref. deletion mutants, and are used to treat or	
PT	prevent HPV infection.	
XX		
XX	Example 3; Page 17; 37pp; English.	
XX		
XX	A variant of the human papilloma virus (HPV) E6 or E7 protein which	
CC	elicits a humoral and/or cellular immune response against HPV can be used	
CC	in vaccines against HPV or to treat HPV infection. The variant is	
CC	preferably a deletion mutant comprising at least half, and preferably two	
CC	-thirds of full length E6 or E7 protein starting from the N- or C-	
CC	terminal, or is a full length E6 moiety fused to a full length E7 moiety.	
CC		

CC	The variant optionally has a linkage moiety and a foreign protein or
CC	peptide which facilitates the purification of, and enhances the
CC	immunogenicity of, the fusion protein. This sequence encodes a fusion
CC	between the C-terminal end of B6 and the N-terminal end of E7. The
CC	protein is also a deletion mutant generated from the sequence described
CC	in AATJ1833. (Updated on 27-AUG-2003 to correct OS field.)
SQ	Sequence 519 BP; 175 A; 92 C; 113 G; 139 T; 0 U; 0 Other;
Query Match	100.0%; Score 28; DB 2; Length 519;
Best Local Similarity	100.0%; Pred. No. 0.41;
Matches	28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Dn	1 GACATTATTGTTATAGTTCGTATGGAC 28 65 GACATTATTGTTATAGTTCGTATGGAC 92
RESULT 10	
AATJ1835	
ID	AATJ1835 standard; DNA; 519 BP.
XX AC	AATJ1835;
XX DT	27-AUG-2003 (revised)
DT	11-JAN-1997 (first entry)
XX DE	Human papilloma virus E6/E7 protein variant.
XX KM	Human papilloma virus; E6; E7; deletion mutant; HPV; immune response;
KM	humoral immune response; cellular immune response; vaccine; ss.
XX OS	Human papillomavirus.
XX FH	Key Location/Qualifiers
FT	CDS 1..519
FT	/tag= a
FT	/product= "E6/E7 fusion protein."
PN	WO9619496-A1.
PD	27-JUN-1996.
XX PF	20-DEC-1995; 95WC-AU000868.
XX PR	20-DEC-1994; 94AU-0000157.
PA	(CSLC-) CSL LTD.
PA	(UYOU) UNIV QUEENSLAND.
PI	Edwards SJ, Cox J, Webb EA, Frazer I;
DR	WPI: 1996-109518/31. P-PADB; AAR97563.
PT	Vaccine variants of human papilloma virus antigens - contain variants of
PT	B6 and/or E7 protein, pref. deletion mutants, and are used to treat or
PS	prevent HPV infection.
PS	Example 3; Page 18; 37pp; English.
XX	A variant of the human papilloma virus (HPV) E6 or E7 protein which
CC	elicits a humoral and/or cellular immune response against HPV can be used
CC	in vaccines against HPV or to treat HPV infection. The variant is
CC	preferably a deletion mutant comprising at least half, and preferably two
CC	-thirds of full length E6 or E7 protein starting from the N- or C-
CC	terminal, or is a full length E6 moiety fused to a full length E7 moiety.
CC	The variant optionally has a linkage moiety and a foreign protein or
CC	peptide which facilitates the purification of, and enhances the fusion
CC	immunogenicity of, the fusion protein. This sequence encodes a fusion
CC	between the C-terminal end of E7 and the N-terminal end of E6. (Updated
CC	on 27-AUG-2003 to correct OS field.)
XX	

Sequence 519 BP; 167 A; 97 C; 111 G; 144 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 2; Length 519;

Best Local Similarity 100.0%; Pred.No. 0.41;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACATTATTGTTATAGTTGTATGGAAC 28
 DB 458 GACATTATTGTTATAGTTGTATGGAAC 485

RESULT 11

AAQ75470
 ID AAQ75470 standard; DNA; 570 BP.

AC AAQ75470;

DT 16-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 28-JUN-1995 (first entry)

DE HPV16 B6/E7 encoding region.

KW HPV; HPV16; E6 protein; E7 protein; diagnosis; cervical dysplasia;

KW cervix cancer; ds.

OS Human papillomavirus; strain 16.

Key Location/Qualifiers

FT CDS 2..478

FT /label= B6_encoding_region

FT /tag= b

FT CDS 481..570

FT /label= E7_encoding_region

FT /tag= b

PN WO9426934-A2.

PD 24-NOV-1994.

PF 06-MAY-1994; 94WO-US005085.

PR 06-MAY-1993; 93US-00058920.

PA (BAXT) BAXTER DIAGNOSTICS INC.

PI Brown JT;

DR WPI; 1995-006821/01.

DR P-PSDB; AAR63865.

PT Human papilloma virus detection assay - by amplification using self

PS sustained sequence replication and hybridisation with a detector probe.

XX Disclosure; Page 24-26; 79pp; English.

CC The sequences of the B6 and E7 polypeptide-encoding regions of human

CC papillomavirus (HPV) 16 and 18 are given in AAQ75470-71 and the encoded

CC proteins in AAR63865-66, respectively. Probes and primers based on these

CC sequences were used for HPV infection diagnosis; expression of B6 and E7

CC 18 diagnostic for cervical cancer or pre-malignant states. (Updated on

CC 25-MAR-2003 to correct PW field.) (Updated on 16-OCT-2003 to standardise

CC OS field)

XX Sequence 570 BP; 199 A; 93 C; 119 G; 159 T; 0 U; 0 Other;

QY Query Match 100.0%; Score 28; DB 2; Length 570;

DB 252 GACATTATTGTTATAGTTGTATGGAAC 279

RESULT 12

AAN91600
 ID AAN91600 standard; DNA; 712 BP.

AC AAN91600;

DT 27-AUG-2003 (revised)

DT 17-JUL-1990 (first entry)

DE Partial nucleotide sequence (5' end) of human papilloma virus (HPV) type

DE 16 (HPV-16).

KW Human papilloma virus; type 16; in situ hybridisation assay;

KW cellular smear; benign cervical wart; cervical cancer.

OS Human papillomavirus.

PN WO8902934-A.

PD 06-APR-1989.

PF 30-SEP-1988; 88WO-US003367.

PR 02-OCT-1987; 87US-00103979.

PA (MICR-) MICROPROBE CORP.

PI Schwartz DE, Adams TH;

DR WPI; 1989-114406/15.

PT Hybridisation test for human papilloma virus in cell smears - by reaction

PT with long labelled probe specific for particular virus types, esp. for

PT examining cervical smears.

PS Disclosure; Page 7; 39pp; English.

CC The patent is for a rapid in situ hybridisation assay for detecting and

CC typing human papilloma virus (HPV) in non-frozen cellular smears fixed to

CC a support in absence of aldehyde-based crosslinking reagents. The assay

CC comprises: (1) combining nucleic acid in the sample with at least one

CC detectable probe able to hybridise with 1 or more HPV types; and (2)

CC are used, eg one for HPV types 6 and 11, associated with benign warts,

CC and one for types 16, 18, 31, 33 and 35, associated with cervical cancer.

CC The assay can differentiate between HPV types. It is esp. used as a

CC secondary test. The probes can be synthesised or cloned. (Updated on 27-

CC AUG-2003 to correct OS field.)

XX Sequence 712 BP; 253 A; 120 C; 155 G; 184 T; 0 U; 0 Other;

QY Query Match 100.0%; Score 28; DB 1; Length 712;

DB 333 GACATTATTGTTATAGTTGTATGGAAC 360

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACATTATTGTTATAGTTGTATGGAAC 28

DB 333 GACATTATTGTTATAGTTGTATGGAAC 360

RESULT 13

ADR47004
 ID ADR47004 standard; DNA; 768 BP.

AC ADR47004;

DT 18-NOV-2004 (first entry)

DE Human papillomavirus type 16 E7 gene for Dengue virus vaccine.

KW ds; gene; cytosstatic; virucide; dengue virus; recombinant replicon;

XX	deltion prem protein; C protein; NS1 protein signal; vaccine;
KM	cervical cancer; viral disease; antigen; dendritic cell; immune response;
OS	Human papillomavirus.
XX	Human papillomavirus type 16.
XX	
FH	Key Location/Qualifiers
FT	1..768
FT	/tag=a
FT	/product= "HPV-16 E7 protein"
PN	MO2004072274-A1.
PD	26-Aug-2004.
XX	
PE	30-JAN-2004; 2004WO-CN000088.
PR	30-JAN-2003; 2003CN-00115272.
PR	30-JAN-2003; 2003CN-00115273.
PA	(SHANGHAI SHANGHAI TENGGEN BIOMEDICAL CO LTD.
PA	(TENG-) TENGGEN BIOMEDICAL CO.
PA	(BEIJ-) BEIJING ORIENTAL TENGGEN TECHNOLOGY DEV C.
XX	
PI	Pang X;
DR	WPI; 2004-625870/60.
DR	P-PSD; ADR47005.
DR	GEMBANK; AF486352.
XX	
PT	Virus-like particle vaccines containing dengue virus recombinant replicon
PT	as core for carrier, applicable in preventives or/and remedies for tumors
PT	like cervical cancer and viral diseases.
PS	Example 2; SEQ ID NO 1; 38pp; Chinese.
XX	
CC	A dengue virus recombinant replicon has a deletion of the complete coding
CC	sequence for prem protein of dengue virus and also includes elements of
CC	e.g. the non-coding region in the whole of the 5'-end, the coding region
CC	of the front 20 amino acids in the C protein, and the coding region of
CC	NS1 protein signal; coding regions of all non-structural proteins. The
CC	obtained vaccines are useful in producing preventives or/and remedies for
CC	cancer like cervical cancer and viral diseases. Such vaccines can
CC	efficiently express antigen in infected cells, which is because dengue
CC	virus can infect dendritic cells, and can effectively present antigen to
CC	provide immunity effect. Different types of dengue virus can be used to
CC	repeatedly produce efficient immune response thereby strengthening the
CC	body's immune system against the pathogen that contains such antigen.
CC	Human papillomavirus (HPV) vaccines were prepared by using a gene-
CC	expressing sytem using of the full-length dengue virus cDNA clone
CC	(pRS/FLD2). The recombinant virus vectors were transfected into baby
CC	hamster kidney (BHK) cells to enable the screening of BHK-21 Tet-off cell
CC	lines. This sequence corresponds to the HPV type 16 E7 gene used as the
CC	gene of interest in the recombinant replicon of the invention.
XX	
SQ	Sequence 768 BP; 255 A; 139 C; 172 G; 202 T; 0 U; 0 Other;
OY	
Db	
Query Match	100.0%; Score 28; DB 13; Length 768;
Best Local Similarity	100.0%; Pred. No. 0.41;
Matches 28; Conservative	0; Mismatches 0; Indels 0; Gaps 0
1	GACATTATGTTAGTTGTATGGAC 28
545	GACATTATGTTAGTTGTATGGAC 572
RESULT 14	
AEF40156	
ID	AEF40156 standard; DNA; 768 BP.
AC	AEF40156;
XX	
DT	23-MAR-2006 (first entry)

XX	Human papillomavirus 16 (HPV-16) E7-E6 oncogene.
DE	
XX	Vaccine; virus-like particle; replicon; therapeutic; cancer; cytostatic;
KM	neoplasm; viral infection; virulence; infection; oncogene;
KM	coding sequence; ds.
XX	
OS	Human papillomavirus type 16.
XX	
PH	Key
FT	Location/Qualifiers
FT	1..768
FT	/*tag=
FT	/partial
FT	/product= "Human papillomavirus 16 (HPV-16) E7-E6
FT	oncoprotein"
FT	/note= "No stop codon"
XX	
FN	US2006018928-A1.
XX	
PD	26-JAN-2006.
XX	
PF	29-JUL-2005; 2005US-00192923.
XX	
PR	30-JAN-2003; 2003CN-00115272.
PR	30-JAN-2003; 2003CN-00115273.
PR	30-JAN-2004; 2004WO-00072274.
XX	
PA	(PANG/) PANG X.
XX	
PI	Pang X;
XX	
DR	WPI; 2006-109169/11.
DR	P-PSDB; AEF40157.
DR	GENBANK; AF486352, AF469197, AF472508.
XX	
PT	New recombinant DEN replicons with a deletion of prem, useful for
PT	producing a drug for the prophylaxis and treatment of cancer or viral
PT	infection.
XX	
PS	Example 2; SEQ ID NO 1; 24pp; English.
XX	
CC	The present invention provides a virus-like particle (VLP) vaccine which
CC	contains dengue virus (DEN) recombinant replicon as its core. The DEN
CC	replicon contains exogenous nucleotide sequences such as human
CC	papillomavirus (HPV) antigen proteins, immune regulators or combination
CC	of HPV antigen and immune regulators. The invention is useful for
CC	producing a drug for the prophylaxis and treatment of cancer or viral
CC	infection. The present sequence is a human papillomavirus oncogene.
XX	
SO	Sequence 768 BP; 255 A; 139 C; 172 G; 202 T; 0 U; 0 Other;
	Query Match 100.0%; Score 28; DB 15; Length 768;
	Best Local Similarity 100.0%; Pred. No. 0.41;
	Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
OY	1 GACATTATTGTTATGTTGATGGAAC 28
Db	545 GACATTATTGTTATGTTGATGGAAC 572
	RESULT 15
	AAT14663
XX	AAT14663 standard; DNA; 776 BP.
XX	
AC	AAT14663;
XX	
DT	27-AUG-2003 (revised)
DT	25-MAR-2003 (revised)
DT	10-OCT-1996 (first entry)
XX	
DE	E6/E7 region of Human Papilloma Virus 16 (HPV 16).
XX	
KM	Human papilloma virus; HPV; detection; cervical cancer; amplification;

```

KW hybridisation; diagnosis; transformed cell; E6; E7; ss.
XX Human papillomavirus type 16.
XX Key Location/Qualifiers
FT primer_bind 1..24
FT /tag= a
FT /note= "Primer BB13 binding site."
FT 30..55
FT /tag= b
FT /note= "Primer H16-58 binding site."
FT 37..57
FT /tag= c
FT /note= "Primer BB4 binding site."
FT 454..474
FT /tag= d
FT /note= "Primer BB14 binding site."
FT 480..503
FT /tag= e
FT /note= "Primer BB11 binding site."
FT 591..621
FT /tag= f
FT /note= "Primer BB109 binding site."
FT 658..681
FT /tag= g
FT /note= "Primer H16-686 binding site."
FT 660..683
FT /tag= h
FT /note= "Primer BB12 binding site."
FT 715..738
FT /tag= i
FT /note= "Primer H16-743 binding site."
FT 745..768
FT /tag= j
FT /note= "Primer H16-773 binding site."
XX
XX US5506105-A.
XX
XX 09-APR-1996.
XX
XX 22-MAR-1994; 94US-00216233.
XX
XX 10-DEC-1991; 91US-00808456.
XX
XX (DADE-) DADE INT INC.
XX
XX Haydock PV;
XX
XX WPI; 1996-200273/20.
XX
XX Detection of low copy number intracellular markers - by 3SR amplification
XX of target RNA in fixed cells then hybridisation with labelled probe, for
XX detecting human papilloma virus in cervical cells.
XX
XX Example 2; Fig 3; 21pp; English.
XX
XX An in situ hybridisation assay for detecting an intracellular marker of
XX low copy number in cells comprises fixing the cells to a support using
XX paraformaldehyde; treating the cells with a protease to permeabilise them
XX without altering morphology; adding amplification reagents; incubating
XX the cells at below fifty degrees celcius to perform amplification by self
XX -sustained sequence replication; adding a labelled probe complementary to
XX the region between the primers; washing cells to remove unhybridised
XX probe and then detecting the labelled probe. The E6/E7 region of human
XX papilloma virus (HPV) 16 is used especially to detect mRNA being
XX transcribed from this region which becomes active in transformed cells.
XX The method can be used for the early diagnosis of cervical cancer.
XX Primers used to amplify fragments of the E6/E7 region are described in
XX AAT14664-t14674. (Updated on 25-MAR-2003 to correct PF field.) (Updated
XX on 27-AUG-2003 to correct OS field.)
XX
XX Sequence 776 BP; 260 A; 139 C; 169 G; 208 T; 0 U; 0 Other;
SQ

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Query Match 100.0%; Score 28; DB 2; Length 776;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GACATTATTGTTATAGTTGATGGAAC 28
DB 251 GACATTATTGTTATAGTTGATGGAAC 278
RESULT 16
AAK89756
ID AAK89756 standard; DNA; 779 BP.
XX
XX AAK89756;
AC
XX
DT 27-AUG-2003 (revised)
DT 12-OCT-1999 (first entry)
XX
XX Probe sequence for HPV 16 E6/E7.
DE
XX
XX human papilloma virus; infection; gene expression; probe; detection;
KW assay; cancer; virus; HPV; ss.
XX
XX Synthetic.
OS
XX Human papillomavirus.
PN
XX
XX WO9929890-A2.
XX
XX 17-JUN-1999.
XX
XX 11-DEC-1998; 98WO-US026447.
XX
XX PF 12-DEC-1997; 97US-0069426P.
XX PR 05-JAN-1996; 98US-0070486P.
XX PR 17-APR-1998; 98US-0082167P.
XX
XX (DIGE-) DIGENE CORP.
XX
XX Lorincz AT;
XX
XX WPI; 1999-443850/37.
XX
XX New method for assessing Human Papilloma Virus (HPV) infection by
XX comparison of gene expression levels.
XX
XX Disclosure; Fig 5; 35pp; English.
XX
XX This nucleotide probe is specific for the HPV16 Human Papilloma Virus
XX (HPV) gene. The degree of HPV infection can be assessed, by measuring the
XX levels of expression of genes involved in the diseased state, and
XX comparing the expression to each other or to reference genes. (Updated on
XX 27-AUG-2003 to correct OS field.)
XX
XX Sequence 779 BP; 259 A; 139 C; 170 G; 211 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 28; DB 2; Length 779;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GACATTATTGTTATAGTTGATGGAAC 28
DB 258 GACATTATTGTTATAGTTGATGGAAC 285
RESULT 17
AAQ29389
ID AAQ29389 standard; DNA; 790 BP.
XX
XX AAQ29389;
AC
XX
XX 24-OCT-2003 (revised)
XX 25-MAR-2003 (revised)
DT 09-MAR-1993 (first entry)

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XX DE DNA encoding HPV 16 E6/E7 proteins obtd. by PCR.
XX KM Virus vector; vaccinia virus; papillomavirus; HPV; human; amplification;
XX KM immunotherapeutic; ss.
XX OS Human papillomavirus type 16.
XX FH Key Location/Qualifiers
XX FT CDS 1..789
XX FT /tag= a
XX FT /note= "reading frame 1"
XX FT CDS 2..790
XX FT /tag= b
XX FT /note= "reading frame 2"
XX FT CDS 3..788
XX FT /tag= d
XX FT /note= "reading frame 3"
XX FT misc_feature 6..482
XX FT /tag= e
XX FT /note= "third reading frame encoding HPV 16 E6"
XX FT misc_feature 485..781
XX FT /tag= c
XX FT /note= "second reading frame encoding HPV 16 E7"
XX PN W0921636-A1.
XX PD 01-OCT-1992.
XX PF 10-MAR-1992; 92WO-GB000424.
XX PR 14-MAR-1991; 91GB-00005383.
XX (IMMU ) IMMUNOLOGY LTD.
XX PA Bourne11 MEG, Inglis SC, Munro AJ;
XX DR WPI, 1992-349219/42.
XX DR P-PSDB; AAR27723, AAR27724, AAR27725.
XX PT Recombinant virus vectors encoding human papillomavirus proteins - for
XX PT treating and vaccinating against HPV infections and conditions caused by
XX PT them, such as cervical cancer.
XX PS Disclosure; Fig 1a; 83pp; English.
XX XX The fragment of DNA contg. the HPV-16 E6/E7 coding region was prepd. by
XX CC PCR from plasmid pBR322/HPV16 (Durst et al., PNAS, 80: 3812 (1983)) using
XX CC oligonucleotides S05 and S06. The DNA prod. has a site for NcoI at the
XX CC beginning of the E6 gene and a SmaI site immediately downstream of the
XX CC termination codon for E7. The E6 and E7 ORFs are fused together to form a
XX CC single continuous ORF via site directed mutagenesis and the immortalising
XX CC potential of E7 is removed by altering two key codons of the HPV E7
XX CC sequence. The single ORF of HPV-16 E6/E7 may be inserted into vaccinia
XX CC virus DNA at neutral sites (pref. by inserting two sets of the DNA in
XX CC opposite orientations to overcome the problem of intertypic
XX CC recombination) to make a recombinant virus vector for use
XX CC immunotherapeutically to activate cells of the immune system against HPV.
XX CC See also AAQ23385-400 and AAQ29450-69. (Updated on 25-MAR-2003 to correct
XX CC PN field.) (Updated on 24-OCT-2003 to standardise OS field)
XX SQ Sequence 790 BP; 262 A; 144 C; 175 G; 209 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 2; Length 790;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACATTATGTTAGTTGTATGAAC 28
DB 256 GACATTATGTTAGTTGTATGAAC 283

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AAT31833
ID AAT31833 standard; DNA; 801 BP.
XX AC AAT31833;
XX XX 27-AUG-2003 (revised)
XX DT 10-JAN-1997 (first entry)
XX XX
XX DE Human papilloma virus E6/E7 protein variant.
XX KM Human papilloma virus; E6; E7; deletion mutant; HPV; immune response;
XX KM humoral immune response; cellular immune response; vaccine; ss.
XX OS Human papillomavirus.
XX FH Key Location/Qualifiers
XX FT CDS 1..801
XX FT /tag= a
XX FT /product= "E6/E7 fusion protein."
XX PN W09619496-A1.
XX PD 27-JUN-1996.
XX PF 20-DEC-1995; 95WO-AU000868.
XX PR 20-DEC-1994; 94AU-00000157.
XX (CSLC-) CSL LTD.
XX PA (UYQU ) UNIV QUEENSLAND.
XX PI Edwards SJ, Cox J, Webb EA, Frazer I;
XX DR WPI, 1996-309518/31.
XX DR P-PSDB; AAR97561.
XX PT Vaccine variants of human papilloma virus antigens - contain variants of
XX PT E6 and/or E7 protein, pref. deletion mutants, and are used to treat or
XX PT prevent HPV infection.
XX PS Example 1; Page 15-16; 37pp; English.
XX XX A variant of the human papilloma virus (HPV) E6 or E7 protein which
XX CC elicits a humoral and/or cellular immune response against HPV can be used
XX CC in vaccines against HPV or to treat HPV infection. The variant is
XX CC preferably a deletion mutant comprising at least half, and preferably two
XX CC -thirds of full length E6 or E7 protein starting from the N- or C-
XX CC terminal, or is a full length E6 moiety fused to a full length E7 moiety.
XX CC The variant optionally has a linkage moiety and a foreign protein or
XX CC peptide which facilitates the purification of, and enhances the
XX CC immunogenicity of, the fusion protein. This sequence encodes a full
XX CC length E6/E7 fusion protein. (Updated on 27-AUG-2003 to correct OS
XX CC field.)
XX SQ Sequence 801 BP; 266 A; 150 C; 174 G; 211 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 2; Length 801;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACATTATGTTAGTTGTATGAAC 28
DB 251 GACATTATGTTAGTTGTATGAAC 278

```

```

DE HPV fusion protein DI/3-E6-His/HPV16 DNA.
XX
XX Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour;
XX immunological fusion partner; CpG oligonucleotide; immune response;
XX HPV antigen; prevention; treatment; ss.
XX
XX Synthetic.
XX Human papillomavirus.
XX WO933868-A2.
XX
XX 08-JUL-1999.
XX
XX 18-DEC-1998; 98WO-EP008563.
XX
XX 24-DEC-1997; 97GB-00027262.
XX
XX (SMK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX Dalemans WLJ, Gerard CMG;
XX
XX WPI. 1999-405485/34.
XX
XX P-PSDB; AAY5376.
XX
XX Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to
XX induce immune response to HPV.
XX
XX Example II; Page 48; 62pp; English.
XX
XX AAY78791-X78801 represent nucleic acid sequences which encode novel
XX constructs comprising an E6 or E7 protein or E6/E7 fusion protein from
XX HPV (represented in AAY5375-Y25386). These constructs are optionally
XX linked to an immunological fusion partner and an immunomodulatory CpG
XX oligonucleotide. The products of the invention can be used to induce an
XX immune response in a patient to an HPV antigen. They can also be used for
XX preventing or treating HPV induced tumours
XX
XX Sequence 822 BP; 277 A; 147 C; 168 G; 230 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 28; DB 2; Length 822;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GACATTATGTTATGTTGATGGAAC 28
DB 569 GACATTATGTTATGTTGATGGAAC 596
RESULT 20
AAX29781
ID AAX29781 standard; DNA; 822 BP.
XX
XX AAX29781;
AC
XX 17-OCT-2003 (revised)
DT 22-JUN-1999 (first entry)
XX
XX Prot.DI/3-E6-His/HPV16 coding sequence.
DE
XX
XX Chimeric; E6; E7; fusion protein; protein D; vaccine; immunotherapy;
XX tumour; lesion; benign; malignant; virus; infection; ss.
XX
XX Human papillomavirus.
XX Haemophilus influenzae.
XX Chimeric.
XX
XX WO9910375-A2.
XX
XX 04-MAR-1999.
XX
XX 17-AUG-1998; 98WO-EP005285.
XX
XX 22-AUG-1997; 97GB-00017953.
XX

```

```

XX
XX (SMK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX Bruck C, Cabezon Silva T, Delisse AEF, Gerard CMG;
XX Lombardo-Bencheikh A;
XX
XX WPI; 1999-190587/16.
XX
XX Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for
XX treatment or prophylaxis of HPV induced lesions.
XX
XX Disclosure; Fig 3; 95pp; English.
XX
XX This sequence represents the coding region for a chimeric E6 or E7
XX protein or E6/E7 fusion protein from Human papillomavirus (HPV) linked to
XX an immunological fusion partner. In this case, a fragment of the
XX Haemophilus influenza B protein D. The sequence also contains a
XX histidine tag at the C-terminus of the encoded protein. The protein can
XX be used in a vaccine, for immuno-therapeutically treating HPV induced
XX tumour lesions (benign or malignant) and preventing HPV viral infection.
XX (Updated on 17-OCT-2003 to standardise OS field)
XX
XX Sequence 822 BP; 277 A; 147 C; 168 G; 230 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 28; DB 2; Length 822;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GACATTATGTTATGTTGATGGAAC 28
DB 569 GACATTATGTTATGTTGATGGAAC 596
RESULT 21
AED52633
ID AED52633 standard; DNA; 822 BP.
XX
XX AED52633;
AC
XX 29-DEC-2005 (first entry)
DT
XX
XX Fusion protein DI/3-E6-His/HPV16, DNA.
DE
XX
XX Fusion protein; vaccine; papilloma; cytostatic; papillomavirus infection;
XX virucide; uterine cervix tumor; E6; ds; gene; D protein.
XX
XX Haemophilus influenzae; strain 772.
XX
XX Human papillomavirus type 16.
XX
XX Synthetic.
XX Chimeric.
XX
XX Key Location/Qualifiers
XX CDS 1..822
XX FT /*tag=a
XX FT /product="Fusion protein DI/3-E6-His/HPV16"
XX
XX IN9801903-14.
XX
XX 04-MAR-2005.
XX
XX 24-AUG-1998; 98IN-CH001903.
XX
XX 22-AUG-1997; 97EP-00179535.
XX
XX (SMK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX Tyrrell AWR;
XX
XX WPI. 2005-557648/57.
XX
XX P-PSDB; AED52634.
XX
XX Vaccine.
XX

```

PS Example 4; Fig 3; 96pp; English.

XX The invention relates to human Papilloma virus (HPV) fusion proteins,
 CC linked to an immunological fusion partner that provides T helper epitopes
 CC to the HPV antigen. Vaccine formulations comprising the fusion proteins
 CC are useful in the treatment or prophylaxis of HPV induced lesions
 CC (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7
 CC proteins (singly, as an E6-E7 fusion or mutated) were fused to either
 CC Haemophilus influenzae D protein (20-127), the C-terminus of
 CC Streptococcus pneumoniae Lyta protein (CLYA) or thiorodoxin. The present
 CC sequence encodes an HPV-H. influenzae D protein, fusion protein of the
 CC invention.

XX Sequence 822 BP; 277 A; 147 C; 168 G; 230 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 28; DB 14; Length 822;
 XX Best Local Similarity 100.0%; Pred. No. 0.41;
 XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACATTATTGTTAGTTTGTATGGAAC 28
 |||
 Db 569 GACATTATTGTTATGTTGTATGGAAC 596

RESULT 22

AAx78795
 ID AAX78795 standard; DNA; 879 BP.

XX AAX78795;
 AC
 XX
 XX 06-SEP-1999 (first entry)
 DT
 XX HPV fusion protein CLYTA-E6-His/HPV16 DNA.
 DE
 XX Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour;
 KW immunological fusion partner; Cpg oligonucleotide; immune response;
 KW HPV antigen; prevention; treatment; ss.
 XX
 XX Synthetic.
 OS Human papillomavirus.
 OS
 XX MO9933868-A2.
 XX
 XX 08-JUL-1999.
 PD
 XX 18-DEC-1998; 98WO-EP008563.
 PF
 XX 24-DEC-1997; 97GB-00027262.
 PR
 XX (SMK) SMITHKLINE BEECHAM BIOLOGICALS.
 PA
 XX Dalemans WLJ, Gerard CMG;
 PI
 XX MPI; 1999-405485/34.
 DR P-PSDB; AAY25379.
 XX
 XX Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to
 PT induce immune response to HPV.
 PT
 XX Example VI; Page 52; 62pp; English.
 PS
 XX AAX78791-X78801 represent nucleic acid sequences which encode novel
 CC constructs comprising an E6 or E7 protein or E6/E7 fusion protein from
 CC HPV (represented in AAY25375-Y25386). These constructs are optionally
 CC linked to an immunological fusion partner and an immunomodulatory Cpg
 CC oligonucleotide. The products of the invention can be used to induce an
 CC immune response in a patient to an HPV antigen. They can also be used for
 CC preventing or treating HPV induced tumours
 CC
 XX Sequence 879 BP; 289 A; 168 C; 209 G; 213 T; 0 U; 0 Other;
 XX
 XX Query Match 100.0%; Score 28; DB 2; Length 879;
 XX Best Local Similarity 100.0%; Pred. No. 0.42;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACATTATTGTTAGTTTGTATGGAAC 28
 |||
 Db 626 GACATTATTGTTATGTTGTATGGAAC 653

RESULT 23

AAx29784
 ID AAX29784 standard; DNA; 879 BP.

XX AAX29784;
 AC
 XX
 XX 17-OCT-2003 (revised)
 DT 22-JUN-1999 (first entry)
 XX
 XX CLYTA-E6-His coding sequence.
 DE
 XX Chimeric; E6; E7; fusion protein; CLYTA; vaccine; immunotherapy; tumour;
 KW lesion; benign; malignant; virus; infection; ss.
 XX
 XX Human papillomavirus.
 OS Streptococcus pneumoniae.
 OS Chimeric.
 OS
 XX MO9910375-A2.
 XX
 XX 04-MAR-1999.
 PD
 XX 17-AUG-1998; 98WO-EP005285.
 PF
 XX 22-AUG-1997; 97GB-00017953.
 PR
 XX (SMK) SMITHKLINE BEECHAM BIOLOGICALS.
 PA
 XX Bruck C, Cabezon Silva T, Delisse AEF, Gerard CMG,
 PI Lombardo-Bencheikh A;
 PI
 XX MPI; 1999-190587/16.
 DR P-PSDB; AAY02635.
 XX
 XX Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for
 PT treatment or prophylaxis of HPV induced lesions.
 PT
 XX Disclosure; Fig 10; 95pp; English.
 PS
 XX This sequence represents the coding region for a chimeric E6 or E7
 CC protein or E6/E7 fusion protein from Human papillomavirus (HPV) linked to
 CC an immunological fusion partner, in this case, a fragment of the
 CC Streptococcus pneumoniae CLYTA protein. The sequence also contains a
 CC histidine tag at the C-terminus of the encoded protein. The protein can
 CC be used in a vaccine, for immuno-therapeutically creating HPV induced
 CC tumour lesions (benign or malignant) and preventing HPV viral infection.
 CC (Updated on 17-OCT-2003 to standardise OS field)
 CC
 XX Sequence 879 BP; 289 A; 168 C; 209 G; 213 T; 0 U; 0 Other;
 XX
 XX Query Match 100.0%; Score 28; DB 2; Length 879;
 XX Best Local Similarity 100.0%; Pred. No. 0.42;
 XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACATTATTGTTAGTTTGTATGGAAC 28
 |||
 Db 626 GACATTATTGTTATGTTGTATGGAAC 653

RESULT 24

AE52641
 ID AED52641 standard; DNA; 879 BP.

XX AED52641;
 AC
 XX
 XX 29-DEC-2005 (first entry)
 DT

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XX XX Fusion protein clyta-E6-His/HPV16, DNA.
DE XX
XX XX Fusion protein; vaccine; papilloma; cytostatic; papillomavirus infection;
KM XX virucide; uterine cervix tumor; E6; de; gene; lyta.
XX XX
OS Streptococcus pneumoniae.
OS Human papillomavirus type 16.
OS Synthetic.
OS Chimeric.
XX XX
FH Key Location/Qualifiers
FT CDS 1..879
FT /tag= a
FT /product= "Fusion protein clyta-E6-His/HPV16"
XX XX
XX IN9801903-14.
XX XX
XX 04-MAR-2005.
XX XX
XX 24-AUG-1998; 98IN-CH001903.
XX XX
XX 22-AUG-1997; 97EP-00179535.
XX XX
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX XX
XX Tyrtrell AMR;
XX XX
XX WPI; 2005-557648/57.
XX DR P-PSDB; AED52642.
XX XX
XX Vaccine.
XX XX
XX Example 10; Fig 10; 96pp; English.
XX XX
XX The invention relates to human Papilloma virus (HPV) fusion proteins,
CC linked to an immunological fusion partner that provides T helper epitopes
CC to the HPV antigen. Vaccine formulations comprising the fusion proteins
CC are useful in the treatment or prophylaxis of HPV induced lesions
CC (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7
CC proteins (singly, as an E6-E7 fusion or mutated) were fused to either
CC Haemophilus influenzae D protein (20-127), the C-terminus of
CC Streptococcus pneumoniae Lyta protein (clyta) or thiodoxin. The present
CC sequence encodes an HPV-Lyta, fusion protein of the invention.
XX XX
XX Sequence 879 BP; 289 A; 168 C; 209 G; 213 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 28; DB 14; Length 879;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GACATTATTGTTATAGTTGTATGGAAC 28
Db 626 GACATTATTGTTATAGTTGTATGGAAC 653

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PD 10-APR-2002.
XX XX
XX 06-OCT-2000; 2000EP-00203472.
XX XX
XX 06-OCT-2000; 2000EP-00203472.
XX XX
XX (UYGR-) RIJCKSUNIV GRONINGEN.
XX XX
XX Regts DG, Wilschut JC, Holtrop M, Daemen CAHH;
XX XX
XX WPI; 2002-354156/39.
XX XX
XX New alphavirus system, useful for genetic immunization against cervical
XX cancer, comprises papilloma virus nucleic acid.
XX XX
XX Example 2; Fig 19; 45pp; English.
XX XX
XX The present invention relates to an alphavirus vector system comprising
XX CC nucleic acid derived from a human papilloma virus (HPV). The invention or
XX cells containing it, are used in treatment and prevention of cervical
XX cancer, particularly as a vaccine. By selecting the nucleic acid that
XX encode E6/E7 proteins without ability to bind to pRb and p53, the risk
XX that cells infected with the alphavirus vector system may become
XX CC oncogenic is avoided (contrast use of other viral vectors). The present
XX sequence is Human papillomavirus enhB6,7 construct DNA
XX XX
XX Sequence 939 BP; 284 A; 197 C; 217 G; 241 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 28; DB 6; Length 939;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GACATTATTGTTATAGTTGTATGGAAC 28
Db 415 GACATTATTGTTATAGTTGTATGGAAC 442

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RESULT 26
AAQ08627
ID AAQ08627 standard; DNA; 1000 BP.
XX XX
XX AAQ08627;
XX AC
XX 24-OCT-2003 (revised)
XX DT
XX 21-APR-1994 (first entry)
XX XX
XX HPV-16 fragment.
XX DE
XX HPV-18; HPV-16; amplification; primer; polymerase chain reaction; PCR;
XX KM ss.
XX XX
XX Human papillomavirus type 16.
XX OS
XX Key Location/Qualifiers
XX FH 198..207
XX FT misc_binding
XX FT /tag= a
XX FT /note= "primer (AAQ08628) binding site"
XX FT /tag= b
XX FT /note= "primer (AAQ08629) binding site"
XX FT 658..677
XX FT /tag= c
XX FT /note= "primer (AAQ08630) binding site"
XX XX
XX DE3838269-A.
XX XX
XX 17-MAY-1990.
XX PD
XX 11-NOV-1988; 88DE-03838269.
XX PF
XX 11-NOV-1988; 88DE-03838269.
XX PR
XX (BEHM ) BEHRINGWERKE AG.
XX PA

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```

XX Cerutti P, Whitcomb J, Zijlstra J, Devilliers EM;
XX WPI; 1990-156905/21.
XX
XX Detection of human papilloma virus - by DNA amplification and analysis.
XX
XX Example 4b; Page 4; 11pp; German.
XX
XX Example 4b describes the results of the amplification of HPV-16 DNA by
XX PCR using primers. (Updated on 24-OCT-2003 to standardise OS field)
XX
XX Sequence 1000 BP; 340 A; 171 C; 230 G; 259 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 28; DB 2; Length 1000;
XX Best Local Similarity 100.0%; Pred. No. 0.42;
XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GACATTATTGTTATAGTTGTATGGAAC 28
Db 333 GACATTATTGTTATAGTTGTATGGAAC 360

RESULT 27
AAN91784
ID AAN91784 standard; DNA; 1005 BP.
XX
XX AAN91784;
XX
XX 27-AUG-2003 (revised)
XX 25-MAR-2003 (revised)
XX 16-MAR-1990 (first entry)
XX
XX DNA probe complementary to human papilloma virus type 16.
XX
XX Cervical cancer.
XX
XX
XX Human papillomavirus type 16.
XX
XX W08909940-A.
XX
XX 19-OCT-1989.
XX
XX 04-APR-1989; 89WO-US001318.
XX
XX 04-APR-1988; 88US-00177404.
XX 31-MAR-1989; 89US-00330381.
XX
XX (ONCO-) ONCOR INC.
XX
XX George AL, Groff DE;
XX
XX WPI; 1989-324314/44.
XX
XX Rapid detection of specific human papilloma virus genotypes - by
XX hybridisation of DNA digest with new labelled nucleic acid probes.
XX
XX Claim 40; Page 46; 81pp; English.
XX
XX Obtd. by cutting HPV16 with BamHI and PvuII. The patent describes probes
XX (DNA or RNA) and their complements capable of detecting one or a
XX combination of HPV types 6, 11, 16, 18, 31, 33 and 35. (Updated on 25-MAR
XX -2003 to correct PR field.) (Updated on 27-AUG-2003 to correct OS field.)
XX
XX Sequence 1005 BP; 325 A; 182 C; 190 G; 308 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 28; DB 1; Length 1005;
XX Best Local Similarity 100.0%; Pred. No. 0.42;
XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GACATTATTGTTATAGTTGTATGGAAC 28
Db 785 GACATTATTGTTATAGTTGTATGGAAC 812

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RESULT 28
AAK78793
ID AAK78793 standard; DNA; 1116 BP.
XX
XX AAK78793;
XX
XX 06-SEP-1999 (first entry)
XX
XX HPV fusion protein DI/3-B6E7-His/HPV16 DNA.
XX
XX Fusion protein; B6 protein; E7 protein; B6/E7; immunomodulator; tumour;
XX immunological fusion partner; CpG oligonucleotide; immune response;
XX HPV antigen; prevention; treatment; ss.
XX
XX Synthetic.
XX
XX Human papillomavirus.
XX
XX W09933868-A2.
XX
XX 08-JUL-1999.
XX
XX 18-DEC-1998; 98WO-EP008563.
XX
XX 24-DEC-1997; 97GB-00027262.
XX
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX Dalemans WLJ, Gerard CMG;
XX
XX WPI; 1999-405485/34.
XX
XX P-PSDB; AAY25377.
XX
XX Composition comprising an E6, E7 or B6/E7 fusion protein from HPV to
XX induce immune response to HPV.
XX
XX Example III; Page 49; 62pp; English.
XX
XX AAK78791-K78801 represent nucleic acid sequences which encode novel
XX constructs comprising an E6 or E7 protein or B6/E7 fusion protein from
XX HPV (represented in AAY25375-125386). These constructs are optionally
XX linked to an immunological fusion partner and an immunomodulatory CpG
XX oligonucleotide. The products of the invention can be used to induce an
XX immune response in a patient to an HPV antigen. They can also be used for
XX preventing or treating HPV induced tumours
XX
XX Sequence 1116 BP; 368 A; 208 C; 235 G; 305 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 28; DB 2; Length 1116;
XX Best Local Similarity 100.0%; Pred. No. 0.42;
XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GACATTATTGTTATAGTTGTATGGAAC 28
Db 569 GACATTATTGTTATAGTTGTATGGAAC 596

RESULT 29
AAK29782
ID AAK29782 standard; DNA; 1116 BP.
XX
XX AAK29782;
XX
XX 17-OCT-2003 (revised)
XX 22-JUN-1999 (first entry)
XX
XX Prot.DI/3-B6-E7-His/HPV16 coding sequence.
XX
XX Chimeric; B6; E7; fusion protein; protein D; vaccine; immunotherapy;
XX tumour; lesion; benign; malignant; virus; infection; ss.
XX
XX Human papillomavirus.
XX

```

```

OS Haemophilus influenzae.
OS Chimeric.
XX
XX WO9910375-A2.
XX
XX 04-MAR-1999.
XX
XX 17-AUG-1998; 98WO-EP005285.
XX
XX 22-AUG-1997; 97GB-00017953.
XX
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX Bruck C, Cabezon Silva T, Delisse AEF, Gerard CMG;
XX Lombardo-Bencheikh A;
XX
XX WPI; 1999-190587/16.
XX
XX P-PSDB; AAY02633.
XX
XX Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for
XX treatment or prophylaxis of HPV induced lesions.
XX
XX Disclosure; Fig 6; 95pp; English.
XX
XX This sequence represents the coding region for a chimeric E6 or E7
XX protein or E6/E7 fusion protein from Human papillomavirus (HPV) linked to
XX an immunological fusion partner, in this case, a fragment of the
XX Haemophilus influenzae B protein D. The sequence also contains a
XX histidine tag at the C-terminus of the encoded protein. The protein can
XX be used in a vaccine, for immuno-therapeutically treating HPV induced
XX tumour lesions (benign or malignant) and preventing HPV viral infection.
XX (Updated on 17-OCT-2003 to standardise OS field)
XX
XX Sequence 1116 BP; 368 A; 208 C; 235 G; 305 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 28; DB 2; Length 1116;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACATTATTGTTATGTTGTTATGGAAC 28
Db 569 GACATTATTGTTATGTTGTTATGGAAC 596

RESULT 30
AED52637
ID AED52637 standard; DNA; 1116 BP.
XX
XX AED52637;
XX
XX 29-DEC-2005 (first entry)
XX
XX Fusion protein D1/3-E6-E7-His/HPV16, DNA.
XX
XX Fusion protein; vaccine; papilloma; cytostatic; papillomavirus infection;
XX virucide; uterine cervix tumor; E7; E6; ds; gene; D protein.
XX
XX Haemophilus influenzae; strain 772.
XX
XX Human papillomavirus type 16.
XX
XX Synthetic.
XX
XX Chimeric.
XX
XX Key Location/Qualifiers
XX CDS 1..1116
XX /tag= a
XX /product= "Fusion protein D1/3-E6-E7-His/HPV16"
XX
XX IN9801903-14.
XX
XX 04-MAR-2005.
XX
XX 24-AUG-1998; 98IN-CH001903.
XX

```

```

PR 22-AUG-1997; 97EP-00179535.
XX
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX Tyrrell AMR;
XX
XX WPI; 2005-557648/57.
XX
XX P-PSDB; AED52638.
XX
XX Vaccine.
XX
XX Example 6; Fig 6; 96pp; English.
XX
XX The invention relates to human Papilloma virus (HPV) fusion proteins,
XX linked to an immunological fusion partner that provides T helper epitopes
XX to the HPV antigen. Vaccine formulations comprising the fusion proteins
XX are useful in the treatment or prophylaxis of HPV induced lesions
XX (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7
XX proteins (singly, as an E6-E7 fusion or mutated) were fused to either
XX Haemophilus influenzae D protein (20-127), the C-terminus of
XX Streptococcus pneumoniae Lyta protein (CLYta) or chlorodoxin. The present
XX sequence encodes an HPV-H. influenzae D protein, fusion protein of the
XX invention.
XX
XX Sequence 1116 BP; 368 A; 208 C; 235 G; 305 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 28; DB 14; Length 1116;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACATTATTGTTATGTTGTTATGGAAC 28
Db 569 GACATTATTGTTATGTTGTTATGGAAC 596

RESULT 31
AAX78797
ID AAX78797 standard; DNA; 1173 BP.
XX
XX AAX78797;
XX
XX 06-SEP-1999 (first entry)
XX
XX HPV fusion protein CLYta-E6E7-His/HPV16 DNA.
XX
XX Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour;
XX immunological fusion partner; CpG oligonucleotide; immune response;
XX HPV antigen; prevention; treatment; ss.
XX
XX Synthetic.
XX
XX Human papillomavirus.
XX
XX WO9933868-A2.
XX
XX 08-JUL-1999.
XX
XX 18-DEC-1998; 98WO-EP008563.
XX
XX 24-DEC-1997; 97GB-00027262.
XX
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX Dalemans WLJ, Gerard CMG;
XX
XX WPI; 1999-405485/34.
XX
XX P-PSDB; AAY25381.
XX
XX Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to
XX induce immune response to HPV.
XX
XX Example VIII; Page 54-55; 62pp; English.
XX
XX AAX78791-X78801 represent nucleic acid sequences which encode novel
XX

```

CC constructs comprising an E6 or E7 protein or E6/E7 fusion protein from
 CC HPV (represented in AAY25375-Y25386). These constructs are optionally
 CC linked to an immunological fusion partner and an immunomodulatory CpG
 CC oligonucleotide. The products of the invention can be used to induce an
 CC immune response in a patient to an HPV antigen. They can also be used for
 CC preventing or treating HPV induced tumours

XX Sequence 1173 BP; 380 A; 229 C; 276 G; 288 T; 0 U; 0 Other;
 SQ

Query Match 100.0%; Score 28; DB 2; Length 1173;
 Best Local Similarity 100.0%; Pred. No. 0.42;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACATTATTGTTATGTTGTATGAAC 28
 Db 626 GACATTATTGTTATGTTGTATGAAC 653

RESULT 32
 AAY29786
 ID AAY29786 standard; DNA; 1173 BP.
 XX
 XX AAY29786;
 AC
 XX 17-OCT-2003 (revised)
 DT 22-JUN-1999 (first entry)
 DT
 XX CLYTA-E6E7-His coding sequence.
 DE
 XX Chimeric; E6; E7; fusion protein; CLYTA; vaccine; immunotherapy; tumour;
 KM lesion; benign; malignant; virus; infection; ss.
 XX
 XX Human papillomavirus.
 OS Streptococcus pneumoniae.
 OS Chimeric.
 OS
 XX WQ9910375-A2.
 PN
 XX 04-MAR-1999.
 PD
 XX 17-AUG-1998; 98WO-EP005285.
 PF
 XX 22-AUG-1997; 97GB-00017953.
 PR
 XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 PA Bruck C, Cabazon Silva T, Delisse AEF, Gerard CMG;
 PI Lombardo-Bencheikh A;
 PI
 XX WPI, 1999-190587/16.
 DR P-PSDB; AAY02637.
 DR
 XX Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for
 PT treatment or prophylaxis of HPV induced lesions.
 PT
 XX Disclosure; Fig 14; 95pp; English.
 PS
 XX This sequence represents the coding region for a chimeric E6 or E7
 CC protein or E6/E7 fusion protein from Human papillomavirus (HPV) linked to
 CC an immunological fusion partner, in this case, a fragment of the
 CC Streptococcus pneumoniae CLYTA protein. The sequence also contains a
 CC histidine tag at the C-terminus of the encoded protein. The protein can
 CC be used in a vaccine, for immuno-therapeutically creating HPV induced
 CC tumour lesions (benign or malignant) and preventing HPV viral infection.
 CC (Updated on 17-OCT-2003 to standardise OS field)
 CC
 XX
 SQ Sequence 1173 BP; 380 A; 229 C; 276 G; 288 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 2; Length 1173;
 Best Local Similarity 100.0%; Pred. No. 0.42;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACATTATTGTTATGTTGTATGAAC 28

Db 626 GACATTATTGTTATGTTGTATGAAC 653

RESULT 33
 AED52645
 ID AED52645 standard; DNA; 1173 BP.
 XX
 XX AED52645;
 AC
 XX 29-DEC-2005 (first entry)
 DT
 XX Fusion protein cLYTA-E6-E7-His/HPV16, DNA.
 DE
 XX Fusion protein; vaccine; papilloma; cytostatic; papillomavirus infection;
 KM viricide; uterine cervix tumor; E7; E6; de; gene; Lyta.
 XX
 XX Streptococcus pneumoniae.
 OS Human papillomavirus type 16.
 OS Synthetic.
 OS Chimeric.
 OS
 XX Key Location/Qualifiers
 FH CDS 1..1173
 FT /*tag= a
 FT /product= "Fusion protein cLYTA-E6-E7-His/HPV16"
 FT
 XX IN9801903-I4.
 FN
 XX 04-MAR-2005.
 PD
 XX 24-AUG-1998; 98IN-CH001903.
 PF
 XX 22-AUG-1997; 97EP-00179535.
 PR
 XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 PA Tyrell AMR;
 PI
 XX WPI, 2005-557648/57.
 DR P-PSDB; AED52646.
 DR
 XX Vaccine.
 PT
 XX Example 12; Fig 14; 96pp; English.
 PS
 XX The invention relates to human Papilloma virus (HPV) fusion proteins,
 CC linked to an immunological fusion partner that provides T helper epitopes
 CC to the HPV antigen. Vaccine formulations comprising the fusion proteins
 CC are useful in the treatment or prophylaxis of HPV induced lesions
 CC (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7
 CC proteins (singly, as an E6-E7 fusion or mutated) were fused to either
 CC Haemophilus influenzae D protein (20-127), the C-terminus of
 CC Streptococcus pneumoniae Lyta protein (cLYTA) or chlorodoxin. The present
 CC sequence encodes an HPV-LyTA, fusion protein of the invention.
 CC
 XX
 SQ Sequence 1173 BP; 380 A; 229 C; 276 G; 288 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 14; Length 1173;
 Best Local Similarity 100.0%; Pred. No. 0.42;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACATTATTGTTATGTTGTATGAAC 28
 Db 626 GACATTATTGTTATGTTGTATGAAC 653

RESULT 34
 AAF55127
 ID AAF55127 standard; DNA; 7840 BP.
 XX
 XX AAF55127;
 AC

DT 29-MAY-2001 (first entry)
XX Nucleotide sequence of the vector pRetrOFF-BEG7.
XX Stem cell; gene therapy; cell therapy; stem cell disorder; ss.
XX Synthetic.
XX
FH Key
FT misc_feature
FT Location/Qualifiers
FT 5600
FT /*tag= d
FT /note= "this base is given as N because it was illegible
FT in the figure"
FT 5650
FT /*tag= e
FT /note= "this base is given as N because it was illegible
FT in the figure"
FT 5700
FT /*tag= f
FT /note= "this base is given as N because it was illegible
FT in the figure"
FT 5750
FT /*tag= g
FT /note= "this base is given as N because it was illegible
FT in the figure"
FT 5800
FT /*tag= h
FT /note= "this base is given as N because it was illegible
FT in the figure"
FT 5850
FT /*tag= i
FT /note= "this base is given as N because it was illegible
FT in the figure"
FT 5850
FT /*tag= a
FT /note= "this base is given as N because it was illegible
FT in the figure"
FT 5900
FT /*tag= j
FT /note= "this base is given as N because it was illegible
FT in the figure"
FT 5900
FT /*tag= b
FT /note= "this base is given as N because it was illegible
FT in the figure"
FT 5950
FT /*tag= k
FT /note= "this base is given as N because it was illegible
FT in the figure"
FT 5950
FT /*tag= c
FT /note= "this base is given as N because it was illegible
FT in the figure"
FT 6000
FT /*tag= l
FT /note= "this base is given as N because it was illegible
FT in the figure"
FT 6050
FT /*tag= m
FT /note= "this base is given as N because it was illegible
FT in the figure"
FT 6100
FT /*tag= n
FT /note= "this base is given as N because it was illegible
FT in the figure"
FT 6150
FT /*tag= o
FT /note= "this base is given as N because it was illegible
FT in the figure"
FT 6200
FT /*tag= p
FT /note= "this base is given as N because it was illegible
FT in the figure"

FT misc_feature
FT 6250
FT /*tag= q
FT /note= "this base is given as N because it was illegible
FT in the figure"
FT 6300
FT /*tag= r
FT /note= "this base is given as N because it was illegible
FT in the figure"
FT 6350
FT /*tag= s
FT /note= "this base is given as N because it was illegible
FT in the figure"
FT 6400
FT /*tag= t
FT /note= "this base is given as N because it was illegible
FT in the figure"
FT 6450
FT /*tag= u
FT /note= "this base is given as N because it was illegible
FT in the figure"
FT 6500
FT /*tag= v
FT /note= "this base is given as N because it was illegible
FT in the figure"
FT 6600
FT /*tag= w
FT /note= "this base is given as N because it was illegible
FT in the figure"
FT 6650
FT /*tag= x
FT /note= "this base is given as N because it was illegible
FT in the figure"
FT 6700
FT /*tag= y
FT /note= "this base is given as N because it was illegible
FT in the figure"
FT 6750
FT /*tag= z
FT /note= "this base is given as N because it was illegible
FT in the figure"
FT 6800
FT /*tag= aa
FT /note= "this base is given as N because it was illegible
FT in the figure"
FT 6850
FT /*tag= ab
FT /note= "this base is given as N because it was illegible
FT in the figure"
FT 6900
FT /*tag= ac
FT /note= "this base is given as N because it was illegible
FT in the figure"
FT 6950
FT /*tag= ad
FT /note= "this base is given as N because it was illegible
FT in the figure"
FT 7000
FT /*tag= ae
FT /note= "this base is given as N because it was illegible
FT in the figure"
FT 7050
FT /*tag= af
FT /note= "this base is given as N because it was illegible
FT in the figure"
FT 7100
FT /*tag= ag
FT /note= "this base is given as N because it was illegible
FT in the figure"
FT 7150
FT /*tag= ah
FT /note= "this base is given as N because it was illegible
FT in the figure"
FT 7200
FT /*tag= ai
FT /note= "this base is given as N because it was illegible
FT in the figure"


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FT CDS 562..858
FT /tag= e
FT /product= "E7 transforming protein"
FT /note= "E7 ORF 544 to 858; putative"
FT CDS 865..2813
FT /tag= f
FT /product= "E1 replication protein"
FT /note= "E1 interrupted ORF from 859 to 2813; putative"
FT CDS 2755..3852
FT /tag= g
FT /product= "E2 regulatory protein"
FT /note= "E2 ORF from 2725 to 3852; putative"
FT CDS 3332..3619
FT /tag= h
FT /product= "E4"
FT /note= "E4 ORF from 3332 to 3619; putative"
FT CDS 3863..4099
FT /tag= i
FT /product= "E5"
FT /note= "E5 ORF from 3863 to 4099; putative"
FT polyA_signal 4213..4218
FT /tag= j
FT /note= "Putative"
FT CDS 4235..5656
FT /tag= k
FT /product= "L2 minor capsid protein"
FT /note= "L2 ORF from 4133 to 5656; putative"
FT TATA_signal 4289..4295
FT /tag= l
FT /product= "L1 major capsid protein"
FT /note= "L1 ORF from 5526 to 7154; putative"
FT polyA_signal 7260..7265
FT /tag= n
XX US679509-A.
XX 21-OCT-1997.
XX 30-SEP-1994; 94US-00316239.
XX 28-SEP-1993; 93US-00127906.
XX (VUNE-) UNIV NEW MEXICO STATE.
XX Wheeler CM, Parmenter CA;
XX PI
XX WPI; 1997-525714/48.
XX P-PSDB; AAM35741.
XX
XX Claim 1; Col 9-16; 33pp; English.
XX
XX Methods have been developed for distinguishing a subset of human
XX papilloma virus (HPV) that is associated with an increased risk of
XX developing cervical dysplasia or cervical cancer. The methods involve:
XX (1) preparing a cervical sample to expose any HPV-16 B6 gene in the
XX sample and determining if the base at position 350 of the B6 gene (see
XX AAM35742 and AAM35744 for comparison) is T or G, where the presence of G
XX at position 350 is associated with an increased risk of developing
XX cervical dysplasia or cervical cancer; and (2) preparing a cervical
XX sample to expose any HPV-16 E6 protein in the sample and determining if
XX the amino acid at position 83 of the protein (see position 90 in AAM35741
XX and AAM35742 for comparison) is Val or Leu, where the presence of Val at
XX position 83 that is associated with an increased risk of developing
XX cervical dysplasia or cervical cancer. The present sequence represents
XX the reference nucleotide sequence for HPV-16 B6. The 350G variant
XX correlates well with Pap scores: 350T:350G ratios among 45 HPV16 samples
XX were 10:4 for negative Pap scores; 4:2 for CIN I, 1:6 for CIN II; 2:9 for
XX CIN III; 0:3 for cancer. (Updated on 25-MAR-2003 to correct PF field.)

```

```

XX SQ Sequence 7904 BP; 2601 A; 1377 C; 1509 G; 2417 T; 0 U; 0 Other;
XX Query Match 100.0%; Score 28; DB 2; Length 7904;
XX Best Local Similarity 100.0%; Pred. No. 0.42;
XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GACATTATGTTATAGTTGTATGGAAC 28
DB 333 GACATTATGTTATAGTTGTATGGAAC 360
XX
XX RESULT 37
XX ID AAX33881 standard; DNA; 7904 BP.
XX AAX33881;
XX AC 17-OCT-2003 (revised)
XX DT 25-JUN-1999 (first entry)
XX XX
XX DE HPV-16 genomic sequence.
XX KW HPV-16; inhibitor; antisense oligonucleotide; E6/E7 gene; human;
XX KW keratinocyte; cervical cell; cervical tumour; PCR primer; beta-actin; ss.
XX OS Human papillomavirus type 16.
XX MO09913071-A1.
XX PN 18-MAR-1999.
XX PD 03-SEP-1998; 98WO-US018320.
XX PF 05-SEP-1997; 97US-00929140.
XX PR (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PA DiPaolo J, Alvarez-Salas L;
XX PI
XX WPI; 1999-243727/20.
XX DR
XX PT New antisense oligonucleotide analogs for inhibiting growth of cervical
XX PT tumors.
XX PS Disclosure; Page 28-32; 40pp; English.
XX XX
XX CC This sequence represents a sequence from the HPV-16 genome. This
XX CC invention relates to antisense oligonucleotide analogs (ONAs) that have a
XX CC sequence complementary to a sequence of nucleotides 415-445 of human
XX CC papilloma virus-16 (HPV-16). The antisense ONAs can be used to inhibit
XX CC expression of HPV gene E6/E7 in living cells, preferably human
XX CC keratinocytes or human cervical cells. They bind to E6/E7 mRNA in the
XX CC cell, prevent mRNA translation and promote mRNA degradation by
XX CC intracellular RNase H. They can be used for preventing transformation of
XX CC living cells by HPV. The antisense ONAs are used particularly for
XX CC inhibiting the growth of cervical tumours. (Updated on 17-OCT-2003 to
XX CC standardise OS field)
XX SQ Sequence 7904 BP; 2601 A; 1377 C; 1509 G; 2417 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 28; DB 2; Length 7904;
XX Best Local Similarity 100.0%; Pred. No. 0.42;
XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GACATTATGTTATAGTTGTATGGAAC 28
DB 333 GACATTATGTTATAGTTGTATGGAAC 360
XX
XX RESULT 38
XX AAV99946
XX ID AAV99946 standard; DNA; 7904 BP.

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XX OS Human papillomavirus.
 XX PN W02003040366-A2.
 XX PD 15-MAY-2003.
 XX PF 08-NOV-2002; 2002MO-FR003843.
 XX PR 09-NOV-2001; 2001FR-00014549.
 XX PR 10-APR-2002; 2002FR-00004474.
 XX PA (CNRS) CNRS CENT NAT RECH SCI.
 XX PI Harel-Bellan A, Alt-Si-Ali S, Cabon-Georget F, Chauchereau A,
 XX PI Dautry F,
 XX DR WPI; 2003-441571/41.
 XX PT New double-stranded oligonucleotides, useful e.g. for treatment and
 XX PT diagnosis of tumors, comprise complementary strands with single-stranded
 XX PT overhangs.
 XX PS Disclosure; Fig 6A; 148bp; French.
 XX CC The invention relates to double-stranded oligonucleotides consisting of
 CC two complementary strands (1a, 1b), each having 1-5 unpaired nucleotides,
 CC at either at their 3' and 5' ends, forming single-stranded overhangs. One
 CC of (1a) and (1b) is complementary to a target sequence, (DNA or RNA),
 CC that is to be specifically repressed. The oligonucleotides are preferably
 CC double stranded inhibitor RNA molecules with a couple of thymidine bases
 CC attached at the 3' or 5' ends. The targets are preferably nucleic acids
 CC that, when repressed, induce apoptosis, necrosis or differentiation of
 CC tumour cells and/or inhibit division of such cells. Typical of many
 CC specified targets include: genes of the Bcl2 family; genes that encode
 CC metalloproteases (matrix or membrane) or their inhibitors; genes encoding
 CC mutant forms of nuclear hormone receptors; a sequence encoding the Httf-
 CC alpha transcription factor; sequences encoding various isoforms of the
 CC vacuolar endothelial growth factor; viral genes; genes that express a
 CC mutated protein, e.g. inactive p53; genes that are formed by a
 CC chromosomal translocation, e.g. where associated with leukaemia, and
 CC genes that express androgen receptors. The oligonucleotides are used: (1)
 CC to study gene function; (11) for therapy or diagnosis, particularly of
 CC conditions caused by expression of a harmful gene or fusion protein,
 CC specifically cancer (e.g. associated with expression of mutant p53 or of
 CC the human papilloma virus B6 protein), viral infections, especially AIDS
 CC or cancer-inducing viruses, or unconventional infections, e.g. BSE or CJD
 CC ; and (111) for treating hypervascular diseases, e.g. age-related macular
 CC degeneration, angiogenesis in tumours, diabetic retinopathy, psoriasis
 CC and rheumatoid arthritis. They may also be used in vitro, e.g. for
 CC treating transplants and for establishing a genetic profile, for
 CC individualization, or modification, of treatment regimes. They provide
 CC very effective and very specific repression of genes. RNA hybrids are
 CC more stable than either hybrids prepared from DNA or single-stranded
 CC sequences; contain only natural components (so will not induce
 CC immunological or intolerance reactions) and they enter tumour cells more
 CC effectively than plasmids. This sequence represents the human
 CC papillomavirus B6 gene to which oligonucleotides can be targeted.
 XX CC
 SQ Sequence 7904 BP; 2601 A; 1377 C; 1509 G; 2417 T; 0 U; 0 Other;
 Query Match 100.0%; Score 28; DB 8; Length 7904;
 Best Local Similarity 100.0%; Pred. No. 0.42; Mismatches 0; Indels 0; Gaps 0;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 GACATTATGTTATAGTTGATGGAAC 28
 ||||||||||||||||||||||||||||
 Db 333 GACATTATGTTATAGTTGATGGAAC 360
 ||||||||||||||||||||||||||||
 RESULT 41
 ADO58335
 ID ADO58335 standard; DNA; 7904 BP.

XX AC ADO58335;
 XX DT 15-JUL-2004 (first entry)
 XX DE Human papillomavirus type 16 L1 capsid protein DNA.
 XX KW gene delivery system; virus-like particle; viral structure protein;
 KW capsid protein; L1; human papillomavirus; HPV; immunity; cytokine;
 KW chemokine; interleukin-2; IL-2; tumour suppressor gene H19; cell cycle;
 KW p21; angiogenesis inhibitor; flk-1; capsomer; HPV16; gene; ds.
 XX OS Human papillomavirus type 16.
 XX PN KR2002084620-A.
 XX PD 09-NOV-2002.
 XX PF 03-MAY-2001; 2001KR-00024124.
 XX PR 03-MAY-2001; 2001KR-00024124.
 XX PA (OHYK/) OH Y K.
 XX PI Kim JG, Ko JY, Oh YK, Shin GS, Son TJ;
 XX DR WPI; 2003-338995/32.
 XX PT Gene delivery system containing desired foreign gene in virus-like
 XX PT particles.
 XX PS Example 1; SEQ ID NO 1; 16bp; Korean.
 XX CC The invention describes a gene delivery system containing a desired
 CC foreign gene in virus-like particles. The desired foreign gene can be
 CC stably delivered into a cell without being decomposed by nucleases and
 CC the desired foreign gene also stable in vivo because the virus-like
 CC particles do not have nucleic acids derived from virus. The gene delivery
 CC system contains a desired foreign gene in virus-like particles consisting
 CC of only viral structure proteins, wherein the viral structure protein is
 CC a capsid protein L1 derived from human papillomavirus (HPV); the foreign
 CC gene is associated with immunity; and the foreign gene associated with
 CC immunity is selected from the group consisting of cytokine gene,
 CC chemokine gene, interleukin-2 (IL-2) gene, tumour suppressor gene H19,
 CC cell cycle participating gene p21 and angiogenesis inhibitor flk-1. The
 CC method for producing the gene delivery system containing the desired
 CC foreign gene comprises the steps of: treating the virus-like particles
 CC with an appropriate reducing agent to be unit capsomer proteins; adding
 CC the desired foreign gene into the unit capsomer protein and allowing them
 CC to react; and removing the reducing agent to refold the unit capsomer
 CC protein. This sequence represents human papillomavirus type 16 (HPV16) L1
 CC capsid protein DNA.
 XX CC
 SQ Sequence 7904 BP; 2601 A; 1377 C; 1509 G; 2417 T; 0 U; 0 Other;
 Query Match 100.0%; Score 28; DB 11; Length 7904;
 Best Local Similarity 100.0%; Pred. No. 0.42; Mismatches 0; Indels 0; Gaps 0;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 GACATTATGTTATAGTTGATGGAAC 28
 ||||||||||||||||||||||||||||
 Db 333 GACATTATGTTATAGTTGATGGAAC 360
 ||||||||||||||||||||||||||||
 RESULT 42
 ADZ45647
 ID ADZ45647 standard; DNA; 7904 BP.
 XX AC ADZ45647;
 XX DT 30-JUN-2005 (first entry)
 XX DE Human papillomavirus type 16 full length genomic clone - SEQ ID 1.

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XX tumor marker; genome; diagnosis; cancer; uterine cervix tumor;
KM rectal tumor; colon tumor; ds.
XX
XX Human papillomavirus type 16.
XX WO2005033333-A2.
XX
XX 14-APR-2005.
XX
XX 04-OCT-2004; 2004WO-DK000670.
XX
XX 07-OCT-2003; 2003DK-00001474.
XX 07-OCT-2003; 2003US-0509205P.
XX 13-FEB-2004; 2004US-0543925P.
XX
XX (DAKO-) DAKOCYTOMATION DENMARK AS.
XX
XX Chau MF, Bisgaard-Franzen K, Lin J, Rasmussen OF, Wang Z, Lusk J,
PI Lindberg M, Ysaac S;
XX
XX WPI; 2005-265441/29.
XX
XX New composition having a nucleic acid molecule identical to genomic clone
PT of human papilloma virus 16, 18 or 51, useful in diagnosing cancer or the
PT risk of developing cancer, in particular cervical, anal, colon and HPV-
PT related cancer.
XX
XX Claim 1; SEQ ID NO 1; 169pp; English.
XX
XX The invention comprises a composition for the detection of cancer
CC markers, the composition contains a nucleic acid molecule which is
CC substantially identical to a full length genomic clone of a human
CC papilloma virus (type 11, 16, 18, 51, 56, 58, 66, 70, or 73). The
CC composition of the invention is useful for diagnosing cancer or the risk
CC of developing cancer, in particular cervical, anal, colon and HPV-related
CC cancer. The present DNA sequence represents a human papilloma virus full
CC length genomic clone of the invention.
XX
XX Sequence 7904 BP; 2601 A; 1377 C; 1509 G; 2417 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 28; DB 14; Length 7904;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GACATTATGTTATGTTGATGGAAC 28
DB 333 GACATTATGTTATGTTGATGGAAC 360

```

```

XX 08-JAN-2001; 2001US-00756095.
XX 08-JAN-2001; 2001US-00756096.
XX 08-JAN-2001; 2001US-00756097.
XX 20-APR-2001; 2001US-00838858.
XX 29-AUG-2001; 2001US-00941492.
XX
XX (INTR-) INTRON INC.
XX
XX Mitchell IG, Garcia-Bianco MA, Baker CC, Puttaraju M;
PI Mansfield GS, Chao H;
XX
XX WPI; 2002-566693/60.
XX
XX Novel cell having pre-trans-splicing molecules with target binding
PT domains that target binding of PTM to pre-mRNA, 3' or 5' splice region,
PT spacer region, nucleotide sequence to be trans-spliced to target-pre-
PT mRNA.
XX
XX Example; Fig 52; 229pp; English.
XX
XX The present invention describes a cell (I) comprising pre-trans-splicing
CC molecules (PTMs) (II) which have one or more target binding domains (IIs)
CC that target binding of PTM to pre-mRNA, 3' splice region (IId) that
CC includes branch point pyrimidine tract and 3' splice acceptor site, or 5'
CC splice site (IId), spacer region (IId) that separates RNA splice site
CC from target binding domain, and nucleotide sequence to (IId) be trans-
CC spliced to target-pre-mRNA. Optionally, the cell comprises (II) either
CC comprising: (A) (IId) and (IId) or (B) (IId) and (IId). The cell
CC may comprise a recombinant vector expressing (II). (I) has cytostatic,
CC immunosuppressive and antimicrobial activities, and can be used in gene
CC therapy. (II) comprising one or more (preferably two or more) (IId) and
CC (IId) (or (IId)), (IId) and (IId), or (II) comprising either (A) or (B)
CC (excluding (IId)), is useful for producing a chimeric RNA molecule in a
CC cell which involves contacting a target pre-mRNA expressed in the cell
CC with (II) that is recognised by nuclear splicing components. The chimeric
CC RNA produced comprises sequences encoding a toxin or translatable
CC protein. The nucleotide sequence to be trans-spliced to target pre-mRNA
CC preferably comprises nucleotide sequences comprising exons 1-10 of cystic
CC fibrosis trans-membrane conductance regulator (CFTR). The chimeric RNA
CC molecule produced using (II) which either comprises (A) or (B) further
CC comprises a nucleotide sequence tag. (I) can be used for gene regulation,
CC gene repair and targeted cell death. (I) can be used for the treatment of
CC various diseases including genetic, infectious or autoimmune diseases and
CC proliferative disorders such as cancer and to regulate gene expression in
CC plants. AB073414 to AB073536 represent sequences used in the
CC exemplification of the present invention
XX
XX Sequence 149 BP; 54 A; 32 C; 12 G; 51 T; 0 U; 0 Other;
SQ
Query Match 94.3%; Score 26.4; DB 6; Length 149;
Best Local Similarity 96.4%; Pred. No. 1.6;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 GACATTATGTTATGTTGATGGAAC 28
DB 88 GACATTATGTTATGTTGATGGAAC 61

```

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RESULT 44
AD037149
ID AD037149 standard; DNA; 459 BP.
XX
XX AD037149;
AC
XX 18-DEC-2003 (first entry)
DT
XX
XX 459bp HPV16 subgenomic fragment DNA sequence.
DE
XX
XX immortalised non-tumorigenic; human Schwann; schwannoma cell line;
KM screening cancer chemotherapeutic; antineoplastic activity;
KM carcinogenicity; neuroprotective; neurodegeneration; SV40;
KM Simian Virus 40; adenovirus; human papilloma virus; B6; E7; cytostatic;

```

KM gene therapy; cancer; HPV16; ds.
XX
OS Human papillomavirus type 16.
XX WO2003073996-A2.
XX
PD 12-SEP-2003.
XX
PF 03-MAR-2003; 2003WO-US006314.
XX
PR 01-MAR-2002; 2002US-0361528P.
XX
PA (HOU-S-) HOUSE EAR INST.
XX
PI Hung G, Li X;
XX
DR WPI; 2003-722006/68.
XX
PT Producing an immortalized non-tumorigenic human Schwann or schwannoma
PT cell line for treating cancer or neurodegenerative disorder comprises
PT selecting for immortalized cells that express the exogenous immortalizing
PT gene.
XX
PS Disclosure; SEQ ID NO 1; 29pp; English.
XX
XX The invention relates to a the production of an immortalised non-
CC tumorigenic human Schwann or schwannoma cell line comprising: providing
CC a cell culture of human Schwann or schwannoma cells, introducing a
CC polynucleotide comprising an exogenous immortalising gene into the cells,
CC and selecting for immortalised cells that express the exogenous
CC immortalising gene and retain phenotypic properties of Schwann or
CC schwannoma cells. The invention further comprises: determining the effect
CC of a pharmacological agent on human Schwann or schwannoma cells;
CC screening cancer chemotherapeutic and antineoplastic activity of an agent
CC ; testing carcinogenicity of an agent; screening the neuroprotective
CC activity of an agent; treating neurodegeneration in a patient; and a kit
CC for screening a pharmacological agent on schwannomas cells. In the method
CC of producing an immortalised non-tumorigenic human Schwann or schwannoma
CC cell line, the polynucleotide is a subgenomic fragment of a virus
CC consisting of SV40 (Simian Virus 40), adenovirus and human papilloma
CC virus, comprising the B6 and E7 genes of the human papilloma virus
CC consisting of types 18, 31, 33 or 35, but preferably 16. The immortalised
CC non-tumorigenic human Schwann or schwannoma cell line has cytostatic and
CC neuroprotective activity and be useful in treating disorders by gene
CC therapy. The method is useful for producing an immortalised non-
CC tumorigenic human Schwann or schwannoma cell line useful for screening
CC cancer chemotherapeutic and antineoplastic activity of an agent, testing
CC carcinogenicity of an agent and screening a neuroprotective activity of
CC an agent and for preparing a composition for diagnosing or treating
CC neurodegenerative disorders and cancer. This polynucleotide represents
CC the DNA of a 459bp HPV16 sequence, a subgenomic fragment used in the
CC production of the immortalised non-tumorigenic human Schwann or
CC schwannoma cell line of the invention.
XX
SQ Sequence 459 BP; 157 A; 71 C; 100 G; 131 T; 0 U; 0 Other;
OY
Query Match 94.3%; Score 26.4; DB 10; Length 459;
Best Local Similarity 96.4%; Pred. No. 1.6;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DB 1 GACATTAATGTTAGTTGTATGGAAC 28
231 GATATATGTTATGTTATGATGGAAC 258
RESULT 45
AAL54445
ID AAL54445 standard; DNA; 477 BP.
XX
XX AAL54445;
XX
XX 03-APR-2003 (first entry)
XX

DE HPV16 E6 siRNA derived DNA sequence.
XX
XX
KM Virucide; cyrostatic; anti-HIV; dermatological; small interfering RNA;
KM selective post-translational silencing; siRNA; oncogene; genital wart;
KM human papilloma virus; HPV gene; cancer; human cervical cancer; HIV;
KM smallpox; flu; common cold; cervical cancer; penile cancer;
KM malignant squamous cell carcinoma; verruca vulgaris; gene therapy; ds.
XX
XX Human papilloma virus.
XX
XX WO2003008573-A2.
XX
XX 30-JAN-2003.
XX
XX 17-JUL-2002; 2002WO-GB003300.
XX
XX 17-JUL-2001; 2001GB-00017358.
XX
XX 14-JAN-2002; 2002GB-00000688.
XX
XX 17-JUN-2002; 2002GB-00013855.
XX
XX (MILN/) MILNER A J.
XX
XX Milner AJ;
XX
XX WPI; 2003-221850/21.
XX
XX
XX Selective post-transcriptional silencing of an exogenous viral gene (e.g.
XX human papilloma virus (HPV) E6), for treating e.g. cancer, comprises
XX PT using a small interfering RNA (siRNA) construct homologous to an mRNA of
XX the gene.
XX
XX Claim 11; Fig 11; 44pp; English.
XX
XX The invention relates to a novel method for selective post-translational
CC silencing in a mammalian cell of the expression of an exogenous gene of
CC viral origin. The method comprises introducing into the cell a small
CC interfering RNA (siRNA) construct that is homologous to a part of the
CC mRNA sequence of the gene. The method is useful for the selective post-
CC transcriptional silencing of an exogenous gene of viral origin (e.g. an
CC oncogene or human papilloma virus (HPV) gene) in a mammalian cell. The
CC method or the siRNA is particularly useful for treating cancer, human
CC cervical cancer, human immunodeficiency virus (HIV), smallpox, flu,
CC common cold, or a disease caused by a HPV (e.g. genital warts, cervical
CC cancer, penile cancer, malignant squamous cell carcinomas or verruca
CC vulgaris). An siRNA construct or vector is useful for use as a medicament
CC for the diseases mentioned. The polynucleotide sequence of the invention
CC can be used to treat disorders by gene therapy. This polynucleotide
CC sequence represents the DNA of a HPV siRNA sequence of the invention
XX
SQ Sequence 477 BP; 167 A; 75 C; 104 G; 131 T; 0 U; 0 Other;
OY
Query Match 94.3%; Score 26.4; DB 10; Length 477;
Best Local Similarity 96.4%; Pred. No. 1.6;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DB 1 GACATTAATGTTAGTTGTATGGAAC 28
251 GACATTAATGTTAGTTGTATGGAAC 278
RESULT 46
AEA51113
ID AEA51113 standard; DNA; 477 BP.
XX
XX AEA51113;
XX
XX 11-AUG-2005 (first entry)
XX
XX Human papillomavirus type 16 E6/E7 gene fragment, SEQ ID NO: 17.
XX
XX Delivery mechanism; gene therapy; cyrostatic; vulnery; virucide;
XX KM injury; infection; cancer; gastrointestinal disease;
XX KM gynecology and obstetrics; tumor; colorectal tumor;
XX

KM uterine cervix tumor; squamous cell carcinoma; neoplasm; E7 gene; ds;
XX B6 gene.
XX Human papillomavirus.
OS WO2005051431-A1.
XX
XX 09-JUN-2005.
PD
XX 25-NOV-2004; 2004WO-GB004979.
PF
XX 25-NOV-2003; 2003GB-00027409.
PR
XX 05-MAR-2004; 2004US-0549919P.
XX
XX (MILN/) MILNER A J.
PA
XX Milner AJ;
PI
XX WPI; 2005-405310/41.
XX
XX Composition useful for delivering an agent into a cell comprises the
PT agent, a transfer agent and a solid or colloidal carrier medium.
XX
XX Disclosure; SEQ ID NO 17; 56pp; English.
XX
XX The present invention relates to a method and composition comprising a
CC transfer agent and a solid or colloidal carrier medium for delivering a
CC biological agents into cells. The invention is useful for the treating
CC of cancer, tumor, carcinoma of cutaneous, squamous or cervical epithelia
CC and colorectal carcinoma, wounds, burns and scars. The invention is also
CC useful in gene therapy. The present sequence is the human papillomavirus
CC type 16 B6/E7 gene fragment. This sequence is useful in a method for
CC treating carcinomas.
XX
XX Sequence 477 BP; 167 A; 75 C; 104 G; 131 T; 0 U; 0 Other;
SQ
Query Match 94.3%; Score 26.4; DB 14; Length 477;
Best Local Similarity 96.4%; Pred. No. 1.6;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GACATTATGTTATAGTTGTATGGAAC 28
DB 251 GACATTATGTTATAGTTGTATGGAAC 278
RESULT 47
ADP31984
ID ADP31984 standard; DNA; 543 BP.
XX
XX ADP31984;
AC
XX
XX 12-FEB-2004 (first entry)
DT
XX
XX Human papillomavirus fusion gene encoding sequence.
DE
XX
XX human papillomavirus; cervix cancer; ds.
KM
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 1..543
FT CDS /*tag= a
FT
XX
XX CN1381583-A.
PN
XX
XX 27-NOV-2002.
PD
XX
XX 24-APR-2002; 2002CN-00117143.
PF
XX
XX 24-APR-2002; 2002CN-00117143.
PR
XX
XX (ONCO-) INST ONCOLOGY TUMOR HOSPITAL CHINESE ACA.
PA
XX

PI Zhao Q;
XX
XX WPI; 2003-258260/26.
DR
XX P-PSDB; ADP31985.
DR
XX
XX Human papillomavirus B6/E7 fusion gene and its efficient expression
PT carrier and fusion protein vaccine.
XX
XX
XX Claim 3; SEQ ID NO 1; 16pp; Chinese.
PS
XX
XX The present invention relates to human papillomavirus B6/E7 fusion gene,
CC its preparing process, the process for configuring the efficient
CC expression carrier containing the gene and resultant expression carrier,
CC the fusion protein prepared from the gene, and the application of the
CC fusion gene and expression protein to medical science and medicine to
CC treat cervix cancer are disclosed. The present sequence represents the
CC human papillomavirus fusion gene encoding sequence.
XX
XX
XX Sequence 543 BP; 185 A; 89 C; 118 G; 151 T; 0 U; 0 Other;
SQ
Query Match 94.3%; Score 26.4; DB 10; Length 543;
Best Local Similarity 96.4%; Pred. No. 1.7;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GACATTATGTTATAGTTGTATGGAAC 28
DB 251 GACATTATGTTATAGTTGTATGGAAC 278
RESULT 48
ADP44067
ID ADP44067 standard; DNA; 747 BP.
XX
XX ADP44067;
AC
XX
XX 15-JUL-2004 (first entry)
DT
XX
XX Nucleotide sequence of an E7B6 fusion protein.
DE
XX
XX E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer;
KM cervical cancer; immune response; lower gastrointestinal tract cancer;
KM anal cancer; reproductive system cancer; penile cancer; vulvar cancer;
KM gene; ss.
XX
XX Human papillomavirus type 16.
OS
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH 1..747
FT CDS /*tag= a
FT /product= "E7B6 fusion protein"
FT
XX
XX WO2004030636-A2.
PN
XX
XX 15-APR-2004.
PD
XX
XX 02-OCT-2003; 2003WO-US031726.
PF
XX
XX 03-OCT-2002; 2002US-0415929P.
PR
XX
XX (AMHP) WYETH HOLDINGS CORP.
PA
XX
XX Smith L, Casasetti MC;
PI
XX
XX WPI; 2004-316328/29.
DR
XX P-PSDB; ADP44066.
DR
XX
XX New polypeptide comprising human papillomavirus B6 and E7 polypeptides,
PT useful for treating or preventing human papillomavirus (HPV)-associated
XX cancers, e.g. cervical cancer.
XX
XX Example 1; Page 73; 101pp; English.
PS

CC The present sequence encodes an E7E6 fusion protein, comprising wild type
CC E7 and E6 polypeptides from human papillomavirus type 16 (HPV16). The
CC specification describes human papillomavirus E6 and E7 polypeptides,
CC where the E7 polypeptide has mutations at any one or more of the amino
CC acids corresponding to amino acids 24, 26 or 91 of the sequence given in
CC ADO44073 and the E6 polypeptide has no mutations or has mutations at any
CC one or more of the amino acids corresponding to amino acids 63 or 106 of
CC the sequence given in ADO44072. The polypeptides of the invention are
CC useful for treating or preventing human papillomavirus (HPV)-associated
CC cancers, such as cervical cancer. The fusion proteins and nucleic acids
CC encoding the fusion proteins are useful for generating immune responses
CC against HPV. They are also useful for treating lower gastrointestinal
CC tract cancer, e.g. anal cancer, and other cancers of the reproductive
CC system, including penile and vulvar cancer.

CC XX
SQ Sequence 747 BP; 247 A; 132 C; 166 G; 202 T; 0 U; 0 Other;

Query Match 94.3%; Score 26.4; DB 12; Length 747;
Best Local Similarity 96.4%; Pred. No. 1.7;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GACATTATTGTTATAGTTGTATGGAAC 28
Db 521 GACATTATTGTTATAGTGTATGGAAC 548

RESULT 49
ADO44065
ID ADO44065 standard; DNA; 747 BP.
XX
AC ADO44065;
XX
DT 15-JUL-2004 (first entry)
XX
DE Nucleotide sequence of a fusion protein designated E6E7Pentm.
XX
XX E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer;
KM cervical cancer; immune response; lower gastrointestinal tract cancer;
KM anal cancer; reproductive system cancer; penile cancer; vulvar cancer;
KM gene; ss.
XX
XX Human papillomavirus type 16.
OS Synthetic.
OS
XX
FH Key Location/Qualifiers
FT 1..747
FT CDS /*tag= a
FT /product= "E6E7Pentm fusion protein"
XX
XX MO2004030636-A2.
XX
XX 15-APR-2004.
XX
XX 02-OCT-2003; 2003WO-US031726.
XX
XX 03-OCT-2002; 2002US-0415929P.
XX
XX (AMHP) WYETH HOLDINGS CORP.
XX
XX Smith L, Caesetti MC;
XX
XX WPI; 2004-316328/29.
XX
XX P-PSDB; ADO44064.
XX
XX New polypeptide comprising human papillomavirus E6 and E7 polypeptides,
XX useful for treating or preventing human papillomavirus (HPV)-associated
XX cancers, e.g. cervical cancer.
XX
XX
XX Claim 24; Page 71; 101pp; English.
XX
XX The present sequence encodes a fusion protein, comprising E6 and E7
XX polypeptides from human papillomavirus type 16 (HPV16). The fusion
XX protein is designated E6E7Pentm, and comprises an E6 amino terminus

CC (where residues 63 and 106 have been replaced with glycine) and an E7
CC carboxy terminus (where residues 24, 26 and 91 have been replaced with
CC glycine). E6E7Pentm is representative of fusion proteins of the
CC invention. The specification describes human papillomavirus E6 and E7
CC polypeptides, where the E7 polypeptide has mutations at any one or more
CC of the amino acids corresponding to amino acids 24, 26 or 91 of the
CC sequence given in ADO44073 and the E6 polypeptide has no mutations or has
CC mutations at any one or more of the amino acids corresponding to amino
CC acids 63 or 106 of the sequence given in ADO44072. The polypeptides of
CC the invention are useful for treating or preventing human papillomavirus
CC (HPV)-associated cancers, such as cervical cancer. The fusion proteins
CC and nucleic acids encoding the fusion proteins are useful for generating
CC immune responses against HPV. They are also useful for treating lower
CC gastrointestinal tract cancers, e.g. anal cancer, and other cancers of
CC the reproductive system, including penile and vulvar cancer.

CC XX
SQ Sequence 747 BP; 246 A; 132 C; 171 G; 198 T; 0 U; 0 Other;

Query Match 94.3%; Score 26.4; DB 12; Length 747;
Best Local Similarity 96.4%; Pred. No. 1.7;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GACATTATTGTTATAGTTGTATGGAAC 28
Db 230 GACATTATTGTTATAGTGTATGGAAC 257

RESULT 50
ADO44061
ID ADO44061 standard; DNA; 747 BP.
XX
XX
AC ADO44061;
XX
DT 15-JUL-2004 (first entry)
XX
DE Nucleotide sequence of an E6E7 fusion protein.
XX
XX E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer;
KM cervical cancer; immune response; lower gastrointestinal tract cancer;
KM anal cancer; reproductive system cancer; penile cancer; vulvar cancer;
KM gene; ss.
XX
XX Human papillomavirus type 16.
OS Synthetic.
OS
XX
FH Key Location/Qualifiers
FT 1..747
FT CDS /*tag= a
FT /product= "E6E7 fusion protein"
XX
XX MO2004030636-A2.
XX
XX 15-APR-2004.
XX
XX 02-OCT-2003; 2003WO-US031726.
XX
XX 03-OCT-2002; 2002US-0415929P.
XX
XX (AMHP) WYETH HOLDINGS CORP.
XX
XX Smith L, Caesetti MC;
XX
XX WPI; 2004-316328/29.
XX
XX P-PSDB; ADO44060.
XX
XX New polypeptide comprising human papillomavirus E6 and E7 polypeptides,
XX useful for treating or preventing human papillomavirus (HPV)-associated
XX cancers, e.g. cervical cancer.
XX
XX
XX Example 1; Page 68; 101pp; English.
XX
XX The present sequence encodes an E6E7 fusion protein, comprising wild type
XX E6 and E7 polypeptides from human papillomavirus type 16 (HPV16). The

CC specification describes human papillomavirus E6 and E7 polypeptides,
CC where the E7 polypeptide has mutations at any one or more of the amino
CC acids corresponding to amino acids 24, 26 or 91 of the sequence given in
CC ADO44073 and the E6 polypeptide has no mutations or has mutations at any
CC one or more of the amino acids corresponding to amino acids 63 or 106 of
CC the sequence given in ADO44072. The polypeptides of the invention are
CC useful for treating or preventing human papillomavirus (HPV)-associated
CC cancers, such as cervical cancer. The fusion proteins and nucleic acids
CC encoding the fusion proteins are useful for generating immune responses
CC against HPV. They are also useful for treating lower gastrointestinal
CC tract cancers, e.g. anal cancer, and other cancers of the reproductive
CC system, including penile and vulvar cancer.

XX
SQ Sequence 747 BP; 247 A; 132 C; 166 G; 202 T; 0 U; 0 Other;

Query Match 94.3%; Score 26.4; DB 12; Length 747;

Best Local Similarity 96.4%; Pred. No. 1.7;

Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GACATTATGTTAGTTGATGGAAC 28
|||
Db 230 GACATTATGTTAGTTGATGGAAC 257

Search completed: May 24, 2006, 05:55:53
Job time : 334.037 secs

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OM nucleic - nucleic search, using sw model

Run on: May 24, 2006, 05:47:01 ; Search time 1932.77 Seconds
(without alignments)
810.102 Million cell updates/sec

Title: US-10-601-913-1

Perfect score: 28

Sequence: 1 GACATTATGTTATGATTGATGAGAC 28

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

EST: *
1: gb_esc1: *
2: gb_esc3: *
3: gb_esc4: *
4: gb_esc5: *
5: gb_esc6: *
6: gb_esc7: *
7: gb_esc8: *
8: gb_esc9: *
9: gb_esc10: *
10: gb_esc11: *
11: gb_esc12: *
12: gb_esc13: *
13: gb_esc14: *
14: gb_esc15: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26.4	94.3	244	3	BO106475
2	22.2	79.3	486	3	BO106475
3	21.6	77.1	499	11	AQ778171
4	21.2	75.7	658	13	CM302859
5	20.6	73.6	261	2	BM183005
6	20.6	73.6	324	2	BM531805
7	20.6	73.6	499	2	DN847201
8	20.6	73.6	692	14	DX977778
9	20.6	73.6	836	10	DT598349
10	20.6	73.6	848	9	CK897969
11	20.6	73.6	906	14	CR065011
12	20.6	73.6	1356	9	DN698710
13	20.4	72.9	677	14	AG11813
14	20.4	72.9	713	3	BM053630
15	20.4	72.9	724	3	BM206337
16	20.2	72.1	305	2	BF820181
17	20.2	72.1	351	9	DR165329
18	20.2	72.1	487	3	BO851812
19	20.2	72.1	543	14	DE110524

C 20	20.2	72.1	583	13	CL387597	CL387597
21	20.2	72.1	621	5	CD820121	CD820121
22	20.2	72.1	645	3	BO854577	BO854577
23	20.2	72.1	693	3	BO864783	BO864783
24	20.2	72.1	706	3	BO853474	BO853474
25	20.2	72.1	728	3	BU007386	BU007386
26	20.2	72.1	758	13	CM371871	CM371871
27	20.2	72.1	760	14	AG529207	AG529207
28	20.2	72.1	528	2	BO021561	BO021561
29	20.2	72.1	534	11	AQ829979	AQ829979
30	20.2	72.1	627	3	BM610169	BM610169
31	20.2	72.1	664	13	CZ821000	CZ821000
32	20.2	72.1	665	1	AL849178	AL849178
33	20.2	72.1	700	9	CK689149	CK689149
34	20.2	72.1	749	9	CK908094	CK908094
35	20.2	72.1	754	13	CZ754866	CZ754866
36	20.2	72.1	763	10	DV932465	DV932465
37	20.2	72.1	832	9	CK896534	CK896534
38	20.2	72.1	954	12	CG920252	CG920252
39	19.8	70.7	511	5	CF091813	CF091813
40	19.8	70.7	536	11	BZ392066	BZ392066
41	19.8	70.7	592	3	BU026745	BU026745
42	19.8	70.7	770	14	DX044921	DX044921
43	19.8	70.7	998	14	CNS07884	CNS07884
44	19.8	70.7	1268	14	AJ854876	AJ854876
45	19.6	70.0	170	5	CK928648	CK928648
46	19.6	70.0	232	2	BI034170	BI034170
47	19.6	70.0	297	10	DV017521	DV017521
48	19.6	70.0	299	5	CK553998	CK553998
49	19.6	70.0	305	2	BU724011	BU724011
50	19.6	70.0	340	3	BM857946	BM857946
51	19.6	70.0	351	10	R33750	R33750
52	19.6	70.0	371	11	AQ005319	AQ005319
53	19.6	70.0	400	14	CRU581204	CRU581204
54	19.6	70.0	405	11	B87841	B87841
55	19.6	70.0	423	11	BF221789	BF221789
56	19.6	70.0	430	7	BF589601	BF589601
57	19.6	70.0	430	7	BF589601	BF589601
58	19.6	70.0	436	12	CC090476	CC090476
59	19.6	70.0	436	11	BH273026	BH273026
60	19.6	70.0	461	13	CM229788	CM229788
61	19.6	70.0	467	14	DU507309	DU507309
62	19.6	70.0	486	5	CK766755	CK766755
63	19.6	70.0	493	13	CL579906	CL579906
64	19.6	70.0	494	13	CZ200459	CZ200459
65	19.6	70.0	519	9	DN303077	DN303077
66	19.6	70.0	524	9	DN290519	DN290519
67	19.6	70.0	552	13	CM881078	CM881078
68	19.6	70.0	558	9	DN293471	DN293471
69	19.6	70.0	571	4	BX564527	BX564527
70	19.6	70.0	573	10	DM126700	DM126700
71	19.6	70.0	579	2	BM029341	BM029341
72	19.6	70.0	580	10	DM552406	DM552406
73	19.6	70.0	601	13	CL583816	CL583816
74	19.6	70.0	608	10	DM082746	DM082746
75	19.6	70.0	613	5	CK763100	CK763100
76	19.6	70.0	615	5	CD304116	CD304116
77	19.6	70.0	615	10	DM141118	DM141118
78	19.6	70.0	617	10	DM141173	DM141173
79	19.6	70.0	618	5	CK551409	CK551409
80	19.6	70.0	622	3	BO995329	BO995329
81	19.6	70.0	623	9	DN290108	DN290108
82	19.6	70.0	624	3	BM319463	BM319463
83	19.6	70.0	633	12	CE817250	CE817250
84	19.6	70.0	634	3	BU006053	BU006053
85	19.6	70.0	635	13	CM151007	CM151007
86	19.6	70.0	636	1	AL883560	AL883560
87	19.6	70.0	637	1	AL893646	AL893646
88	19.6	70.0	639	3	BM372638	BM372638
89	19.6	70.0	645	3	BO991858	BO991858
90	19.6	70.0	653	10	DM081330	DM081330
91	19.6	70.0	654	3	BO985822	BO985822
92	19.6	70.0	655	10	DM143566	DM143566

969	19	67.9	289	2	BM159112	BM159112	fw27c12.y
970	19	67.9	289	2	BM181586	BM181586	fw43h04.y
971	19	67.9	289	2	BM532234	BM532234	fy06g11.y
972	19	67.9	289	3	BM811666	BM811666	fw09a08.y
973	19	67.9	289	3	BM811785	BM811785	fx10d12.y
974	19	67.9	289	3	BM077247	BM077247	fx16d12.y
975	19	67.9	289	3	B0077437	B0077437	fx16e06.y
976	19	67.9	289	3	BM617859	BM617859	faa81c11.y
977	19	67.9	290	2	B1840218	B1840218	fw71a09.y
978	19	67.9	290	2	BM266109	BM266109	fw39e12.y
979	19	67.9	290	2	BM530701	BM530701	fw67a01.y
980	19	67.9	290	3	B0075369	B0075369	fw04a08.y
981	19	67.9	290	3	B0077226	B0077226	fw14e07.y
982	19	67.9	290	3	B0077436	B0077436	fw17c02.y
983	19	67.9	290	3	B0077555	B0077555	fw17h05.y
984	19	67.9	290	3	B0077638	B0077638	fw21h06.y
985	19	67.9	290	3	B0078146	B0078146	fw85a11.y
986	19	67.9	290	3	B0078202	B0078202	fw85f12.y
987	19	67.9	290	3	B0480236	B0480236	faa87f04.y
988	19	67.9	290	3	B0480563	B0480563	faa91c04.y
989	19	67.9	290	3	B0618072	B0618072	faa83f08.y
990	19	67.9	290	3	B0618830	B0618830	faa08d03.y
991	19	67.9	291	2	BM157312	BM157312	fw41h06.y
992	19	67.9	291	2	BM159129	BM159129	fw27h10.y
993	19	67.9	291	2	BM315189	BM315189	fw23a06.y
994	19	67.9	291	3	B0076227	B0076227	fw22a11.y
995	19	67.9	291	3	B0076523	B0076523	fw22d04.y
996	19	67.9	291	3	B0076530	B0076530	fw88g07.y
997	19	67.9	291	3	B0076554	B0076554	fw89a05.y
998	19	67.9	291	3	B0076560	B0076560	fw89c02.y
999	19	67.9	291	3	B0076884	B0076884	fw02d10.y
1000	19	67.9	291	3	B0076889	B0076889	fw02c03.y

ALIGNMENTS

RESULT 1
 BQ106475
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

BQ106475 244 bp mRNA linear EST 16-APR-2002
 fc2102.e Rose Petals (Fragrant Cloud) Lambda Zap Express Library
 Rosa hybrid cultivar cDNA clone fc2102.e 5', mRNA sequence.
 BQ106475
 BQ106475.1 GI:20156137
 EST.
 Rosa hybrid cultivar
 Rosa hybrid cultivar
 Euryotia, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons, core eudicotyledons;
 rosoids; eurosids 1; Rosales; Rosaceae; Rosoideae; Rosa.
 1 (bases 1 to 244)
 Guernan,I., Shallit,M., Menda,N., Plestun,D., Dafny-Yelin,M.,
 Shalev,G., Bar,E., Davydov,O., Ovadis,M., Emanuel,M., Wang,J.,
 Adom,Z., Pichersky,E., Lewinsohn,E., Zamir,D., Vainstein,A. and
 Weiss,D.
 Rose Scent: Genomics Approach to Discovering Novel Floral
 Fragrance-Related Genes
 Plant Cell 14 (10), 2325-2338 (2002)
 Contact: Naama Menda
 Petal Genomics
 Faculty of Agricultural, Food and Environmental Quality Sciences,
 The Hebrew University of Jerusalem
 P.O. Box 12, Rehovot, 76100, Israel
 Tel: 972 8 9489 683
 Fax: 972 8 9468 265
 Email: shaham@agri.huji.ac.il
 Seq primer: 73 forward.
 Location/Qualifiers
 1..244

```
/organism="Rosa hybrid cultivar"  
/mol_type="mRNA"  
/strain="Fragrant Cloud"  
/db_xref="taxon:128735"
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Query Match	94.3%	Score 26.4	DB 3	Length 244
Best Local Similarity	96.4%	Pred. No. 15		
Matches 27	Conservative 0	Mismatches 1	Indels 0	Gaps 0

```

QY      1 GACATTATTGTTAAGTTGTATGGAAC 28
         |||||
Db      14 GACTTATTGTTAAGTTGTATGGAAC 41

```

RESULT 2				
LOCUS	DN832021/c			
DEFINITION	DN832021	486 bp	mRNA	linear
	PO6 Opiechorchis viverrini lambda Triplex2 Library Opiechorchis viverrini cDNA 5', mRNA sequence.			EST 18-APR-2005

VERSION	DN832021.1	GI:62727557
KEYWORDS	EST.	
SOURCE	Opisthorchis viverrini	
ORGANISM	Opisthorchis viverrini	

REFERENCE 1 (bases 1 to 486)

TITLE	Expressed sequence tags (ESTs) from cDNA libraries of adult stages
JOURNAL	<i>Ophiosthorchis viverrini</i>
COMMENT	Unpublished (2005) Contact: Brindley, PJ

Department of Tropical Medicine
Tulane University, Health Sciences Center
1430 Tulane Avenue, New Orleans, LA 70112, USA
Tel.: 1 504 988 4645
Fax: 1 504 988 6586
Email: paul.brindley@tulane.edu
Insert Length: 486 Std Error: 0.00
Seq primer: 5' triplex sequencing primer, CTCGAGATCTGCACAGC
POLYA=Yes.

```

FEATURES
source
location/Qualifiers
1..486
/organism="Opisthorchis viverrini"
/mol_type="mRNA"
/strain="Khon Kaen Province, Thailand isolate"
/db_xref="taxon:6198"
/sex="hermaphrodite"
/tissue_type="whole body"
/dev_stage="adult"
/clone_id="Opisthorchis viverrini lambda Triplex2
library"

```

Query Match	79.3%	Score 22.2	DB 9	Length 486
Best Local Similarity	88.9%	Pred. No. 5.8e+02		
Matches 24; Conservative	0	Mismatches 3	Indels 0	Gaps 0

```

QY      2 ACATTATTGTTATAGTTTGATGGAAC 28
        |||||
DB      72 ACATTATGTTATAGTTTGATGGAAC 46

```

RESULT 3	LOCUS	DEFINITION
A0778171	499 bp DNA	linear GSS 02-AUG-1991
HS_3206_A1_B05_MR_C1T	Approved Human Genomic Sperm Library D Homo	
sapiens genomic clone	Plate=3206 Col=9 Row=c,	genomic survey

sequence.
 accession AQ78171 GI:5681131
 version AQ78171.1
 keywords Homo sapiens (human)
 source Homo sapiens
 organism Homo sapiens
 reference 1 (bases 1 to 499)
 authors Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
 title Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
 journal Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 comment 10449764
 contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 clones may be purchased from Research Genetics (info@resgen.com).
 BAC end Web Server: http://www.htsc.washington.edu
 plate: 3206 row: C column: 9
 seq primer: M13 Reverse
 class: BAC ends
 high quality sequence stop: 499.
 location/Qualifiers
 1..499
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="plate=3206 Col=9 Row=C"
 /sex="male"
 /clone_11b="CIT Approved Human Genomic Sperm Library D"
 /note="Organ: Sperm; Vector: pBelobAC11; BAC clones in E-coli DH10B"
 ORIGIN
 Query Match 77.1%; Score 21.6; DB 11; Length 499;
 Best Local Similarity 85.7%; Pred. No. 9.7e+02;
 Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 GACATTATGTTATGATTGTATGAGAAC 28
 Db 266 GAAACTACTCTTATAGTTGTATGAGAAC 293
 RESULT 4
 CWM302859 658 bp DNA linear GSS 31-OCT-2004
 LOCUS 104.787.11464939.116.35676.078 Sorghum methylation filtered library
 DEFINITION (LifID: 104) Sorghum bicolor genomic clone 11464939, genomic survey
 accession CWM302859
 version CWM302859.1
 keywords GSS.
 source Sorghum bicolor (sorghum)
 organism Sorghum bicolor
 reference 1 (bases 1 to 658)
 authors Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D., Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K., McNamey,J., Smith,M., Hoteman,H., Roe,B.A., Wiley,G., Korfi,I.F., Rabinowitz,P.D., Lakey,N., McComble,W.R., Jeddeloh,D.A. and Martensen,R.A.
 title Sorghum genome sequencing by methylation filtration
 journal Plos Biol. 3 (1), e13 (2005)

PUBMED 15660154
 comment Contact: Bedell JA
 Orion Genomics, LLC
 4041 Forest Park Ave, St. Louis, MO 63108, USA
 Tel: 314 615 6979
 Fax: 314 615 5975
 Email: jbedell@oriongenomics.com
 plate: 787 row: d column: 19
 seq primer: T3 Reverse
 class: methylation filtered
 high quality sequence stop: 658.
 location/Qualifiers
 1..658
 /organism="Sorghum bicolor"
 /mol_type="genomic DNA"
 /cultivar="Atx623"
 /db_xref="taxon:4558"
 /clone="11464939"
 /clone_11b="Sorghum methylation filtered library (LifID: 104)"
 /note="Organ: leaf; Vector: pBCSK(-); Site: 1; HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a methylation filtered library."
 ORIGIN
 Query Match 75.7%; Score 21.2; DB 13; Length 658;
 Best Local Similarity 88.5%; Pred. No. 1.4e+03;
 Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 ACATTATGTTATGATTGTATGAGAA 27
 Db 559 AAATTATTTTATGATTGTCTGAGAA 584
 RESULT 5
 BWM183005 261 bp mRNA linear EST 11-DEC-2001
 LOCUS IMAGR:5566067 5', mRNA sequence.
 DEFINITION BWM183005
 accession BWM183005
 version BWM183005.1
 keywords EST.
 source Danto rerio (zebrafish)
 organism Danto rerio (zebrafish)
 reference 1 (bases 1 to 261)
 authors Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Pearson,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurr,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
 title Washu Zebrafish EST Project 1998
 comment Unpublished (1998)
 title JOURNAL
 journal Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: zbratfish@wustl.edu
 cDNA library construction by: Joe Barnes and Steve Johnson. DNA sequencing by: Washington University Genome Sequencing Center Clone distribution: Research Genetics web address: http://www.researchgenetics.com/
 putative full length read
 The vector to vector length is 262
 zebrafish identity (p-value greater than 1e-99) found to: g[13461292]gb[AI105787]AI105787 db03d09 pl zf adult heart library

Danio rerio
Seq primer: T3 ET from Amerham.
Location/Qualifiers

1.261
/organism="Danio rerio"
/mol_type="mRNA"
/strain="C32"
/db_xref="taxon:7955"
/clone="IMAGE:556067"
/tissue_type="embryo, 14 somite"
/lab_host="DH10B"
/clone_1lb="zebrafish C32 14 somite embryo"
/note="Vector: pAMP1; Site 1: EcoRI; Site 2: NotI; First strand cDNA synthesis was primed using oligo-dt on magnetic beads with an additional primer
5'-ggcgccgataatagcactcacta-agg-3'. Second strand synthesis was a 3-cycle PCR using the primers
5'-ggcgccgataatagcactcacta-agg-3'
5'-aagcagtggtacacagcagagctt-ctttttttttt-3'. cDNA was subsequently amplified in a 7-cycle PCR with the following primers: 5'-ggcgccgataatagcactcacta-agg-3', 5'-aagcagtggt-aaacacgagc. Deoxy-UMP adaptors were added in a third PCR (5 cycles) and the primers
5'-caucaucaucaagcgccgataatagcactcacta-agg-3' and
5'-caucaucaucaagcgagtggtacacagcagagctac-3'. Ends were treated with uracil DNA glycosylase and product with 3' overhangs was annealed to complementary ends of pAMP1. Insert can be excised using EcoRI and NotI. Library constructed by Joe Barnes and Steve Johnson (Washington University)."

ORIGIN

Query Match 73.6%; Score 20.6; DB 2; Length 261;
Best Local Similarity 85.2%; Pred. No. 2.3e+03;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GACATTATTGTATAGTTGTATGAA 27
7 GACCTATTGTATAGTTATGTA 33

RESULT 6
BMS31805 324 bp mRNA linear EST 19-FEB-2002
LOCUS f91d07.y1 zebrafish sjd 2 day embryo Danio rerio cDNA clone
DEFINITION IMAGE:560652 5', mRNA sequence.
ACCESSION BMS31805
VERSION BMS31805.1 GI:18740694
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 324)
Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Bddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Stepcoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk, R., Rutter, B., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
Washu Zebrafish EST Project 1998
Unpublished (1998)
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrfish@wustl.edu
cDNA library construction by: Joe Barnes and Steve Johnson. DNA sequencing by: Washington University Genome Sequencing Center Clone distribution: ResourcenzentrumPrimarDatenbank, Berlin, Germany (web address: www.rzpd.de)

zebrafish identity (p-value greater than 1e-99) found to:
gt|3461292|gb|AI105787|AI105787 db03d09_pi zf adult heart library
Danio rerio
Seq primer: T3 ET from Amerham
High quality sequence stop: 324.
Location/Qualifiers

1.324
/organism="Danio rerio"
/mol_type="mRNA"
/strain="SJD"
/db_xref="taxon:7955"
/clone="IMAGE:5630652"
/tissue_type="whole embryo, 2 day"
/lab_host="DH10B"
/clone_1lb="zebrafish SJD 2 day embryo"
/note="Vector: pAMP1; Site 1: EcoRI; Site 2: NotI; First strand cDNA synthesis was primed using oligo-dt on magnetic beads with an additional primer
5'-ggcgccgataatagcactcacta-agg-3'. Second strand synthesis was a 3-cycle PCR using the primers
5'-ggcgccgataatagcactcacta-agg-3' and
5'-aagcagtggtacacagcagagctt-ctttttttttt-3'. cDNA was subsequently amplified in a 7-cycle PCR with the following primers: 5'-ggcgccgataatagcactcacta-agg-3' and 5'-aagcagtggt-aaacacgagc. Deoxy-UMP adaptors were added in a third PCR (5 cycles) and the primers
5'-caucaucaucaagcgccgataatagcactcacta-agg-3' and
5'-caucaucaucaagcgagtggtacacagcagagctac-3'. Ends were treated with uracil DNA glycosylase and product with 3' overhangs was annealed to complementary ends of pAMP1. Insert can be excised using EcoRI and NotI. Library constructed by Joe Barnes and Steve Johnson (Washington University)."

ORIGIN

Query Match 73.6%; Score 20.6; DB 2; Length 324;
Best Local Similarity 85.2%; Pred. No. 2.3e+03;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GACATTATTGTATAGTTGTATGAA 27
7 GACCTATTGTATAGTTATGTA 33

RESULT 7
DN847201/c 499 bp mRNA linear EST 20-APR-2005
LOCUS KECB31-081.g-T7 NHA bovine early embryo cDNA library KECB Bos
DEFINITION taurus cDNA 3', mRNA sequence.
ACCESSION DN847201
VERSION DN847201.1 GI:62806361
KEYWORDS EST.
SOURCE Bos taurus (cattle)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 499)
Olaseker, I. and Laerdahl, J.K.
Production of ESTs from a cDNA library of flushed bovine preimplantation embryos
Unpublished (2005)
Contact: Olaseker, I.
Dept. of Basic Sciences and Aquatic Medicine
Norwegian School of Veterinary Science
P.O. Box 8146 Dep, NO-0033 Oslo, Norway
Tel: +47 22964779
Fax: +47 22964758
Email: ingrid.olaseker@vet.hi.no
Single pass sequencing. Bases called and trimmed with Phred. Vector pCMV-PCR identified with cross_match. EST name is Clone.g-T7
Seq primer: T7.
Location/Qualifiers

FEATURES

```

source
1. .499
/organism="Bos taurus"
/mol_type="mRNA"
/strain="NRF Norwegian Red"
/db_xref="taxon:9913"
/tissue_type="20 flushed preimplantation embryos"
/dev_stage="compact morula - expanded blastocyst"
/clone_lib="NVH bovine early embryo cDNA library KECB"
/note="Vector: pCMV-PCR; The library was constructed using the Stratagene PCR cDNA Library Construction Kit (Stratagene Cloning Systems, USA) according to the suppliers protocol. This includes PCR amplification of cDNA with adapter-based primers followed by ligation-independent directional cloning into the vector based on the same adapters (Lfc-R and Lfc-L)."

ORIGIN
Query Match 73.6%; Score 20.6; DB 9; Length 499;
Best Local Similarity 85.2%; Pred. No. 2.3e+03;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 2 ACATTATGTTATGATTGTATGGAAC 28
|||||
348 ACAAAAGTTATATATTGTATGGAAC 322

RESULT 8 692 bp DNA linear GSS 05-JUL-2004
LOCUS BX977778
DEFINITION Reverse strand read from insert in 5'HPT insertion targeting and chromosome engineering clone MHPN317a23, genomic survey sequence.
ACCESSION BX977778
KEYWORDS BX977778.1 GI:49709201
VERSION GSI; genome survey sequence; MICER.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.
Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L., Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y., Rogers,J. and Bradley,A.
Direct Submision
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. http://www.sanger.ac.uk/MICER
location/Qualifiers
1. .692
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPN317a23"
/clone_lib="MHPN"

FEATURES
Source
location/Qualifiers
1. .692
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPN317a23"
/clone_lib="MHPN"

ORIGIN
Query Match 73.6%; Score 20.6; DB 14; Length 692;
Best Local Similarity 85.2%; Pred. No. 2.3e+03;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 GACATTATGTTATGATTGTATGGAA 27
|||||
572 GACATGATTGTTATGATTGTATGGTA 598

RESULT 9 836 bp mRNA linear EST 02-SEP-2005
LOCUS DT598349
DEFINITION wmi103-4ma2-c01 wmi103 welwitschia mirabilis cDNA clone
wmi103-4ma2-c01 5', mRNA sequence.
ACCESSION DT598349
VERSION DT598349.1 GI:74109622
KEYWORDS EST.
SOURCE welwitschia mirabilis

```

ORGANISM	REFERENCE	TITLE	JOURNAL	COMMENT
<p> <i>Melwitschia mirabilis</i> Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Gnecophyta; Gnecopsida; <i>Melwitschiales</i>; <i>Melwitschiaceae</i>; <i>Melwitschia</i>. 1 (bases 1 to 836) dePamphilis, C., Carlson, J., Ma, H., Soltis, D., Soltis, P., Oppenheimer, D., Frohlich, M., Doyle, J., Tanksley, S., Webb, M., Leebens-Mack, J., McNeal, J., Landherr, L., Ilu, D. and Wall, K. Generation of ESTs from early flower buds of <i>Melwitschia mirabilis</i> Unpublished (2003) Contact: Claude dePamphilis or James Leebens-Mack Muller Laboratory Penn State University 208 Muller Laboratory, Department of Biology, ATTN Rm212, Penn State University, University Park, PA 16802, USA Tel: 814 863 6413 Fax: 814 865 9131 Email: cwm3@psu.edu or jh110@psu.edu The sequence provided is trimmed of vector and low quality regions. Full sequence and original trace file are available from the Plant Genome Network website (http://psn.cornell.edu) Plate: wmi03-4ma2 row: c column: 01 Seq primer: M13P. </p>	<p> Location/Qualifiers 1. 836 /organism="Melwitschia mirabilis" /mol_type="mRNA" /db_xref="PGN:wmi03-4ma2-c01" /db_xref="taxon:3377" /clone="wmi03-4ma2-c01" /cisue_type="young female scrobilla" /lab_host="SOLR" /clone_1b="Wmi03" /notc="vector: Bluescript; site 1: EcoRI; site 2: XhoI; This is directionally cloned, non-normalized library. This library has been generated by the Floral Genome Project (FGP). The Floral Genome Project is funded by NSF's Plant Genome Research Program (DBI-0115684). More information about the project can be obtained at http://fgp.bio.psu.edu" </p>	<p> Query Match 73.6%; Score 20.6; DB 10; Length 836; Best Local Similarity 85.2%; Pred. No. 2.3e+03; Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0; </p>	<p> OY 1 GACATTATTGTTAGTTGATGGA 27 DB 546 GACATGATGTTAGTTAGTGGA 572 </p>	<p> RESULT 10 CX897969/c 848 bp mRNA linear EST 04-FEB-2005 DEFINITION JGI CAAM7770.fcd NIH XGC (c) Xenopus tropicalis cDNA clone ACCESSION IMAGE:7681489 5', mRNA sequence. VERSION CX897969 KEYWORDS CX897969.1 GI:58637313 EST. Xenopus tropicalis (western clawed frog) Xenopus tropicalis Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae; Xenopus; Silurana. 1 (bases 1 to 848) Richardson, P., Lucas, S., Rokhsar, D., Dettner, J.C., Ng, D.C., Brokstein, P. and Lindquist, E.A. DOG Joint Genome Institute Xenopus tropicalis EST project Unpublished (2004) Other ESTs: JGI CAAM7770.rev Contact: Lindquist, E.A., Richardson, P. DOG Joint Genome Institute 2800 Mitchell Drive, Walnut Creek, CA 94598, USA </p>

Tel: 925 296 5600
 Fax: 925 296 5710
 Email: cdna@jgi-pbf.org
 Tissue Procurement: Timothy Grammer (Richard M. Harland Laboratory,
 University of California, Berkeley)
 http://tropicalis.berkeley.edu/home
 cDNA Library Preparation: DOE Joint Genome Institute:
 http://www.jgi.doe.gov
 DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
 Clone Distribution: I.M.A.G.E. Consortium/LNL:
 http://image.lnl.gov
 Naming Conventions: EST name is generated by the concatenation of
 the JGI Clone id and the direction of sequencing. The suffix '.fwd'
 indicates a forward sequencing read of the insert. It does not
 necessarily reflect the orientation of the insert.
 Plate: CAA0081 row: C column: 23
 High quality sequence stop: 767.
 Location/Qualifiers

FEATURES

source

1. 848
 /organism="Xenopus tropicalis"
 /mol_type="mRNA"
 /db_xref="taxon:8364"
 /clone="IMAGE:7681489"
 /sex="male"
 /tissue_type="Testes"
 /dev_stage="Adult"
 /lab_host="Electromax DH10B"
 /clone_lib="NIH XGC tropt63"
 /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
 This library was made from dt primed cDNA and cloned into
 Invitrogen pCMVSPORT6 vector. The work was done at DOE
 Joint Genome Institute. Poly A RNA were primed with 5'
 GACTAGTTCAGATCCGAG CGACGCCCTTTTCTTTT 3'. cDNA
 were ligated to SalI adapter (5' TCGACCGACGCTCCG and
 5'CGGACGCTGGG), digested with NotI, size fractionated in
 1.1% agarose gel electrophoresis and ligated into NotI and
 SalI digested pCMVSPORT6 vector."

ORIGIN

Query Match 73.6%; Score 20.6; DB 9; Length 848;
 Best Local Similarity 85.2%; Pred. No. 2.3e+03;
 Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACATTATGTTATGATTGTATGGAAC 28
 |||||
 Db 244 ACATTATGTTATGATTGTATGATC 218

RESULT 11 906 bp DNA linear GSS 05-JUL-2004
 CRO65011 Reverse strand read from insert in 5'HRPT insertion targeting and
 LOCUS chromosome engineering clone MHPN42e12, genomic survey sequence.
 DEFINITION CRO65011
 ACCESSION CRO65011 GI:49798601
 VERSION GSS; genome survey sequence; MISCER.
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 906)
 Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
 Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
 Rogers,J. and Bradley,A.
 Direct Submission
 TITLE Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
 JOURNAL CB10 15A, UK. http://www.sanger.ac.uk/MISCER
 FEATURES location/Qualifiers

FEATURES

source

1. 906
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"

ORIGIN

Query Match 73.6%; Score 20.6; DB 14; Length 906;
 Best Local Similarity 85.2%; Pred. No. 2.3e+03;
 Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GACATTATGTTATGATTGTATGGA 27
 |||||
 Db 572 GACATTATGTTATGATTGTATGGA 598

RESULT 12 1356 bp mRNA linear EST 30-MAR-2005
 DN698710
 LOCUS Cluj19-B11 3', mRNA sequence.
 DEFINITION Cluj19-B11.x1d-t SHGC-CLJ Gaerosteus aculeatus cDNA clone

ACCESSION DN698710 GI:62060219
 VERSION DN698710
 KEYWORDS EST.
 SOURCE Gaerosteus aculeatus (three spined stickleback)
 ORGANISM Gaerosteus aculeatus

REFERENCE 1 (bases 1 to 1356)
 Kingsley,D.M., Petchel,C., Balabhadra,S., Grimwood,J., Dickson,M.,
 Schmutz,J. and Myers,R.M.
 Expressed sequence tags from Gaerosteus aculeatus
 Unpublished (2003)

TITLE JOURNAL
 COMMENT Contact: Grimwood, Jane
 Stanford Human Genome Center
 Stanford University School of Medicine
 975 S California Ave, Palo Alto, CA 94304, USA
 Tel: 650 320 5917
 Fax: 650 320 5801
 Email: jane@hgc.stanford.edu

High quality sequence start: 11
 High quality sequence stop: 899.
 Location/Qualifiers

FEATURES

source

1. 1356
 /organism="Gaerosteus aculeatus"
 /mol_type="mRNA"
 /strain="Bictrufjordur marine sticklebacks, Iceland"
 /db_xref="taxon:69293"
 /clone="Cluj19-B11"
 /sex="mixed male and female"
 /tissue_type="whole larva"
 /dev_stage="21 day old larvae collected at Svarup Stage 30
 (J Embryol. Exp. Morphol 6: 373-383,1958)"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="SHC-CLJ"
 /note="Vector: Express 1; Total and poly A+ RNA was
 isolated from the indicated stickleback tissue, and a cDNA
 library was constructed in the Express 1 plasmid vector by
 Open Biosystems. First strand cDNA synthesis was primed
 with an 54 bp linker primer containing an oligodT sequence
 preceded by a synthetic NotI site (first strand primer:
 5'-GACTAGTTCAGATCCGAGCGGCCCGCC(T)25-3'). Following
 second strand synthesis, cDNAs were made blunt at the end
 corresponding to the original 5 prime end of mRNA, and
 cloned directionally into the NotI and EcoRV sites of
 Express 1. Note that the EcoRV site is typically destroyed
 in the blunt end cloning, leaving a junction of the EcoRV
 'xxATC' (where is ATC is the second half of the EcoRV
 site, and xxx is derived from the cDNA sequence). A map of
 the Express 1 vector is available at:
 http://www.openbiosystems.com/cdna_library construction fa
 q.php# The primary library was transformed and amplified
 in DH10B (T1 phage resistant) bacteria. Clones available

from Open Biosystems:
http://www.openbiosystems.com/stickleback"

ORIGIN

Query Match 73.6%; Score 20.6; DB 9; Length 1356;
Best Local Similarity 85.2%; Pred. No. 2.3e+03;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GACATTATGTTATAGTTGTATGGA 27
|||||
Db 35 GACATTATGTTATAGTTGTATGTA 9

RESULT 13

AG111813 677 bp DNA linear GSS 03-NOV-2001
LOCUS AG111813
DEFINITION Pan troglodytes DNA, clone: PTB-117P07.F, genomic survey sequence.
ACCESSION AG111813
VERSION AG111813.1 GI:16732332
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
AUTHORS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Pan.

REFERENCE 1 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Toto, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of library PTB
Unpublished
2 (bases 1 to 677)

TITLE Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Toto, Y., Watanabe, H. and Sakaki, Y.
Submitted (02-AUG-2001) Aseo Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9111, Fax: 81-45-503-9170
E-mail: chimpbes@sc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/,
Clones are derived from the chimpanzee BAC library PTB This BAC end
clone tracking errors.
PRIMERS
Sequencing: -21M13
LIBRARY Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.

FEATURES
source location/Qualifiers
1..677
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-117P07.F"
/sex="male"
/cell_type="lymphoblast"
/clone_id="PTB Chimpanzee Male BAC library"

COMMENT

Query Match 72.9%; Score 20.4; DB 14; Length 677;
Best Local Similarity 95.5%; Pred. No. 2.7e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 TATTGTTATAGTTGTATGGA 27
|||||
Db 357 TATTGTTATAGTTGTATGGA 336

ORIGIN

Query Match 72.9%; Score 20.4; DB 14; Length 677;
Best Local Similarity 95.5%; Pred. No. 2.7e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 TATTGTTATAGTTGTATGGA 27
|||||
Db 357 TATTGTTATAGTTGTATGGA 336

RESULT 14

BM053630 713 bp mRNA linear EST 19-OCT-2002
LOCUS BM053630
DEFINITION BM053630 Nori Satoh unpublished cDNA library, blood cells cDNA
intestinalis cDNA clone cibd079b12 5', mRNA sequence.

ACCESSION BM053630
VERSION BM053630.1 GI:24154326
KEYWORDS EST.
SOURCE Ciona intestinalis
ORGANISM Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Clonidae; Ciona.
1 (bases 1 to 713)
REFERENCE 1 Satou, Y., Satake, M., Azumi, K., Nonaka, M., Shin-i, T., Kohara, Y. and
Satou, N.
Expressed genes in Ciona intestinalis (2002)
Unpublished (2002)
Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.

REFERENCE

Qy 4 ATTATGTTATAGTTGTATG 25
|||||
Db 351 ATTATGTTATAGTTGTATG 372

FEATURES

source location/Qualifiers
1..713
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="cibd079b12"
/issue_type="blood cells"
/clone_id="Nori Satoh unpublished cDNA library, blood
cells"

ORIGIN

Query Match 72.9%; Score 20.4; DB 3; Length 713;
Best Local Similarity 95.5%; Pred. No. 2.7e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 ATTATGTTATAGTTGTATG 25
|||||
Db 351 ATTATGTTATAGTTGTATG 372

RESULT 15
LOCUS BM206337
DEFINITION BM206337 Nori Satoh unpublished cDNA library, cleaving embryo Ciona
intestinalis cDNA clone c1c1093n06 5', mRNA sequence.
ACCESSION BM206337
VERSION BM206337.1 GI:24620951
KEYWORDS EST.
SOURCE Ciona intestinalis
ORGANISM Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Clonidae; Ciona.
1 (bases 1 to 724)
REFERENCE 1 Satou, Y., Shin-i, T., Kohara, Y. and Satou, N.
Expressed genes in Ciona intestinalis (2002c)
Unpublished (2002)
Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.

REFERENCE

Qy 1 (bases 1 to 724)
Db 351 ATTATGTTATAGTTGTATG 372

FEATURES

source location/Qualifiers
1..724
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="c1c1093n06"
/issue_type="whole body"
/db_xref="cleaving embryo"
/clone_id="Nori Satoh unpublished cDNA library, cleaving
embryo"

ORIGIN

Query Match 72.9%; Score 20.4; DB 3; Length 724;
 Best Local Similarity 95.5%; Pred. No. 2.8e+03;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 ATTATGTTATAGTTGTATG 25
 |||||
 DB 508 ATTATGTTATAGTTGTATG 529

RESULT 16
 BEF20181 205 bp mRNA linear EST 13-JAN-2001
 LOCUS M1-RT0025-171100-003-e09 RT0025 Homo sapiens cDNA, mRNA sequence.
 DEFINITION
 ACCESSION BEF20181
 VERSION
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM

REFERENCE
 AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Negai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
 O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

TITLE
 JOURNAL
 PUBLISHED
 COMMENT
 1073800
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the PAPSP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?cl=MR1ct2-MR1-RT0025-
 171100-003-e09&ct3=2000-11-17&ct4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 21
 High quality sequence stop: 94.
 Location/Qualifiers

FEATURES
 source

1. 205
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_1lb="RT0025"
 /note="Organ: kidney tumor; Vector: puc18; Site 1: SmaI;
 Site 2: SmaI; A mini-library was made by cloning products
 derived from ORSSTES PCR (U.S. letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the puc 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

ORIGIN

Query Match 72.1%; Score 20.2; DB 2; Length 205;
 Best Local Similarity 88.0%; Pred. No. 3.2e+03;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ACATATGTTATAGTTGTATGA 26
 |||||
 DB 90 ACATTTGTTATAGTTTCTATGA 114

RESULT 17
 DR165329 351 bp mRNA linear EST 20-JUN-2005
 LOCUS RRP0501_4_F02.b1_A029 Roots minus phosphorous Pinus taeda cDNA
 DEFINITION
 RRP0501_4_F02_A029 3', mRNA sequence.
 ACCESSION DR165329
 VERSION DR165329.1 GI:68023291
 KEYWORDS
 SOURCE EST.
 ORGANISM Pinus taeda (loblolly pine)

REFERENCE
 AUTHORS Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
 1 (bases 1 to 351)
 Pratt,L., Cordonnier-Pratt,M.M., Lorenz,W.W., Zimmermann,C. and
 Dean,J.F.D.
 An EST database from phosphorous-deficient loblolly pine (Pinus
 taeda) roots
 Unpublished (2005)
 Other ESTs: RRP0501_4_F02.g1_A029
 Contact: Cordonnier-Pratt MM
 Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210
 Email: mmp@plantuga.edu
 RNA prepared and library constructed by W. Walter Lorenz (School of
 Forest Resources, University of Georgia); plant material prepared
 by Craig Zimmermann (School of Forest Resources, University of
 Georgia) using rooted cuttings provided by the Forest Biology
 Research Cooperative (FBRC) and the CCLONBS project a the
 University of Florida; sequencing done in the Laboratory for
 Genomics and Bioinformatics, University of Georgia. Sequence ends
 have been trimmed to exclude vector and regions below Phred quality
 16. Three-prime sequences are presented as their reverse complement
 and have been trimmed to exclude polyA.
 Seq primer: M13-21 (TGTAAACGACGCGCCAGT)
 POLYA=yes.
 Location/Qualifiers

1. 351
 /organism="Pinus taeda"
 /mol_type="mRNA"
 /strain="3 CCLONBS"
 /db_xref="taxon:3352"
 /clone="RRP0501_4_F02_A029"
 /lab_host="DH10B-T1 phage-resistant E. coli"
 /clone_1lb="Roots minus phosphorous"
 /note="Organ: Root; Vector: pSL1180; Site 1: EcoRI;
 Site 2: XhoI; The library was prepared from polyA+ RNA
 from the roots of 1-year-old loblolly pine (Pinus taeda)
 cuttings that were rooted and then planted in washed sand.
 The rooted cuttings were maintained for 139 days (July 28
 2003 harvest) under ambient conditions in a local
 greenhouse. They were kept on a weekly regimen of 0.5x
 nutrient-complete Hoagland's solution and supplemented
 with additional water sufficient to maintain a 15% soil
 moisture content. Starting five weeks prior to harvesting
 roots for RNA preparation, the weekly fertilizer regimen
 for the potted trees was modified to omit phosphorus from
 the 0.5x Hoagland's solution (5 applications). For two
 days prior to starting the modified fertilizer regimen,
 pots were flushed extensively with water to reduce
 residual levels of phosphorus. Double-stranded cDNA was
 cloned unidirectionally into pSL1180. Inserts can be
 excised with EcoRI (5' end) and XhoI (3' end)."

FEATURES
 source

ORIGIN

Query Match 72.1%; Score 20.2; DB 9; Length 351;
 Best Local Similarity 88.0%; Pred. No. 3.2e+03;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ACATATGTTATAGTTGTATGA 26
 |||||

Db 83 ACATTATGTTATGATTGGACAGA 107

RESULT 18
BO851812
LOCUS
DEFINITION BO851812.487 bp mRNA linear EST 14-AUG-2002
OSB16F20.yg.ab1 OG ABCDI lettuce salinas Lactuca sativa cDNA clone
OSB16F20. mRNA sequence.

ACCESSION BO851812
VERSION BO851812.1 GI:22237277
KEYWORDS
SOURCE Lactuca sativa
ORGANISM Lactuca sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
Cichorieae; Lactuca.

REFERENCE
AUTHORS Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J.,
Ellison,P., Kolman,J., Slabaugh,M.S., Livingston,K., Zhou,Y.,
Lai,Z., Church,S., Jackson,L. and Bradford,K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compomics.ucdavis.edu/
Unpublished (2002)

JOURNAL
COMMENT Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Aamundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]
belongs to contig OG_Ca_Contig6733, see http://cgdb.ucdavis.edu/
for details.
Plate: OG816 row: F column: 20.

FEATURES
source
1..487
location/Qualifiers
/organism="Lactuca sativa"
/mol_type="mRNA"
/cultivar="Salinas"
/db_xref="taxon:4236"
/clone="OG816F20"
/lab_host="E.coli"
/clone_lib="OG_ABCDI lettuce salinas"
/note="Vector: pBRCDNA51AB; The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgdb.ucdavis.edu/
TAG_LIB=OG_ABCDI lettuce salinas
TAG_SEQ=TTTACCGGG"

ORIGIN

Query Match 72.1%; Score 20.2; DB 3; Length 487;
Best Local Similarity 88.0%; Pred. No. 3.2e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GACATTATTGTTATGATTGGATG 25
|||||
Db 102 GACATTCTGTATGATTGGATG 126
|||||

RESULT 19
DE110524
LOCUS
DEFINITION DE110524.543 bp DNA linear GSS 02-AUG-2005
Oryzias latipes DNA, reverse end of BAC clone: Md0153B05, genomic
survey sequence.

ACCESSION DE110524

VERSION DE110524.1 GI:71610277
KEYWORDS GSS.
SOURCE Oryzias latipes (Japanese medaka)
ORGANISM Oryzias latipes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percormorpha; Atherinomorpha;
Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.

REFERENCE
AUTHORS Shimizu,N., Asakawa,S., Shimizu,A. and Sasaki,T.
TITLE The BAC end sequence of Oryzias latipes
JOURNAL Published Only in Database (2005)
REFERENCE 2 (bases 1 to 543)
AUTHORS Shimizu,N., Asakawa,S., Sasaki,T. and Shimizu,A.
TITLE Direct Submission
JOURNAL Submitted (30-JUN-2005) Nobuyoshi Shimizu, Keio University, School
of Medicine, Molecular Biology; 35 Shinanomachi, Shinjuku-Ku,
Tokyo, 160-8582, Japan (E-mail:nshimizu@med.keio.ac.jp,
Tel:81-3-3351-2370, Fax:81-3-3351-2370)

FEATURES
source
1..543
location/Qualifiers
/organism="Oryzias latipes"
/mol_type="genomic DNA"
/db_xref="taxon:8090"
/clone="Md0153B05"
/clone_lib="Medaka Hdr BAC library"
/note="This sequence is reverse end of BAC clone
Md0153B05."

ORIGIN

Query Match 72.1%; Score 20.2; DB 14; Length 543;
Best Local Similarity 88.0%; Pred. No. 3.3e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 ATTATGTTATGATTGATGAAC 28
|||||
Db 272 ATTATGTTATGATTGATGAAC 296
|||||

RESULT 20
CL387597/c 583 bp DNA linear GSS 19-AUG-2004
LOCUS RCI144.281113.r RPI1-44 Sus scrofa genomic clone RPI144_281113,
DEFINITION genomic survey sequence.
ACCESSION CL387597
VERSION CL387597.1 GI:51439557
KEYWORDS GSS.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
1 (bases 1 to 583)
1 Regatcheva,M.B., Meyers,S., He,W., Latkin,D.M., Marron,B.M.,
Bever,J.B. and Schook,L.B.
Piggy-BACing the Human Genome: Constructing a Porcine Physical Map
Through Comparative Genomics
Unpublished (2004)
Other GSSs: RPI144.281113.f
Contact: Lawrence B. Schook
Department of Animal Sciences
University of Illinois at Urbana Champaign
1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 217 265 5326
Fax: 217 244 5617
Email: schook@uiuc.edu
Clones are derived from the porcine BAC library RPI1-44
(http://www.bacpac.chori.org/porcine242.htm). For BAC library
availability, please contact Pieter de Jong (pdjong@chori.org).
Clones may be purchased from BACPAC Resources
(http://BACPACresources.chori.org). This work was undertaken as part
of the international Swine Genome Sequencing Consortium by
University of Illinois at Urbana Champaign, USA with funds provided

by grant No. AG2002-34480-11828 from USDA-CSREES and
AG2001-35205-09965 from USDA/NRI (Livestock Genome Sequencing
Initiative)
Plate: 281 row: L column: 13
Seq primer: SP6
Class: BAC ends.

FEATURES

source

1. .583
/organism="Sus scrofa"
/mol_type="genomic DNA"
/strain="four pigs (bred: 37.5% Yorks Landrace and 25%
Meishan)"
/db_xref="taxon:9823"
/clone="RPC14_281L13"
/sex="male"
/cell_type="blood"
/clone_1ib="RPC1-44"
/note="Vector: pFARAC2; Site_1: EcoRI; Site_2: EcoRI;
porcine male BAC library produced by Pieter de Jong"

ORIGIN

Query Match 72.1%; Score 20.2; DB 13; Length 583;
Best Local Similarity 88.0%; Pred. No. 3.3e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CATTATTGTTATGTTGATGGA 27
|||||
Db 459 CATTATTGTTATGTTTGGTA 435

RESULT 21 621 bp mRNA linear EST 10-JUL-2003
CD820121 BN20.051E05F011220 BN20 Brassica napus cDNA clone BN20051B05, mRNA
LOCUS
DEFINITION
Sequence.
CD820121 GI:32502061
VERSION
CD820121.1
KEYWORDS
EST.
SOURCE
Brassica napus (rape)
ORGANISM
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 621)
Genoplante.
Genoplante, a major partnership french program in plant genomics
unpublished (2003)
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (<http://www.genoplante.com>
and <http://genoplante-info.infobiogen.fr>).
Location/Qualifiers
1. .621
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jec Neuf"
/db_xref="taxon:3708"
/clone="BN20051B05"
/issue_type="seed"
/clone_1ib="BN20"

FEATURES

source

1. .621
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jec Neuf"
/db_xref="taxon:3708"
/clone="BN20051B05"
/issue_type="seed"
/clone_1ib="BN20"

ORIGIN

Query Match 72.1%; Score 20.2; DB 5; Length 621;
Best Local Similarity 88.0%; Pred. No. 3.3e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ACATTATGTTATGTTGATGGA 26
|||||
Db 517 AGATTATGTTATGTTGATGGA 541

RESULT 22 645 bp mRNA linear EST 14-AUG-2002
B0854577 OGB23K09.yg.ab1 OG ABCDI lettuce salinas Lactuca sativa cDNA clone
LOCUS
DEFINITION
Sequence.
OGB23K09, mRNA sequence.
B0854577
B0854577.1 GI:22240042
VERSION
B0854577
KEYWORDS
EST.
SOURCE
Lactuca sativa
ORGANISM
Lactuca sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
Cichorieae; Lactuca.
1 (bases 1 to 645)
Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J.,
Billson,P., Kolkmann,J., Slabaugh,M.S., Livingston,K., Zhou,Y.,
Lai,Z., Church,S., Jackson,L. and Bradford,K.
Lettuce and Sunflower ESTs from the Composite Genome Project
<http://comgenomics.ucdavis.edu/>
Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Amundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]
belongs to contig OG_CA_Config6733, see <http://cspdb.ucdavis.edu/>
for details.
Plate: OGB23 row: K column: 09.

FEATURES

source

1. .645
/organism="Lactuca sativa"
/mol_type="mRNA"
/cultivar="Salinas"
/db_xref="taxon:4236"
/clone="OGB23K09"
/lab_host="E.coli"
/clone_1ib="OG_ABCDI lettuce salinas"
/note="Vector: pBRCDNA5f1AB; The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at <http://cspdb.ucdavis.edu/>
TAG_LIB-OG_ABCDI lettuce salinas
TAG_SEQ=GTGACCGGG"

ORIGIN

Query Match 72.1%; Score 20.2; DB 3; Length 645;
Best Local Similarity 88.0%; Pred. No. 3.3e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GACATTATGTTATGTTGATGGA 25
|||||
Db 102 GACATTCTGTTATGTTGATGGA 126

RESULT 23 693 bp mRNA linear EST 14-AUG-2002
B0864783 OGB27K11.yg.ab1 OG ABCDI lettuce salinas Lactuca sativa cDNA clone
LOCUS
DEFINITION
Sequence.
OGB27K11, mRNA sequence.
B0864783
B0864783.1 GI:22250248
VERSION

KEYWORDS EST.
SOURCE Lactuca sativa
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; campanulids; Asterales; Asteraceae; Cichorioideae; Cichorieae; Lactuca.
 1 (bases 1 to 693)
REFERENCE Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L., Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J., Ellison,P., Kolkmann,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z., Church,S., Jackson,L. and Bradford,K.
 Lettuce and Sunflower ESTs from the Compositae Genome Project
<http://compomics.ucdavis.edu/>
 Unpublished (2002)
JOURNAL Contact: Alexander Kozik [R.W.Michelmore]
 Department of Vegetable Crops, R.W.Michelmore Lab
 University of California at Davis (UCD)
 Aamundson Hall, UCD, Davis, CA 95616, USA
 Tel: 1-(530)-742-1742
 Fax: 1-(530)-752-9659
 Email: akozik@ucdavis.org [michelmore@vegmail.ucdavis.edu]
 belongs to contig Q3_CA_Contig6733, see <http://cgpdb.ucdavis.edu/> for details.
FEATURES Plate: QGB27 row: K column: 11.
 source Location/Qualifiers
 1..693
 /organism="Lactuca sativa"
 /mol_type="mRNA"
 /cultivar="Salinas"
 /db_xref="taxon:4236"
 /clone="QGB27K11"
 /lab_host="E.coli"
 /clone_lib="Q3 ABCDI lettuce salinas"
 /note="Vector: pBRCDNA5flab; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at <http://cgpdb.ucdavis.edu/>
 TAG_LIB=Q3 ABCDI lettuce salinas
 TAG_SEQ=TGTAGCCGG3"

ORIGIN
 Query Match 72.1%; Score 20.2; DB 3; Length 693;
 Best Local Similarity 88.0%; Pred. No. 3.3e+03;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GACATTATGTTATGATTGATG 25
 Db 102 GACATTCTTGTATGTTTGATG 126

RESULT 24
 B0853474 706 bp mRNA linear EST 14-AUG-2002
LOCUS OGB20J20.yg.ab1 QG_ABCDI lettuce salinas Lactuca sativa cDNA clone
DEFINITION OGB20J20.yg.ab1 QG_ABCDI lettuce salinas Lactuca sativa cDNA clone
ACCESSION B0853474 mRNA sequence.
VERSION B0853474.1 GI:22238939
KEYWORDS EST.
SOURCE Lactuca sativa
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; campanulids; Asterales; Asteraceae; Cichorioideae; Cichorieae; Lactuca.
 1 (bases 1 to 706)
REFERENCE Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,

TITLE Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J., Ellison,P., Kolkmann,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z., Church,S., Jackson,L. and Bradford,K.
 Lettuce and Sunflower ESTs from the Compositae Genome Project
<http://compomics.ucdavis.edu/>
 Unpublished (2002)
JOURNAL Contact: Alexander Kozik [R.W.Michelmore]
 Department of Vegetable Crops, R.W.Michelmore Lab
 University of California at Davis (UCD)
 Aamundson Hall, UCD, Davis, CA 95616, USA
 Tel: 1-(530)-742-1742
 Fax: 1-(530)-752-9659
 Email: akozik@ucdavis.org [michelmore@vegmail.ucdavis.edu]
 belongs to contig Q3_CA_Contig6733, see <http://cgpdb.ucdavis.edu/> for details.
FEATURES Plate: QGB20 row: J column: 20.
 source Location/Qualifiers
 1..706
 /organism="Lactuca sativa"
 /mol_type="mRNA"
 /cultivar="Salinas"
 /db_xref="taxon:4236"
 /clone="QGB20J20"
 /lab_host="E.coli"
 /clone_lib="Q3 ABCDI lettuce salinas"
 /note="Vector: pBRCDNA5flab; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at <http://cgpdb.ucdavis.edu/>
 TAG_LIB=Q3 ABCDI lettuce salinas
 TAG_SEQ=TGTAGCCGG3"

ORIGIN
 Query Match 72.1%; Score 20.2; DB 3; Length 706;
 Best Local Similarity 88.0%; Pred. No. 3.3e+03;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GACATTATGTTATGATTGATG 25
 Db 102 GACATTCTTGTATGTTTGATG 126

RESULT 25
 B0007386 728 bp mRNA linear EST 03-OCT-2005
LOCUS B0007386
DEFINITION QGH2a10.yg.ab1 QG_EFGHJ lettuce serritola Lactuca serritola cDNA clone QGH2a10, mRNA sequence.
ACCESSION B0007386
VERSION B0007386.1 GI:22441781
KEYWORDS EST.
SOURCE Lactuca serritola
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; campanulids; Asterales; Asteraceae; Cichorioideae; Cichorieae; Lactuca.
 1 (bases 1 to 728)
REFERENCE Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L., Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J., Ellison,P., Kolkmann,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z., Church,S., Jackson,L. and Bradford,K.
 Lettuce and Sunflower ESTs from the Compositae Genome Project
<http://compomics.ucdavis.edu/>
 Unpublished (2002)
JOURNAL Contact: Alexander Kozik [R.W.Michelmore]
 Department of Vegetable Crops, R.W.Michelmore Lab
 University of California at Davis (UCD)

Asmundson Hall, UCD, Davis, CA 95616, USA
 Tel: 1-(530)-742-1742
 Fax: 1-(530)-752-9659
 Email: akozik@atgc.org [michelmore@veeemail.ucdavis.edu]
 belongs to config Q3_CA_Config6733, see http://cgpdb.ucdavis.edu/
 for details.
 Plate: OGH2 row: a column: 10.
 Location/Qualifiers

FEATURES

source

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1..728
/organism="Lactuca serriola"
/mol_type="mRNA"
/db_xref="taxon:75943"
/clone_lib="OGH2a10"
/lab_host="E.coli"
/clone_lib="OG FRGHJ lettuce serriola"
/notes="Vector: pBRCDNA5flab; The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgpdb.ucdavis.edu/
TAG_LIB=OG FRGHJ lettuce serriola
TAG_SEQ=GCTAGTCGGG"
```

ORIGIN

Query Match 72.1%; Score 20.2; DB 3; Length 728;
 Best Local Similarity 88.0%; Pred. No. 3.3e+03;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GACATTATGTTATGTTGATG 25
 Db 644 GACATCTCTGTATGTTGATG 668

RESULT 26 758 bp DNA linear GSS 01-NOV-2004
 CM371871
 LOCUS fdbb001f0471110 Sorghum methylation filtered library (Libid: 104)
 DEFINITION Sorghum bicolor genomic clone fdbb001f047111, genomic survey
 sequence.

ACCESSION CM371871 GI:55090315
 VERSION CM371871
 KEYWORDS GSS.
 SOURCE Sorghum bicolor (Sorghum)
 ORGANISM Sorghum bicolor

REFERENCE Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoidae; Andropogoneae; Sorghum.

1 (bases 1 to 758)
 Bedell, V.A., Budiman, M.A., Nunberg, A., Citek, R.W., Robbins, D.,
 Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K.,
 McMenamy, J., Smith, M., Holman, H., Roe, B.A., Wiley, G., Korff, I.F.,
 Rabinowicz, P.D., Lakey, N., McCombie, W.R., Jeddeloh, J.A. and
 Marienissen, R.A.

REFERENCE Sorghum genome sequencing by methylation filtration
 JOURNAL PLOS Biol. 3 (1), e13 (2005)
 PUBMED 15660154

TITLE Contact: Bedell JA
 JOURNAL Orion Genomics, LLC
 PUBMED 4041 Forest Park Ave, St. Louis, MO 63108, USA
 COMMENT Tel: 314 615 6879
 Fax: 314 615 5975
 Email: jbedell@oriongenomics.com
 Plate: fdbb001f047 row: 1 column: 11
 Seq primer: K Reverse
 Class: methylation filtered
 High quality sequence stop: 758.
 Location/Qualifiers

1..758

FEATURES

source

1..758

ORIGIN

Query Match 72.1%; Score 20.2; DB 13; Length 758;
 Best Local Similarity 88.0%; Pred. No. 3.3e+03;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ACATTATGTTATGTTGATGGA 26
 Db 173 ACATGTTGTTATGTTGATGGA 197

RESULT 27 760 bp DNA linear GSS 23-DEC-2004
 AG529207
 LOCUS Mus musculus molossinus DNA, clone:MSMg01-438K16.T7, genomic survey
 DEFINITION sequence.

ACCESSION AG529207 GI:48236620
 VERSION AG529207.1
 KEYWORDS GSS.
 SOURCE Mus musculus molossinus (Japanese wild mouse)
 ORGANISM Mus musculus molossinus

REFERENCE Rukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

Abe, K., Noguchi, H., Tagawa, K., Yuzurika, M., Toyoda, A., Kojima, T.,
 Ezawa, K., Saitou, N., Hattori, M., Sakaki, Y., Moriwaki, K. and
 Shiroishi, T.

REFERENCE Contribution of Asian mouse subspecies Mus musculus molossinus to
 genomic constitution of strain C57BL/6J, as defined by BAC-end
 sequence-SNP analysis
 JOURNAL Genome Res. 14 (12), 2439-2447 (2004)
 PUBMED 15574823

2 (bases 1 to 760)
 Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.

REFERENCE Direct Submission
 TITLE Submitted (17-NOV-2003) Masahito Hattori, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
 Tel: 81-45-503-9111, Fax: 81-45-503-9170
 E-mail: hattori@gsc.riken.jp, URL: http://hgp.gsc.riken.go.jp/

COMMENT Clones are derived from the mouse BAC library MSMg01. For BAC
 library availability, please contact Kunya Abe (abe@crc.riken.jp).
 The Institute of Physical and Chemical Research (RIKEN) 3-1-1
 Koyada, Tsukuba, 305-0074 Japan
 phone: 81-298-36-9189, fax: 81-298-36-9199
 e-mail: abe@crc.riken.jp

PRIMERS
 Sequencing : T7
 LIBRARY : pBAC3.6
 Vector 1 : SCORI
 R Site 1 : SCORI
 R Site 2 : SCORI.

FEATURES

source

1..760
 /organism="Mus musculus molossinus"
 /mol_type="genomic DNA"
 /sub_species="molossinus"
 /db_xref="taxon:57486"

ORIGIN
 /clone="MSG01-438K16.T7"
 /sex="male"
 /tissue type="mixture of kidney and spleen"
 /clone_id="MSG01 Mouse Male BAC Library"

Query Match 72.1%; Score 20.2; DB 14; Length 760;
 Best Local Similarity 88.0%; Pred. No. 3.3e+03;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GACATTATGTTATAGTTGTATGCG 25
 |||||
 Db 289 GACATTATGTTATAGTTGTATGCG 265

RESULT 28
 BG021561/c 528 bp mRNA linear EST 19-FEB-2003
 LOCUS dg32b09.x1 Xenopus laevis gastrula non normalized Xenopus laevis
 DEFINITION cDNA clone IMAGE:3750473 3', mRNA sequence.

ACCESSION BG021561
 VERSION BG021561.1 GI:12477640
 KEYWORDS EST.
 SOURCE Xenopus laevis (African clawed frog)
 ORGANISM Xenopus laevis

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 Anopodinae; Xenopus; Xenopus.
 1 (bases 1 to 528)
 Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L.,
 Pape, D., Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y.,
 Peterson, B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R.,
 Watsen, R., and Wilson, R.
 Washu Xenopus EST project, 1999
 Unpublished (1999)

TITLE
 JOURNAL
 COMMENT
 Contact: Sandy Clifton, Ph.D.
 Washu Xenopus EST project, 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu

Library constructed by Bruce Blumberg
 DNA sequencing by: Washington University Genome Sequencing Center
 Source Lab clone id - xlmga09c18 This clone is available
 royalty-free through LNL; contact the IMAGE Consortium
 (image@image.lnl.gov) for further information.
 Seq primer: -40up from Gibco
 High quality sequence stop: 476.
 Location/Qualifiers

FEATURES
 SOURCE
 1. .528
 Location/Qualifiers

/organism="Xenopus laevis"
 /mol_type="mRNA"
 /db_xref="taxon:8355"
 /clone="IMAGE:3750473"
 /tissue type="gastrula (stages 10.5, 11.5 mixed)"
 /lab host="Top-10 P"
 /clone_id="Xenopus laevis gastrula non normalized"
 /note="Vector: pBluescript SK-; site 1: EcoRI; site 2:
 XhoI; cDNA was prepared from 2 ug of poly A+ RNA (equal
 parts from stage 10.5 and stage 11.5 gastrulae).
 EcoRI-XhoI cut cDNA was then ligated into XhoI-XR
 (Stratagene) with EcoRI at the 5' end and XhoI at the 3'
 end. The library was mass excised and used to infect
 Top10P. Clones were picked into freezing medium (per
 liter 15 g tryptone, 10g yeast extract, 5g NaCl, 36 mM
 KH2PO4, 13.2 mM KH2PO4, 1.7 mM Na-citrate, 0.4 mM MgSO4 7
 H2O, 6.8 mM (NH4)2SO4, 4 % w/v glycerol) and grown for 24
 hours. Original library construction by Bruce Blumberg
 (Cho et al 1991 Cell 67, 1111-1120)."

ORIGIN

Query Match 71.4%; Score 20; DB 2; Length 528;
 Best Local Similarity 82.1%; Pred. No. 3.9e+03;
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 GACATTATGTTATAGTTGTATGGAAC 28
 |||||
 Db 44 GACATTATGTTATAGTTGTATGTAATTAAC 17

RESULT 29
 AQ829979/c 534 bp DNA linear GSS 27-AUG-1999
 LOCUS HS 4828 B1 F06 T7A CIT Approved Human Genomic Sperm Library D Homo
 DEFINITION sapiens genomic clone Plate=4828 Col=11 Row=L, genomic survey
 sequence.

ACCESSION AQ829979
 VERSION AQ829979.1 GI:5796041
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 534)
 Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
 Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
 Hood, L.
 Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome
 Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 10449764
 Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones may be purchased from Research Genetics (info@resgen.com).
 BAC end Web Server: http://www.htsc.washington.edu
 Plate: 4828 row: L column: 11
 Seq primer: T7
 Class: BAC ends
 High quality sequence stop: 534.
 Location/Qualifiers

FEATURES
 SOURCE
 1. .534
 Location/Qualifiers

/organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="plate=4828 Col=11 Row=L"
 /sex="male"
 /clone_id="CIT Approved Human Genomic Sperm Library D"
 /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
 E-Coli DH10B"

ORIGIN

Query Match 71.4%; Score 20; DB 11; Length 534;
 Best Local Similarity 100.0%; Pred. No. 3.9e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ATTATGTTATAGTTGTAT 23
 |||||
 Db 365 ATTATGTTATAGTTGTAT 346

RESULT 30
 BM610169/c 627 bp mRNA linear EST 25-FEB-2002
 LOCUS 17000687110115 A.Gam.ad.cDNA.blood1 Anopheles gambiae cDNA clone
 DEFINITION 13600449718565 5', mRNA sequence.

ACCESSION BM610169
 VERSION BM610169.1 GI:18908273
 KEYWORDS EST.

```

SOURCE      Anopheles gambiae (African malaria mosquito)
ORGANISM    Anopheles gambiae
REFERENCE   1 (bases 1 to 627)
AUTHORS     Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L.,
            Charlab,R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
            Celeris Anopheles gambiae EST project
            Unpublished (2002)
TITLE       Celeris Anopheles gambiae EST project
JOURNAL     Unpublished (2002)
COMMENT     Contact: Holt R.A.
            Celeris Genomics
            45 W. Gude Dr., Rockville, MD 20850, USA
            Tel: 2404533151
            Fax: 2404534580
            Email: HoltR@celera.com
            Plate: NU010049VR row: N column: 23
            Seq primer: M13 Reverse.
FEATURES    source
            1..627
            Location/Qualifiers
            /organism="Anopheles gambiae"
            /mol_type="mRNA"
            /strain="RSP-ST (Reduced susc. to Permethrin - std.
            chromosome)"
            /db_xref="taxon:7165"
            /clone="1960049718565"
            /dev_stage="Adult"
            /lab_host="DH10B"
            /clone_1lb="A.Gam.ad.cdna.blood1"
            /note="Vector: pSport1; Site_1: SalI; Site_2: NotI; Whole
            adult mosquitoes (mixed sex) frozen on liquid nitrogen 24
            hours after human blood feeding. cDNA inserts >500 bp
            cloned directionally into pSport 1. Not 1 site is 3'.
            Clones available through the Malaria Research and
            Reference Reagent Resource Center (www.malaria.mri.org)"

ORIGIN
Query Match      71.4%; Score 20; DB 3; Length 627;
Best Local Similarity 82.1%; Pred. No. 3.9e+03;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1 GACATTATGTTAGTTGTATGGAAC 28
        |||||
        424 GACATTATGTTAGTTAGTATGGAAC 397

RESULT 31
LOCUS      CZ821000        664 bp      DNA      linear      GSS 26-JUL-2005
DEFINITION OC_Ba0199G04.f OC_Ba Oryza coarctata genomic clone OC_Ba0199G04
VERSION     CZ821000
KEYWORDS    CZ821000.1 GI:71260853
SOURCE      GSS.
ORGANISM    Oryza coarctata (Porteresia coarctata)
REFERENCE   Oryza coarctata
AUTHORS     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
            clade; Ehrhartoideae; Oryzaceae; Oryza.
            1 (bases 1 to 664)
            Kim,H., Collura,K., Wisotski,M., Byrne,M., Stum,D., Smart,D.,
            Rao,K., Luo,M., Jetly,R., Kudrna,D., Muller,C., Soderlund,C. and
            Wang,R.
            OMAP (Oryza Map Alignment Project) - Arizona Genomics Institute
            Unpublished (2005)
TITLE       OMAP (Oryza Map Alignment Project) - Arizona Genomics Institute
JOURNAL     Unpublished (2005)
COMMENT     Contact: Rod A. Wang
            Arizona Genomics Institute
            University of Arizona
            Forbes Building Room 303, Tucson, AZ 85721-0036, USA
            Tel: 520 626 9595
            Fax: 520 621 1259
            Email: rwing@genome.arizona.edu
            PCR Primers

```

```

FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0199 row: G column: 04
Seq primer: TAA TAC GAC TCA CTA TAG GG
Class: BAC ends.
FEATURES    Location/Qualifiers
            1..664
            /organism="Oryza coarctata"
            /mol_type="genomic DNA"
            /db_xref="taxon:77588"
            /clone="OC_Ba0199G04"
            /issue_type="leaves"
            /dev_stage="mature"
            /lab_host="DH10B"
            /clone_1lb="OC_Ba"
            /note="Vector: pAG1BAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN
Query Match      71.4%; Score 20; DB 13; Length 664;
Best Local Similarity 82.1%; Pred. No. 3.9e+03;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1 GACATTATGTTAGTTGTATGGAAC 28
        |||||
        492 GACATTATGCCAAGTTGTATGGAAC 519

RESULT 32
LOCUS      AL849178        665 bp      mRNA      linear      EST 26-NOV-2003
DEFINITION AL849178 XGC-egg Xenopus tropicalis cDNA clone TB99002h04 5', mRNA
SEQUENCE     AL849178
VERSION     AL849178.2 GI:38560538
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
ORGANISM    Xenopus tropicalis
REFERENCE   Eukaryota; Metazoa; Chordata; Vertebrata; Buteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
            Xenopodinae; Xenopus; Silurana.
            1 (bases 1 to 665)
            Cronling,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
            Sanger Xenopus tropicalis EST project 2001 (11_2003)
            Unpublished (2003)
            On Sep 15, 2002 this sequence version replaced gi:22869400.
            Contact: Taylor R
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS SEQUENCE ID: TB99002h04.PIKSP6
            Sequencing primer: SP6
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
            cDNA was oligo dt primed from Sug of poly A+ RNA from egg.
            EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
            5' end and NotI at the 3' end.
            Vector: pCS107; Site 1: EcoRI; Site 2: NotI
            Host: Escherichia coli XL1-blue.
FEATURES    Location/Qualifiers
            1..665
            /organism="Xenopus tropicalis"
            /mol_type="mRNA"
            /db_xref="taxon:8364"
            /clone="TB99002h04"
            /dev_stage="egg"
            /lab_host="Escherichia coli XL1-blue"
            /clone_1lb="XGC-egg"
            /note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA
            was oligo dt primed from Sug of poly A+ RNA from egg.
            EcoRI-NotI cut cDNA was then ligated into pCS107 with
            EcoRI at the 5' end and NotI at the 3' end"

ORIGIN

```

Query Match 71.4%; Score 20; DB 1; Length 665;
 CX689149/c 700 bp mRNA linear EST 19-JAN-2005
 LOCUS ydc08b02.y2 Sea urchin EST lib1 Strongylocentrotus purpuratus cDNA
 DEFINITION
 ACCESSION CX689149
 VERSION CX689149
 KEYWORDS EST.
 SOURCE Strongylocentrotus purpuratus
 ORGANISM Strongylocentrotus purpuratus
 Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 Echinozoa; Euechinozoa; Echinodermata; Echinodermata;
 Strongylocentrotidae; Strongylocentrotus.
 1 (bases 1 to 700)
 Coffman,J.A., Robertson,A.J., Clifton,S., Pape,D., Hillier,L.,
 Martin,J., Wyllie,T., Dante,M., Meyer,R., Theising,B., Bowers,Y.,
 Gibbons,M., Konko,T., Tsagaris,W., Rutter,E., Kennedy,S. and
 Wilson,R.
 Washu Sea Urchin EST Project
 Unpublished (2004)
 Contact: Dr. James A. Coffman
 Washu Sea Urchin EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 DNA sequencing by: Washington University Genome Sequencing Center
 Seq primer: -28RFPOT
 High quality sequence stop: 700.
 Location/Qualifiers
 1..700
 /organism="Strongylocentrotus purpuratus"
 /mol_type="mRNA"
 /db_xref="taxon:7668"
 /clone="ydc08b02"
 /lab_host="DH10B"
 /note="Vector: pCMVSPORT6.1 (Invitrogen); Site 1: NotI;
 Site 2: SmaI; Arrayed normalized library of full-length
 cDNAs representing blaescula stage transcriptome of the sea
 urchin Strongylocentrotus purpuratus, cloned into the
 vector pCMVSPORT6.1 (Invitrogen)"

ORIGIN
 Query Match 71.4%; Score 20; DB 9; Length 700;
 Best Local Similarity 82.1%; Pred. No. 3.9e+03;
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Oy 1 GACATATTTGTTATGTTTGTATGAAC 28
 |||||
 Db 533 GACAGTATGCTTACGTTTGTATGAAC 506

RESULT 34
 LOCUS CX908094 749 bp mRNA linear EST 04-FEB-2005
 DEFINITION JGI CAAN728.fwd NIH XGC tropic4 Xenopus tropicalis cDNA clone
 IMAGE:7686784 5', mRNA sequence.
 ACCESSION CX908094
 VERSION CX908094.1 GI:58647438
 KEYWORDS EST.
 SOURCE Xenopus tropicalis (western clawed frog)

ORGANISM Xenopus tropicalis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 Xenopodidae; Xenopus; Silurana.
 1 (bases 1 to 749)
 Richardson,P., Lucas,S., Rokhsar,D., Dettter,J.C., Ng,D.C.,
 Brokstein,P. and Lindquist,E.A.
 DOE Joint Genome Institute Xenopus tropicalis EST project
 Unpublished (2004)
 Other ESTs: JGI CAAN728.rev
 Contact: Lindquist,E.A., Richardson,P.
 DOE Joint Genome Institute
 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 Tel: 925 296 5700
 Fax: 925 296 5710
 Email: cnae@jgi-psf.org
 Tissue Procurement: Timothy Grammer (Richard M. Harland Laboratory,
 University of California, Berkeley:
 http://tropicalis.berkeley.edu/home)
 cDNA Library Preparation: DOE Joint Genome Institute:
 http://www.jgi.doe.gov
 DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
 Clone Distribution: I.M.A.G.E. Consortium/LNL:
 http://image.llnl.gov
 Naming Conventions: EST name is generated by the concatenation of
 the JGI Clone id and the direction of sequencing. The suffix '.fwd'
 indicates a forward sequencing read of the insert. It does not
 necessarily reflect the orientation of the insert.
 Plate: CAN 0005 row: P column: 14
 High quality sequence stop: 684.
 Location/Qualifiers
 1..749
 /organism="Xenopus tropicalis"
 /mol_type="mRNA"
 /db_xref="taxon:8364"
 /clone="IMAGE:7686784"
 /sex="male"
 /tissue_type="Testes"
 /dev_stage="Adult"
 /lab_host="Electromax DH10B"
 /clone_lib="NIH XGC tropic4"
 /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
 This library was made from dt primed cDNA and cloned into
 Invitrogen pCMVSPORT6 vector. The work was done at DOE
 Joint Genome Institute. Poly A RNA were primed with 5'
 GACTAGTCTTAGATGCGAG CGAGCGCCCTTTTCTTTTCTTTT 3'. cDNA
 were ligated to SalI adapter (5' TCGACCGACGCGTCG and
 5'CGAGCGCGTCG), digested with NotI, size fractionated in
 1.1% agarose gel electrophoresis and ligated into NotI and
 SalI digested pCMVSPORT6 vector."

ORIGIN
 Query Match 71.4%; Score 20; DB 9; Length 749;
 Best Local Similarity 82.1%; Pred. No. 3.9e+03;
 Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Oy 1 GACATTTTGTATGTTTGTATGAAC 28
 |||||
 Db 242 GAATTTTCTTAATATGATGGAAC 269

RESULT 35
 LOCUS C2754866 754 bp DNA linear GSS 26-JUL-2005
 DEFINITION OC_Ba0106B12.f OC_Ba Oryza coarctata genomic clone OC_Ba0106B12
 5', genomic survey sequence.
 ACCESSION C2754866
 VERSION C2754866.1 GI:71194717
 KEYWORDS GSS.
 SOURCE Oryza coarctata (Porteresia coarctata)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BBP

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 754)
Kim.H., Collura,K., Wisotski,M., Byrne,M., Stum,D., Smart,D.,
Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Soderlund,C. and
Wing,R.
OMAP (Oryza Map Alignment Project) - Arizona Genomics Institute
Unpublished (2005)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: twing@genome.arizona.edu
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: GAC TCA TTA GGC ACC CCA
Plate: 0106 row: B column: 12
Seq primer: TAA TAC GAC TCA CTA TAG GG
Class: BAC ends.
Location/Qualifiers
1..754
/organism="Oryza coarctata"
/mol_type="genomic DNA"
/db_xref="taxon:7588"
/clone="OC_Ba0106B12"
/issue_type="leaves"
/dev_stage="mature"
/lab_host="DH10B"
/clone_1lb="OC_Ba"
/note="Vector: pAG1BAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN

Query Match 71.4%; Score 20; DB 13; Length 754;
Best Local Similarity 82.1%; Pred. No. 3.9e+03;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GACATTATGTTATGATTGTATGAAC 28
Db 597 GATATGAGCTTATAGTTGTTGTGATC 624

RESULT 36
DV932465 763 bp mRNA linear EST 01-DEC-2005
LOCUS LB03025_CR_019 GC_BGC-30 Bos taurus cDNA clone IMAGE:8141805, mRNA
DEFINITION sequence.
ACCESSION DV932465
VERSION DV932465.1 GI:82989654
KEYWORDS EST.
SOURCE Bos taurus (cattle)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 763)
Moore,S., Alexander,L., Brownstein,M., Guan,L., Lobo,S., Meng,Y.,
Taneguchi,M., Wang,Z., Yu,J., Prange,C., Schreiber,K., Shennen,C.,
Wagner,L., Bala,M., Barbazuk,S., Barber,S., Babakaiff,R.,
Beland,J., Chun,E., Del Rio,L., Gibson,S., Hanson,R., Scott,J.,
Kirpatrick,R., Liu,J., Matsuo,C., Mayo,M., Santos,R.R., Tsai,J.,
Tsai,M., Wong,D., Siddiqui,A., Holt,R., Jones,S.J. and Marra,M.A.
Bovine Genome Sequencing Program: Full-length cDNA sequencing
Unpublished (2005)
Contact: Robert Kirkpatrick
Canada's Michael Smith Genome Sciences Centre
BC Cancer Agency
Suite 100, 570 West 7th Avenue, Vancouver, British Columbia,
Canada, V5Z 4S6
Tel: 1-604-707-5900 x5406
Fax: 1-604-876-3561
Email: robertk@bcgsc.ca
Insert length: 763 Std Error: 0.00

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Plate: LB03025 row: 0 column: 19
High quality sequence stop: 763.
Location/Qualifiers
1..763
/organism="Bos taurus"
/mol_type="mRNA"
/strain="U1 Hereford"
/db_xref="taxon:9913"
/clone="IMAGE:8141805"
/sex="female"
/issue_type="Muscle"
/dev_stage="6 months old fetus"
/lab_host="E. coli DH10B T1 Phage resistant"
/clone_1lb="GC_BGC-30"
/note="Vector: pEXpress 1; Site_1: blunt (5' end of cDNA);
Site_2: NotI (3' end of cDNA)"

ORIGIN

Query Match 71.4%; Score 20; DB 10; Length 763;
Best Local Similarity 82.1%; Pred. No. 3.9e+03;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GACATTATGTTATGATTGTATGAAC 28
Db 703 GCCATTGTTGTTATGATGATTAAC 730

RESULT 37
CX896534 832 bp mRNA linear EST 04-FEB-2005
LOCUS JGI_CAAM6990.fwd NIH XGC_tropres Xenopus tropicalis cDNA clone
DEFINITION IMAGE:7680909 5', mRNA sequence.
ACCESSION CX896534
VERSION CX896534.1 GI:58635878
KEYWORDS EST.
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 832)
Richardson,P., Lucas,S., Rohsard,D., Dettler,J.C., Ng,D.C.,
Brokstein,P. and Lindquist,E.A.
DOE Joint Genome Institute Xenopus tropicalis EST project
Unpublished (2004)
Other ESTs: JGI CAAM6990.rev
Contact: Lindquist,E.A., Richardson,P.
DOE Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 296 5600
Fax: 925 296 5710
Email: cdna@jgi-psf.org
Tissue Procurement: Timothy Grammer (Richard M. Harland Laboratory,
University of California, Berkeley;
http://tropicalis.berkeley.edu/home)
cDNA Library Preparation: DOE Joint Genome Institute:
http://www.jgi.doe.gov
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
clone Distribution: I.M.A.G.E. Consortium/LNL:
http://image.lnl.gov
Naming Conventions: EST name is generated by the concatenation of
the JGI Clone id and the direction of sequencing. The suffix '.fwd'
indicates a forward sequencing read of the insert. It does not
necessarily reflect the orientation of the insert.
Plate: CAAM 0073 row: k column: 19
High quality sequence stop: 724.
Location/Qualifiers
1..832
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="IMAGE:7680909"
/sex="male"

FEATURES
source

```

/tissue type="Testes"
/lab stage="Adult"
/clone_lib="NIH_XC_cryptes"
/notes="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
This library was made from dt primed cDNA and cloned into
Invitrogen pCMVSPORT6 vector. The work was done at DOE
Joint Genome Institute. Poly A RNA were primed with 5'
GACTAGTCTTAGATCGGAG CGAGCCGCCCTTTTCTTTTCTTTT 3'. cDNA
were ligated to SalI adapter (5' TCGACCCAGCGCTCG and
5'CGAGCGCGTGG), digested with NotI, size fractionated in
1.1% agarose gel electrophoresis and ligated into NotI and
SalI digested pCMVSPORT6 vector."

ORIGIN
Query Match 71.4%; Score 20; DB 9; Length 832;
Best Local Similarity 82.1%; Pred. No. 3.9e+03;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GACATTATGTTAAGTTGTATGGAAC 28
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 637 GAATTATGCTGTAATAGTAGGAAC 664

RESULT 38
LOCUS CG920252 954 bp DNA linear GSS 12-DEC-2003
DEFINITION MBEN064TR mch2 Medicago truncatula genomic clone 10K7, genomic
survey sequence.
ACCESSION CG920252
VERSION CG920252.1 GI:39779935
KEYWORDS GSS.
SOURCE Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
Medicago.
1 (bases 1 to 954)
Town, C.D., Shetty, J., Koo, H. and Feldblum, T. F.
Sequencing of BAC ends from Medicago truncatula
Unpublished (2003)
Other GSSs: MBEN064TF
Contact: Chris Town
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
Seq primer: CAGGAAACAGCTATGACC
Class: BAC ends.
Location/Qualifiers
1..954
/organism="Medicago truncatula"
/mol_type="genomic DNA"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone_lib="10K7"
/clone_libs="mch2"
/notes="Vector: pBeloBAC11; Site 1: HindIII; Site 2:
HindIII; Cook, D.R. and Kim, D.J., unpublished"

ORIGIN
Query Match 71.4%; Score 20; DB 12; Length 954;
Best Local Similarity 82.1%; Pred. No. 3.9e+03;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GACATTATGTTAAGTTGTATGGAAC 28
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 68 GAAGTATTTAATAGTTGTATGGAAC 95

RESULT 39

```

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CF091813/c
LOCUS CF091813 511 bp mRNA linear EST 22-JUN-2003
DEFINITION QHM9H07.yg.ab1 QH M sunflower H. argophyllus Helianthus argophyllus
cDNA clone QHM9H07, mRNA sequence.
ACCESSION CF091813
VERSION CF091813.1 GI:33130880
KEYWORDS EST.
SOURCE Helianthus argophyllus
ORGANISM Helianthus argophyllus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
Heliantheae; Helianthus.
1 (bases 1 to 511)
Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Riesberg, L.,
Lin, H., Van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J.,
Ellison, P., Kolman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,
Lai, Z., Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compositae.ucdavis.edu/
Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Aamundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.edu [michelmoreveg@mail.ucdavis.edu]
belongs to contig QH_CA_contig4705, see http://cspdb.ucdavis.edu/
for details.
Plate: QHM9 row: H column: 07.
Location/Qualifiers
1..511
/organism="Helianthus argophyllus"
/mol_type="mRNA"
/db_xref="taxon:73275"
/clone="QH9H07"
/lab_host="E.coli"
/clone_lib="QH M sunflower H. argophyllus"
/notes="Vector: pRCNBS11ab; The library was constructed
from three different sources (seedling, root and leaf) of
RNA from a single genotype. cDNAs were pooled and
directionally cloned into a custom medium-copy vector.
Details of library construction can be obtained at
http://cspdb.ucdavis.edu/"

ORIGIN
Query Match 70.7%; Score 19.8; DB 5; Length 511;
Best Local Similarity 91.3%; Pred. No. 4.6e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CATTATGTTAATAGTTGTATGG 25
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 306 CAATTATGCTATAGTTGTATGG 284

RESULT 40
LOCUS BZ392066 536 bp DNA linear GSS 30-APR-2003
DEFINITION EINCK17TF BL 10.12 KB Entamoeba invadens genomic clone EINCK17,
genomic survey sequence.
ACCESSION BZ392066
VERSION BZ392066.1 GI:30238603
KEYWORDS GSS.
SOURCE Entamoeba invadens
ORGANISM Entamoeba invadens
Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 536)
Wang, Z., Samuelson, J., Clark, C.G., Eichinger, D., Paul, J., van
Dellen, K., Hall, N., Anderson, I. and Lotz, B.
Gene discovery in the Entamoeba invadens genome
Mol. Biochem. Parasitol. 129 (1), 23-31 (2003)
12798503
FUJMED

```

COMMENT Other_GSSs: EINCK17R
Contact: Brendan Loftus
Department of Eukaryotic Genomics
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: ent@tigr.org
DNA was provided by Daniel Bichinger
Seq primer: TP
Class: sheared ends.

FEATURES
source
1..536
Location/Qualifiers
/organism="Entamoeba invadens"
/mol_type="genomic DNA"
/strain="IP-1"
/db_xref="taxon:33085"
/clone="EINCK17"
/clone_1lb="SI_10_12_KB"
/note="Vector: pHO2; Site 1: BstXI; Total genomic DNA was isolated from early log phase trophozoites of E. invadens IP-1 using a Qiagen plant DNA extraction kit. A shotgun medium-size plasmid library (average insert size of 10-12 kb) was generated by random mechanical shearing of E. invadens genomic DNA, repairing the ends of DNA fragments with T4 polymerase, adding BstXI adaptors and ligating into the BstXI site of a pUC-derived vector pHO2."

ORIGIN
Query Match 70.7%; Score 19.8; DB 11; Length 536;
Best Local Similarity 91.3%; Pred. No. 4.6e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GACATTATGTTAGTTGTAT 23
186 GACATTATGTTATATTGTTT 208

Db 186 GACATTATGTTATATTGTTT 208

RESULT 41
BU026745/c 592 bp mRNA linear EST 23-AUG-2002
LOCUS OHG17014.yg.ab1 QH_EFGHJ sunflower RHA280 Helianthus annuus cDNA
DEFINITION OHG17014.yg.ab1 QH_EFGHJ sunflower RHA280 Helianthus annuus cDNA
VERSION BU026745
KEYWORDS BU026745.1 GI:22462265
SOURCE EST.
ORGANISM Helianthus annuus (common sunflower)
Helianthus annuus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; campanulids; Asterales; Asteraceae; Asteroideae; Helianthaceae; Helianthus.
1 (bases 1 to 592)
Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Riesberg,L., Lin,H., Van Damme,M., Laveille,D., Chevalier,P., Ziegler,J., Ellison,P., Kolman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z., Church,S., Jackson,L. and Bradford,K.
Lecture and Sunflower ESTs from the Compositae Genome Project
http://compogenomics.ucdavis.edu/
unpublished (2002)
Contact: Alexander Kozik (R.W.Michelmore)
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Aamundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.org [michelmore@vegmail.ucdavis.edu]
Singleton, see http://cspdb.ucdavis.edu/ for details.
Plate: OHG17 row: O column: 14.
Location/Qualifiers
1..592
/organism="Helianthus annuus"
/mol_type="mRNA"

FEATURES
source

COMMENT /cultivar="RHA280"
/db_xref="taxon:4232"
/clone="OHG17014"
/lab_host="E.coli"
/clone_1lb="QH_EFGHJ sunflower RHA280"
/note="Vector: pBRCDNA5flAB; The library was constructed from 11 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cspdb.ucdavis.edu/TAG_TISSUE=hu11s
TAG LIB=QH_EFGHJ sunflower RHA280
TAG_SRQ=GCTACTCCGG"

ORIGIN
Query Match 70.7%; Score 19.8; DB 3; Length 592;
Best Local Similarity 91.3%; Pred. No. 4.6e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CATTATGTTATGTTGTATGC 25
419 CAATATGTCATAGTTGTATGG 397

Db 419 CAATATGTCATAGTTGTATGG 397

RESULT 42
DX044921/c 770 bp DNA linear GSS 10-JAN-2006
LOCUS DX044921
DEFINITION KBRB046A24R KBRB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBRB046A24, genomic survey sequence.
VERSION DX044921
KEYWORDS DX044921.1 GI:84739218
SOURCE GSS.
ORGANISM Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 770)
Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M., Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S., Hahn,J.H. and Park,B.S.
End sequence of Brassica rapa BamHI (KBRB) BAC clone
unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.90.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone KBRB046A24
Seq primer: M13 Reverse
Class: BAC ends.
Location/Qualifiers
1..770
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBRB046A24"
/lab_host="E.coli DH10B"
/clone_1lb="KBRB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa ssp. pekinensis var. Chifu BAC library (KBRB BAC) is provided by Yong-Pyo Lim (CNU)."

FEATURES
source

ORIGIN

Query Match 70.7%; Score 19.8; DB 14; Length 770;
 Best Local Similarity 91.3%; Pred. No. 4.6e+03;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACATTATGTTATGATTGATG 24
 |||||
 248 ACATTATGTTATGATTGTTG 226

RESULT 43
 CINS07B84/c
 LOCUS
 DEFINITION T7 end of clone BC0A010A01 of library BC0A from strain CBS 767 of
 Debaryomyces hansenii, genomic survey sequence.
 AL437546
 AL437546.1 GI:12220959
 GSS.
 Debaryomyces hansenii var. hansenii
 Debaryomyces hansenii var. hansenii
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 Saccharomycetales; Saccharomycetaceae; Debaryomyces.
 1 (bases 1 to 998)
 Souciet,J., Aigle,M., Artiguenave,F., Blandin,G.,
 Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S., de
 Montigny,J., Dujon,B., Durrens,P., Galliardin,C., Lepingle,A.,
 Floerente,B., Maupertuy,A., Neuvéglise,C., Ozier-Kalogeropoulos,O.,
 Potier,S., Saurin,W., Tekala,F., Toffano-Nioche,C.,
 Wesolowski-Louvel,M., Wincker,P. and Weissenbach,J.
 Genomic exploration of the hemiascomycetous yeasts: 1. A set of
 yeast species for molecular evolution studies
 FEMS Lett. 487 (1), 3-12 (2000)

JOURNAL 1152876
 2 (bases 1 to 998)
 Lepingle,A., Casaregola,S., Neuvéglise,C., Bon,E., Nguyen,H.,
 Artiguenave,F., Wincker,P. and Galliardin,C.
 Genomic exploration of the hemiascomycetous yeasts: 14.
 Debaryomyces hansenii var. hansenii
 FEMS Lett. 487 (1), 82-86 (2000)
 1152889
 3 (bases 1 to 998)
 Genoscope.
 Direct Submission
 Submitted (08-SEP-2000) Genoscope - Centre National de Séquençage,
 2 rue Gaston Crémieux, CP 5706, 91057 EVRY cedex - FRANCE (E-mail :
 reggie@genoscope.cns.fr - Web : www.genoscope.cns.fr)
 This GSS is part of a random genomic sequencing program of thirteen
 yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
 exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
 Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
 lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
 angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
 Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
 5 kb were prepared and both extremities were sequenced. See
 keywords for description of this sequence and for the sequence of
 the other extremity of this insert.
 Location/Qualifiers
 1..998
 /organism="Debaryomyces hansenii var. hansenii"
 /mol_type="genomic DNA"
 /strain="CBS 767"
 /variety="hansenii"
 /db_xref="taxon:58641"
 /clone="BC0A010A01"
 /clone_1lb="BC0A"
 /note="end : T7"

ORIGIN
 Query Match 70.7%; Score 19.8; DB 14; Length 998;
 Best Local Similarity 91.3%; Pred. No. 4.6e+03;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 TTATGTTATGATTGATGAA 27

Db 764 TTATGTTATGATTGATGAA 742
 |||||
 192 ACATTATGTTATGATTGTTG 170

RESULT 44
 AJ854876/c
 LOCUS
 DEFINITION Brassica rapa subsp. pekinensis GSS, clone KBRH051F18, end read,
 primer M13(forward), genomic survey sequence.
 AJ854876
 AJ854876.1 GI:55651482
 GSS; genome survey sequence.
 KEYWORDS
 SOURCE
 ORGANISM
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 1
 Bancroft,I., Huckle,B.J., Trick,M. and Beckett,P.
 BAC end sequence of Brassica rapa
 Unpublished
 2 (bases 1 to 1268)
 Beckett,P.
 Direct Submission
 Submitted (05-NOV-2004) Beckett P., Computational Biology, John
 Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk, NR4
 7UH, UNITED KINGDOM
 Contact: Ian Bancroft
 John Innes Centre Norwich Research Park, Colney, Norwich, NR4 7UH.
 Tel: +44 1603 450843
 Fax: +44 1603 450021
 Email: ian.bancroft@bbsrc.ac.uk
 BAC End sequence of Brassica rapa BAC clone KBRH051F18 Seq primer:
 M13(forward)
 Class: BAC ends.
 Location/Qualifiers
 1..1268
 /organism="Brassica rapa subsp. pekinensis"
 /mol_type="genomic DNA"
 /cultivar="Chilly"
 /sub_species="pekinensis"
 /db_xref="taxon:51351"
 /clone="KBRH051F18"
 /clone_1lb="Brassica rapa BAC library (KBRH), Vector:
 pCG186cl; Site_1: HindIII"

ORIGIN
 Query Match 70.7%; Score 19.8; DB 14; Length 1268;
 Best Local Similarity 91.3%; Pred. No. 4.7e+03;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACATTATGTTATGATTGATG 24
 |||||
 192 ACATTATGTTATGATTGTTG 170

RESULT 45
 CK928648/c
 LOCUS
 DEFINITION p5mrgcr_004935 Normalized Magnaporthe grisea cDNA pgem-T Easy
 library Magnaporthe grisea cDNA clone p5mrgcr_004935, mRNA
 sequence.
 CK928648
 CK928648.1 GI:45416499
 EST.
 Magnaporthe grisea (anamorph: Pyricularia grisea)
 Magnaporthe grisea
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Sordariomycetes; incertae sedis; Magnaporthaceae; Magnaporthe.
 1 (bases 1 to 170)
 Chen,B., Li,Y., Peng,Y., Dong,H. and Li,D.
 Large-scale identification of ESTs from Magnaporthe grisea by
 normalized cDNA library sequencing

JOURNAL COMMENT
 Unpublished (2004)
 Contact: Baozhan Chen, Youzhi Li
 Laboratory of Subtropical Bioresource Conservation and Utilization
 Guangxi University, China Agricultural University, Zhejiang
 University
 Daxue Road 100#, Nanning, Guangxi, 530004, China
 Tel: 0086-771-3239566
 Fax: 0086-771-3237873
 Email: chenbzh@n-gx.cninfo.net, URL: http://www.estarray.org
 Seq primer: M13 forward primer.

FEATURES
 source
 1..170
 /organism="Magnaporthe grisea"
 /mol_type="mRNA"
 /db_xref="taxon:148305"
 /clone="p5imgcr.004935"
 /csize_type="Myccellium, conidium, germinating conidium, swelling appressorium, mature appressorium, penetration peg"
 /dev_stage="Myccellium, conidium, germinating conidium, swelling appressorium, mature appressorium, penetration peg"
 /clone_1lb="Normalized Magnaporthe grisea cDNA pGEM-T Easy library"
 /note="Vector: pGEM-T Easy"

ORIGIN
 Query Match 70.0%; Score 19.6; DB 5; Length 170;
 Best Local Similarity 84.6%; Pred. No. 5.4e+03;
 Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY
 2 ACATTATGTTATGTTGTTGATGGA 27
 52 ACATTGCTGTTATGTTGTTGATGGA 27

Db

RESULT 46
 LOCUS BI034170 232 bp mRNA linear EST 14-JUN-2001
 DEFINITION PM2-NN0169-190301-006-b03 NN0169 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BI034170
 VERSION BI034170.1 GI:14440796
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 232)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsumura,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 10737800
 Contact: Simpson A.J.C.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-27049922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM2&ct=PM2-NN0169-190301-006-b03&ct3=2001-03-19&ct4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 5

FEATURES
 source
 High quality sequence stop: 231.
 Location/Qualifiers
 1..232
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_1lb="NN0169"
 /note="Organ: nervous normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from OREGRES PCR (U.S. Letters Patent application No.196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN
 Query Match 70.0%; Score 19.6; DB 2; Length 232;
 Best Local Similarity 84.6%; Pred. No. 5.4e+03;
 Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY
 3 CATTATGTTATGTTGTTGATGGA 28
 24 CAGTATGTAATCTGTTATGAC 49

Db

RESULT 47
 LOCUS DV017521 297 bp mRNA linear EST 23-SEP-2005
 DEFINITION Zp-e5 Lku Zmimia elegans cDNA clone Zp-e5, mRNA sequence.
 ACCESSION DV017521
 VERSION DV017521.1 GI:76151574
 KEYWORDS EST.
 SOURCE Zmimia elegans
 ORGANISM Zmimia elegans
 Zmimia elegans
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; campanulids; Asterales; Asteraceae; Asteroideae; Heliantheae; Zimnia.
 1 (bases 1 to 297)
 Pasquet,B., Ranocha,P., Legay,S., Digonnet,C., Barbier,O., Pichon,M. and Goffner,D.
 Novel markers of xylogenesis in zmimia are differentially regulated by auxin and cytokinin
 Plant Physiol. 139 (4), 1821-1839 (2005)
 16306148
 Contact: Deborah Goffner
 Differenciation du xyleme : Signaux cellulaires et dynamique parietale
 UR 5546 CNRS/Universite Paul Sabatier Surfaces cellulaires et signalisations chez les vegetaux
 Pile de Biotechnologies Vegetales, 24, chemin de Borde Rouge, B.P. 17 Auserville, 31326 CASTANET-TOLOSAN, FRANCE
 Tel: 33 5 62 19 35 23
 Fax: 33 5 62 19 35 02
 Email: goffner@cecy.ups-clse.fr
 EST from differentiating TE SSH library - dehydration-induced protein RD22 - singulet
 PCR Primers
 FORWARD: TCGAGCGCGCCGCCGCGAGT
 BACKWARD: AGCGTGTGCGCGCGAGT
 Insert Length: 297 Std Error: 0.00
 Plate: 2p row: e column: 05
 Seq primer: M13-reverse
 POLYA=No.
 Location/Qualifiers
 1..297
 /organism="Zmimia elegans"
 /mol_type="mRNA"
 /cultiar="Bany"
 /db_xref="taxon:34245"
 /clone="Zp-e5"
 /cell_type="TE differentiating cell cultures"

/dev stage="Late TE differentiation processes (48, 60 and 72h of culture in NAA+BAP medium)"
 /lab_host="B.coli DH5alpha"
 /clone_id="LXL"
 /note="Vector: pGEM-T; Site 1: SalI; Site 2: NdeI; LXL (Late Xylogenesis Library). SSH (suppression subtractive hybridization) library made with tester sample comprising pooled RNA from 48, 60 and 72h of cell culture in differentiation medium (supplemented with auxin NAA and cytokinin BAP) and driver sample comprising pooled RNA from 0h of culture and 48, 60 and 72h in control conditions (with NAA only, with BAP only and with no hormone)"

ORIGIN

Query Match 70.0%; Score 19.6; DB 10; Length 297;
 Best Local Similarity 84.6%; Pred. No. 5.4e+03;
 Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACATTATGTTATGTTGATGGA 27
 |||||
 Db 204 ACATCATGTTATGTTATGGA 179

RESULT 48
 CK553998/c 299 bp mRNA linear EST 05-OCT-2004
 LOCUS rsw1a0_015679.y1 sw1 Bombyx mori cDNA, mRNA sequence.
 ACCESSION CK553998
 VERSION CK553998.1 GI:40938452
 KEYWORDS EST.

SOURCE Bombyx mori (domestic silkworm)
 ORGANISM Bombyx mori

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pelegrypota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea; Bombycidae; Bombyx.

REFERENCE

1 (bases 1 to 299)

Xia, Q., Zhou, Z., Lu, C., Cheng, D., Dai, F., Li, B., Zhao, P., Zha, X., Cheng, T., Chai, C., Pan, G., Xu, J., Liu, C., Lin, Y., Qian, J., Hou, Y., Wu, Z., Li, G., Pan, M., Li, C., Shen, Y., Lan, X., Yuan, L., Li, T., Yu, H., Yang, G., Wan, Y., Zhu, Y., Yu, M., Shen, W., Wu, D., Xiang, Z., Yu, J., Wang, J., Li, R. Q., Shi, J. P., Li, H., Li, G. Y., Su, J. N., Wang, X. L., Li, G. Q., Zhang, Z. J., Wu, Q. F., Li, J., Zhang, Q. P., Wei, N., Xu, J. Z., Sun, H. B., Dong, L., Liu, D. Y., Zhao, S. L., Zhao, X. L., Meng, Q. S., Lan, F. D., Huang, X. G., Li, Y. Z., Fang, F., Li, C. F., Li, D. W., Sun, Y. Q., Zhang, Z. P., Yang, Z., Huang, Y. Q., Xi, Y., Qi, Q. H., He, D. D., Huang, H. Y., Zhang, X. W., Wang, Z. Q., Li, W. J., Cao, Y. Z., Yu, Y., Yu, H., Ji, H., Ye, J., Chen, H., Zhou, Y., Liu, B., Wang, J., Ye, J., Li, H., Li, S., Ni, P., Zhang, J., Zhang, Y., Zheng, H., Mao, B., Mao, B., Ye, C., Li, S., Wang, J., Wong, G. K. and Yang, H.

A draft sequence for the genome of the domesticated silkworm (Bombyx mori)

Science 306 (5703), 1937-1940 (2004)

JOURNAL PUBMED COMMENT

Contact: Zhonghui Xiang
 Southwest Agricultural University
 Chongqing Beibei
 Tel: 86-23-68251123
 Fax: 86-23-68251128
 Email: xzh@swau.cq.cn.

FEATURES

Location/Qualifiers
 1..299
 /organism="Bombyx mori"
 /mol_type="mRNA"
 /strain="Dazhao(P50)"
 /db_xref="taxon:7091"
 /sex="mixed"
 /tissue_type="fat body (pupa)"
 /dev_stage="p0"
 /clone_id="sw1"
 /note="Vector: pBlueScript II SK(+)"

ORIGIN

Query Match 70.0%; Score 19.6; DB 5; Length 299;
 Best Local Similarity 84.6%; Pred. No. 5.4e+03;
 Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACATTATGTTATGTTGATGGA 27
 |||||
 Db 100 ACATTATGTTACGTTTTCGGGA 75

RESULT 49
 BJ724011 305 bp mRNA linear EST 09-MAR-2004
 LOCUS BJ724011 MF01FPA cDNA Oryzias latipes cDNA clone MF01FPA031d06 3', mRNA sequence.
 DEFINITION BJ724011.1 GI:45265103
 ACCESSION BJ724011.1
 VERSION BJ724011.1
 KEYWORDS EST.
 SOURCE Oryzias latipes (Japanese medaka)
 ORGANISM Oryzias latipes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Perciformes; Atherinomorpha; Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.

1 (bases 1 to 305)

Kohara, Y., Shin-I, T., Kimura, T., Narita, T., Jindo, T. and Takeda, H. Medaka EST Project in Takeda's lab

Unpublished (2001)
 Contact: Tadashi Shin-I
 Center For Genetic Resource Information
 National Institute of Genetics
 111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6855
 Fax: 81-559-81-6855
 Email: tshin@genes.nig.ac.jp.

Location/Qualifiers

FEATURES

1..305
 /organism="Oryzias latipes"
 /mol_type="mRNA"
 /strains="Hyd-R"
 /db_xref="taxon:8090"
 /clone="MF01FPA031d06"
 /sex="mixture of female and male"
 /tissue_type="whole embryo"
 /dev_stage="fry stage 40"
 /clone_id="MF01FPA cDNA"

ORIGIN

Query Match 70.0%; Score 19.6; DB 2; Length 305;
 Best Local Similarity 81.5%; Pred. No. 5.4e+03;
 Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ACATTATGTTATGTTGATGGAAC 28
 |||||
 Db 6 ACATTCTGCATGTTGATGGAAC 32

RESULT 50
 BM857946 340 bp mRNA linear EST 07-MAR-2002
 LOCUS BM857946
 DEFINITION f417a03.y1 zebrafish sjd day 3 embryo Danio rerio cDNA clone IMAGE:5620108 5', mRNA sequence.
 ACCESSION BM857946
 VERSION BM857946.1 GI:19225628
 KEYWORDS EST.

SOURCE Danio rerio (zebrafish)
 ORGANISM Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 340)

Clark, M., Johnson, S. L., Lehrach, H., Lee, R., Li, F., Narita, M., Bddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Stepec, M., Theising, B., Allen, M., Bowers, Y.,

TITLE
JOURNAL
COMMENT

Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurr, R.,
Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Waterson, R. and Wilson, R.
Washu Zebrafish EST Project 1998
Unpublished (1998)
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrfish@watson.wustl.edu
cDNA library construction by: Joe Barnes and Steve Johnson. DNA
Sequencing by: Washington University Genome Sequencing Center Clone
distribution: ResourceCenter/PrimateDatabase, Berlin, Germany
(web address: www.rzpd.de)
zebrfish1998 (p-value greater than 1e-99) found to:
g134612921gb|AI105787|AI105787 db03d09_p1 zF adult heart library
Danio rerio
Seq primer: T3 ET from Amersham
High quality sequence, stop: 318.

ORIGIN

Query Match	70.0%	Score 19.6	DB 3	Length 340
Best Local Similarity	81.5%	Pred. No. 5	4e-03	
Matches	22	Conservative	0	Mismatches 5, Indels 0, Gaps 0
Qy	1	GACATTAATGTTATAGTTGATATGAA	27	
Db	22	GACCTTTTGTGTAATAGTTATATGAA	48	

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 24, 2006, 05:34:58 ; Search time 342.899 Seconds
(without alignments)
650.664 Million cell updates/sec

Title: us-10-601-913-121

Perfect score: 32
Sequence: 1 TTATTAATAGTGCCTCGCGGTGCCAGAAACC 32

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

N_Geneseq.8:*
1: geneseqn1980s:*
2: geneseqn1980s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description
C	1	100.0	32	2	AAT72389			Aact72389 Human Pap
	2	100.0	32	2	AAT72397			Aact72397 Human Pap
	3	100.0	32	2	AAT72398			Aact72398 Human Pap
C	4	100.0	32	2	AAT72390			Aact72390 Human Pap
	5	100.0	476	2	AAQ97848			Aag97848 HPV-18 E6
	6	100.0	476	2	AAZ27568			Aaz27568 HPV-18 E6
	7	100.0	476	3	AA661623			Aa661623 CDNA enco
	8	100.0	477	10	AAU54443			Aal54443 HPV18 E6
	9	100.0	477	14	AD044101			Ad044101 Nucleotid
	10	100.0	483	2	AAO75471			Aea51111 Human pap
	11	100.0	477	14	AEA51111			Aea51111 HPV18 B6/
	12	100.0	802	1	AAN91786			Aan91786 DNA probe
	13	100.0	817	2	AAQ29390			Aag29390 DNA enco
	14	100.0	837	2	AAK78800			Aak78800 HPV fusio
	15	100.0	837	14	AAZ29789			Aaz29789 Pict. DI/3
	16	100.0	843	14	AED52652			Aed52652 Fusion pr
	17	100.0	843	14	ADV85648			Adv85648 Human pap
	18	100.0	1000	2	AAQ08623			Aaq08623 HPV-18 tr

19	32	100.0	1152	2	AAK78801			Aax78801 HPV fusio
20	32	100.0	1152	2	Aax29790			Aax29790 Pict. DI/3
21	32	100.0	1152	14	AED52656			Aed52656 Fusion pr
22	32	100.0	1731	1	AAN80161			Aan80161 Human pap
23	32	100.0	7857	12	AD245648			Ad245648 Human pap
24	30.4	95.0	477	14	AD044106			Ad044106 Nucleotid
25	24	75.0	477	12	AD044105			Ad044105 Nucleotid
26	24	75.0	477	12	AD044112			Ad044112 Nucleotid
27	24	75.0	1095	2	AAZ31781			Aaz31781 HPV68 DNA
28	24	75.0	1108	2	AAZ31783			Aaz31783 HPV68 E6
29	24	75.0	3283	2	AAZ31789			Aaz31789 HPV70 DNA
30	24	75.0	7833	2	AAQ25937			Aaq25937 Human pap
31	24	75.0	7905	14	AD245655			Ad245655 Human pap
32	23.8	74.4	630	6	ABK62613			Abk62613 Rat seque
33	23.8	74.4	630	6	ABK62613			Abk62613 Rat seque
34	23.8	74.4	885	4	AAZ31789			Aaz31789 HPV70 DNA
35	23.8	74.4	885	4	AAZ31789			Aaz31789 HPV70 DNA
36	23.2	72.5	40	2	AAT71196			Aat71196 HPV type
37	23	71.9	30	2	AAQ44290			Aaq44290 Sequence
38	23	71.9	30	2	AAZ07822			Aaz07822 Oligo 2PV
39	23	71.9	30	14	ADZ64772			Adz64772 HPV 18 E6
40	22.6	70.6	167	5	ABV07997			Abv07997 Human pro
41	22.2	69.4	159	12	ACH89313			Ach89313 Human gen
42	22.2	69.4	297	5	AAZ78228			Aaz78228 DNA enco
43	22.2	69.4	421	8	ABX40477			Abx40477 Bovine ES
44	22.2	69.4	460	4	AAI10129			Aai10129 Probe #62
45	22.2	69.4	460	4	ABAS1759			Abas1759 Human foe
46	22.2	69.4	460	4	AAI31375			Aai31375 Probe #61
47	22.2	69.4	460	4	ABA21587			Ab21587 Probe #53
48	22.2	69.4	460	4	AAK25505			Aak25505 Human bon
49	22.2	69.4	460	4	AAK00066			Aak00066 Human bra
50	22.2	69.4	460	4	ABZ52073			Abz52073 Human liv
51	22.2	69.4	460	5	AAI00070			Aai00070 Probe #61
52	22.2	69.4	460	6	ABS00071			Abs00071 Human gen
53	22.2	69.4	581	14	AE814480			Aee14480 Hamster S
54	22.2	69.4	581	14	AE810838			Aee10838 Hamster c
55	22.2	69.4	593	12	ACH75587			Ach75587 Human gen
56	22.2	69.4	659	4	AAZ31155			Aaz31155 Human dia
57	22.2	69.4	750	4	AAI19425			Aai19425 Probe #93
58	22.2	69.4	750	4	ABA64438			Ab64438 Human foe
59	22.2	69.4	750	4	AAI44613			Aai44613 Probe #13
60	22.2	69.4	750	4	ABA46575			Ab446575 Human bre
61	22.2	69.4	750	4	ABA31574			Ab31574 Probe #10
62	22.2	69.4	750	4	AAK38624			Aak38624 Human bon
63	22.2	69.4	750	4	AAK12895			Aak12895 Human bra
64	22.2	69.4	750	4	ABES38189			Abes38189 Human liv
65	22.2	69.4	750	5	AAI05150			Aai05150 Probe #51
66	22.2	69.4	750	6	ABS12691			Abs12691 Human gen
67	22.2	69.4	828	13	ACN38704			Acn38704 Tumour-as
68	22.2	69.4	925	6	ABN74633			Abn74633 Bovine em
69	22.2	69.4	925	6	ABN74632			Abn74632 Bovine em
70	22.2	69.4	1023	5	ABV25873			Abv25873 Human pro
71	22.2	69.4	1023	5	ABV25550			Abv25550 Human pro
72	22.2	69.4	1023	5	ABV25127			Abv25127 Human pro
73	22.2	69.4	1023	5	ABV22488			Abv22488 Human pro
74	22.2	69.4	1023	5	ABV24989			Abv24989 Human pro
75	22.2	69.4	1023	5	ABV28303			Abv28303 Human pro
76	22.2	69.4	1023	5	ABV25223			Abv25223 Human pro
77	22.2	69.4	38703	14	AED83346			Aed83346 Human cos
78	22.2	69.4	55008	4	AAK80495			Aak80495 Human imm
79	22.2	69.4	154702	8	ACF62730			Acf62730 Cancer ba
80	22.2	69.4	154702	8	ADB20845			Adb20845 MRP1 base
81	22.2	69.4	154702	10	ADB87934			Adb87934 Human UGT
82	22.2	69.4	154702	10	ADB86917			Adb86917 Human MDR
83	22.2	69.4	164702	10	ADB82108			Adb82108 Human MDR
84	22.2	69.4	231222	10	ADL13693			Adl13693 Osteoarth
85	22	68.8	51	10	ADD36630			Add36630 Human pap
C	86	22	51	10	ADD22208			Add22208 HPV B6 ge
	87	66.9	410	9	ACH50121			Ach50121 Human leu
	88	66.2	123	4	AAI26856			Aai26856 Probe #16
	89	66.2	123	4	ABA75108			Ab75108 Human foe
	90	66.2	123	4	AAI55647			Aai55647 Probe #24
	91	66.2	123	4	ABA39789			Ab39789 Probe #18

C 968	17	53.1	170469	13	ABD33314	Abd33314 Human can
C 969	17	53.1	170506	14	ADZ13520	Adz13520 Human can
C 970	17	53.1	176594	13	ABD33387	Abd33387 Murine ca
C 971	17	53.1	180000	15	AER49487	Aer49487 Marfians'
C 972	17	53.1	180000	15	AER49487	Aer49487 Marfians'
C 973	16.8	52.5	180000	13	AER49487	Aer49487 Marfians'
C 974	16.8	52.5	180000	13	ADM14220	Adm14220 Human bas
C 975	16.8	52.5	180000	13	AAA69132	Aaa69132 Bacterioph
C 976	16.8	52.5	180000	13	ADSG67083	Adsg67083 Corn seed
C 977	16.8	52.5	180000	13	AAG68668	Aag68668 Human ant
C 978	16.8	52.5	180000	13	ACA93325	Aca93325 Recombina
C 979	16.8	52.5	180000	13	ACDA5332	Acda5332 Anti-Rh(D
C 980	16.8	52.5	180000	13	AEE74495	Aee74495 Anti-Rh(D
C 981	16.8	52.5	180000	13	AA503518	Aa503518 DNA encod
C 982	16.8	52.5	180000	13	AHA42399	Aha42399 Nucleotid
C 983	16.8	52.5	180000	13	ACH23299	Ach23299 Human adu
C 984	16.8	52.5	180000	13	ABV56062	Abv56062 Human pro
C 985	16.8	52.5	180000	13	ABK62800	Abk62800 Rat seque
C 986	16.8	52.5	180000	13	ACN45597	Acn45597 Cotton pr
C 987	16.8	52.5	180000	13	ADN74362	Adn74362 Thale cre
C 988	16.8	52.5	180000	13	ADT18740	Adt18740 Plant cDN
C 989	16.8	52.5	180000	13	ADR41251	Adr41251 Human CD-
C 990	16.8	52.5	180000	13	AAZ65342	Aaz65342 Human sec
C 991	16.8	52.5	180000	13	ACC50506	Acc50506 Human sec
C 992	16.8	52.5	180000	13	ABZ71280	Abz71280 Secreted
C 993	16.8	52.5	180000	13	ADB91186	Adb91186 Human sec
C 994	16.8	52.5	180000	13	ADC73566	Adc73566 Human sec
C 995	16.8	52.5	180000	13	ADR11731	Adr11731 E. faeciu
C 996	16.8	52.5	180000	13	ADC90401	Adc90401 E. faeciu
C 997	16.8	52.5	180000	13	AED12469	Aed12469 Anti-Nogo
C 998	16.8	52.5	180000	13	ADG30518	Adg30518 Human GMB
C 999	16.8	52.5	180000	13	AED12432	Aed12432 Anti-Nogo
C1000	16.8	52.5	180000	13	AB877115	Ab877115 Frog embr
					AED12478	Aed12478 Anti-Nogo

ALIGNMENTS

RESULT 1
AAT72389/c
AAT72389 standard; DNA; 32 BP.

AC AAT72389;
AT 09-FEB-1998 (first entry)
DE Human Papillomavirus Type 18 target region.
KW Human Papillomavirus; probe; target region; genital cancer; HPV;
KW cervical smear; ss.
OS Human papillomavirus.
PN EP774518-A2.
PD 21-MAY-1997.
PF 15-NOV-1996; 96EP-00308264.
PR 15-NOV-1995; 95US-0006854P.
PA (GENP-) GEN-PROBE INC.
PI Gordon P, Brentano ST, Carter NM, Hammond PW;
PI WPI; 1997-274349/25.
PT Probes for detection of Human Papillomavirus Type 16 and Type 18 - can
PT distinguish between Type 16 and 18, associated with genital cancers.
PS Claim 16; Page 61; 70pp; English.
CC Novel hybridisation assay probes have been developed comprising an

CC oligonucleotide which will hybridise under selected conditions to Human
CC Papillomavirus (HPV) Type 16 and/or 18 (but not Types 6, 11, 31, 33, 35,
CC 39, 45, 51, 52, or 58) target nucleic acids to form detectable target;
CC probe duplex. The present sequence represents a specifically claimed
CC target sequence. Oligonucleotides are useful to detect HPV Type 16 and/
CC or 18 in samples e.g. cervical smears, body fluid, and distinguish these
CC from other HPV variants. Papillomaviruses are small DNA viruses and HPV
CC Types 16 and 18 are associated with genital cancers. HPV PCR primers can
CC amplify HPV Type 16 and/or 18 nucleic acid in a sample. HPV Type 16
CC and/or 18 can be detected by adding a probe and detecting probe:target
CC duplex formation; target nucleic acid is optionally amplified. Type 16 or
CC 18 can be specifically detected by amplifying nucleic acids with at least
CC one specifically claimed PCR primer. For Type 18 detection, a helper
CC probe may be used. Oligonucleotides can distinguish target sequences from
CC phylogenetically close HPV Types 16 and 18 whilst available detection
CC sera react with antigens of all papillomaviruses

CC Sequence 32 BP; 8 A; 8 C; 7 G; 9 T; 0 U; 0 Other;

Query Match 100.0%; Score 32; DB 2; Length 32;

Best local Similarity 100.0%; Pred. No. 9.2e-05; Mismatches 0; Indels 0; Gaps 0;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTATTATTAAGTGGCTGCGGTCCGAAACC 32
32 TTATTATTAAGTGGCTGCGGTCCGAAACC 1

RESULT 2
AAT72397
AAT72397 standard; DNA; 32 BP.

AC AAT72397;
AT 09-FEB-1998 (first entry)
DE Human Papillomavirus Type 18 helper probe.
KW Human Papillomavirus; probe; target region; genital cancer; HPV;
KW cervical smear; ss.
OS Synthetic.
PN EP774518-A2.
PD 21-MAY-1997.
PF 15-NOV-1996; 96EP-00308264.
PR 15-NOV-1995; 95US-0006854P.
PA (GENP-) GEN-PROBE INC.
PI Gordon P, Brentano ST, Carter NM, Hammond PW;
PI WPI; 1997-274349/25.
PT Probes for detection of Human Papillomavirus Type 16 and Type 18 - can
PT distinguish between Type 16 and 18, associated with genital cancers.
PS Claim 20; Page 60; 70pp; English.
CC Novel hybridisation assay probes have been developed comprising an
CC oligonucleotide which will hybridise under selected conditions to Human
CC Papillomavirus (HPV) Type 16 and/or 18 (but not Types 6, 11, 31, 33, 35,
CC 39, 45, 51, 52, or 58) target nucleic acids to form detectable target;
CC probe duplex. The present sequence represents a specifically claimed
CC target sequence. Oligonucleotides are useful to detect HPV Type 16 and/
CC or 18 in samples e.g. cervical smears, body fluid, and distinguish these
CC from other HPV variants. Papillomaviruses are small DNA viruses and HPV
CC Types 16 and 18 are associated with genital cancers. HPV PCR primers can
CC amplify HPV Type 16 and/or 18 nucleic acid in a sample. HPV Type 16

CC and/or 18 can be detected by adding a probe and detecting probe:target
CC duplex formation; target nucleic acid is optionally amplified. Type 16 or
CC 18 can be specifically detected by amplifying nucleic acids with at least
CC one specifically claimed PCR primer. For Type 18 detection, a helper
CC probe may be used. Oligonucleotides can distinguish target sequences from
CC phylogenetically close HPV Types 16 and 18 whilst available detection
CC sera react with antigens of all papillomaviruses
XX
SQ Sequence 32 BP; 9 A; 7 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 32; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 9.2e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DQ 1 TTATTAATAGTGCTGCGTCCAGAAACC 32
1 TTATTAATAGTGCTGCGTCCAGAAACC 32

RESULT 3
AAT72398
ID AAT72398 standard; RNA; 32 BP.
XX AAT72398;
XX
DT 09-FEB-1998 (first entry)
XX
DE Human Papillomavirus Type 18 helper probe.
XX Human Papillomavirus; probe; target region; genital cancer; HPV;
KM cervical smear; ss.
XX
OS Synthetic.
OS Human papillomavirus.
XX
PN EP74518-A2.
XX
PD 21-MAY-1997.
XX
PF 15-NOV-1996; 96BP-00308264.
XX
PR 15-NOV-1995; 95US-0006854P.
XX
PA (GENP-) GEN-PROBE INC.
PI Gordon P, Brentano ST, Carter NM, Hammond PW;
XX
DR WPI; 1997-274349/25.
XX
PT Probes for detection of Human Papillomavirus Type 16 and Type 18 - can
PT distinguish between Type 16 and 18, associated with genital cancers.
XX
PS Claim 20; Page 61; 70pp; English.
XX
CC Novel hybridisation assay probes have been developed comprising an
CC oligonucleotide which will hybridise under selected conditions to Human
CC Papillomavirus (HPV) Type 16 and/or 18 (but not Types 6, 11, 31, 33, 35,
CC 39, 45, 51, 52, or 58) target nucleic acids to form detectable target;
CC probe duplex. The present sequence represents a specifically claimed
CC helper probe. Oligonucleotides are useful to detect HPV Type 16 and/or
CC 18 in samples e.g. cervical smears, body fluid, and distinguish these
CC from other HPV variants. Papillomaviruses are small DNA viruses and HPV
CC Types 16 and 18 are associated with genital cancers. HPV PCR primers can
CC amplify HPV Type 16 and/or 18 nucleic acid in a sample. HPV Type 16
CC and/or 18 can be detected by adding a probe and detecting probe:target
CC duplex formation; target nucleic acid is optionally amplified. Type 16 or
CC 18 can be specifically detected by amplifying nucleic acids with at least
CC one specifically claimed PCR primer. For Type 18 detection, a helper
CC probe may be used. Oligonucleotides can distinguish target sequences from
CC phylogenetically close HPV Types 16 and 18 whilst available detection
CC sera react with antigens of all papillomaviruses
XX
SQ Sequence 32 BP; 9 A; 7 C; 8 G; 0 T; 8 U; 0 Other;

Query Match 100.0%; Score 32; DB 2; Length 32;
Best Local Similarity 75.0%; Pred. No. 9.2e-05;
Matches 24; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

DQ 1 TTATTAATAGTGCTGCGTCCAGAAACC 32
1 UUAUUAUAAAGUGCGTCCGUGCCAGAAACC 32

RESULT 4
AAT72390/C
ID AAT72390 standard; RNA; 32 BP.
XX
AC AAT72390;
XX
DT 09-FEB-1998 (first entry)
XX
DE Human Papillomavirus Type 18 target region.
XX
KM Human Papillomavirus; probe; target region; genital cancer; HPV;
KM cervical smear; ss.
XX
OS Human papillomavirus.
XX
PN EP74518-A2.
XX
PD 21-MAY-1997.
XX
PF 15-NOV-1996; 96BP-00308264.
XX
PR 15-NOV-1995; 95US-0006854P.
XX
PA (GENP-) GEN-PROBE INC.
PI Gordon P, Brentano ST, Carter NM, Hammond PW;
XX
DR WPI; 1997-274349/25.
XX
PT Probes for detection of Human Papillomavirus Type 16 and Type 18 - can
PT distinguish between Type 16 and 18, associated with genital cancers.
XX
PS Claim 16; Page 61; 70pp; English.
XX
CC Novel hybridisation assay probes have been developed comprising an
CC oligonucleotide which will hybridise under selected conditions to Human
CC Papillomavirus (HPV) Type 16 and/or 18 (but not Types 6, 11, 31, 33, 35,
CC 39, 45, 51, 52, or 58) target nucleic acids to form detectable target;
CC probe duplex. The present sequence represents a specifically claimed
CC target sequence. Oligonucleotides are useful to detect HPV Type 16 and/
CC or 18 in samples e.g. cervical smears, body fluid, and distinguish these
CC from other HPV variants. Papillomaviruses are small DNA viruses and HPV
CC Types 16 and 18 are associated with genital cancers. HPV PCR primers can
CC amplify HPV Type 16 and/or 18 nucleic acid in a sample. HPV Type 16
CC and/or 18 can be detected by adding a probe and detecting probe:target
CC duplex formation; target nucleic acid is optionally amplified. Type 16 or
CC 18 can be specifically detected by amplifying nucleic acids with at least
CC one specifically claimed PCR primer. For Type 18 detection, a helper
CC probe may be used. Oligonucleotides can distinguish target sequences from
CC phylogenetically close HPV Types 16 and 18 whilst available detection
CC sera react with antigens of all papillomaviruses
XX
SQ Sequence 32 BP; 8 A; 8 C; 7 G; 0 T; 9 U; 0 Other;

Query Match 100.0%; Score 32; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 9.2e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DQ 1 TTATTAATAGTGCTGCGTCCAGAAACC 32
32 TTATTAATAGTGCTGCGTCCAGAAACC 1

```

RESULT 5
ID AAQ97848 standard; cDNA; 476 BP.
XX
AC AAQ97848;
XX
DT 25-MAR-2003 (revised)
XX
DT 06-DEC-1995 (first entry)
XX
DE HPV-18 E6 cDNA.
XX
KM Ubiquitin-conjugating enzyme; HPV-18 E6 protein; cell cycle;
KM cell proliferation; cancer; psoriasis; fibrosis; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..477
FT /tag= a
XX
XX MO9518974-A2.
XX
XX 13-JUL-1995.
XX
XX 04-JAN-1995; 95MO-US000164.
XX
XX 04-JAN-1994; 94US-00176937.
XX 23-MAY-1994; 94US-00247904.
XX 27-MAY-1994; 94US-00250795.
XX 13-SEP-1994; 94US-00305520.
XX
XX (MITO-) MITOTIX INC.
XX
XX Draetta G, Rolfe M, Eckstein JM, Cottarel G, Gyuris J;
XX
XX WPI, 1995-255137/33.
XX
XX P-PSDB; AAY9656.
XX
XX Identifying inhibitors of ubiquitin mediated proteolysis of cell cycle
XX regulatory proteins - also new ubiquitin conjugating enzymes, their
XX related nucleic acid, vectors, antibodies etc., useful for regulating
XX e.g. cell proliferation.
XX
XX Disclosure; Page 100-101; 157p; English.
XX
XX HPV-18 E6 cDNA (given in AAQ97848) was amplified from a HeLa cell cDNA
XX library using the primers given in AAQ97846-47. The gene was subcloned
XX into a baculovirus vector for expression of recombinant E6 in Sf9 insect
XX cells for use as a component of an in vitro ubiquitin conjugating system.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 476 BP; 163 A; 95 C; 100 G; 118 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 32; DB 2; Length 476;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 TTATTAATAAGTGCTGCGTCCAGAAACC 32
XX ||||||||||||||||||||||||||||
XX Db 301 TTATTAATAAGTGCTGCGTCCAGAAACC 332
XX
RESULT 6
ID AA227568 standard; cDNA; 476 BP.
XX
AC AA227568;
XX
DT 15-DEC-1999 (first entry)
XX
DE HPV-18 E6 coding sequence.
XX
KM Ubiquitin conjugating enzyme; UbCE, ubiquitin-mediated proteolysis;

```

```

KM cell-cycle regulatory protein; ubiquitination inhibitor; atherosclerosis;
KM proliferative disorder; cancer; restenosis; tissue connective disorder;
KM wound healing; fibrosis; cancer; rheumatoid arthritis; scleroderma;
KM insulin dependent diabetes mellitus; glomerulonephritis; cirrhosis;
KM diagnosis; therapy; E6; ds.
XX
XX Human papillomavirus.
XX
XX US9568761-A.
XX
XX 19-OCT-1999.
XX
XX 07-JUN-1995; 95US-00486663.
XX
XX 04-JAN-1994; 94US-00176937.
XX 23-MAY-1994; 94US-00247904.
XX 27-MAY-1994; 94US-00250795.
XX 13-SEP-1994; 94US-00305520.
XX
XX (MITO-) MITOTIX INC.
XX
XX Chiu MI, Cottarel G, Berlin V, Damagnez V, Draetta G, Rolfe M;
XX
XX WPI, 1999-590402/50.
XX
XX P-PSDB; AAY39568.
XX
XX Identifying ubiquitination inhibitors using novel ubiquitin conjugating
XX enzymes.
XX
XX Example 2; Col 89-92; 61pp; English.
XX
XX This sequence encodes the human papillomavirus E6 protein. The invention
XX relates to assays for identifying an inhibitor of ubiquitin-mediated
XX proteolysis of a cell-cycle regulatory protein comprising contacting a
XX candidate agent with an ubiquitin-conjugating system and measuring the
XX level of ubiquitination. The ubiquitin-conjugating system comprises: (a)
XX a reconstituted protein mixture including a ubiquitin conjugating enzyme
XX (UbCE) produced by the expression of a nucleic acid which hybridizes
XX under high stringency conditions to human UbCE, Candida albicans UbCE, or
XX Schizosaccharomyces pombe UbCE coding sequences; (b) a regulatory protein
XX ; and (c) ubiquitin. The polynucleotides are useful for identifying
XX ubiquitination inhibitors. The polynucleotides are useful for identifying
XX compounds and antibodies against them may also be useful for the
XX treatment and/or diagnosis of proliferative disorders (e.g. cancer,
XX atherosclerosis, or restenosis), tissue connective disorders, controlling
XX wound healing, and disorders characterized by fibrosis (e.g. rheumatoid
XX arthritis, insulin dependent diabetes mellitus, glomerulonephritis,
XX cirrhosis, and scleroderma)
XX
SQ Sequence 476 BP; 163 A; 95 C; 100 G; 118 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 32; DB 2; Length 476;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 TTATTAATAAGTGCTGCGTCCAGAAACC 32
XX ||||||||||||||||||||||||||||
XX Db 301 TTATTAATAAGTGCTGCGTCCAGAAACC 332
XX
RESULT 7
ID AAA61623 standard; cDNA; 476 BP.
XX
AC AAA61623;
XX
DT 15-SEP-2003 (revised)
XX
DT 23-OCT-2000 (first entry)
XX
DE cDNA encoding HPV-18 E6 protein.
XX
KM HPV-18 E6; ubiquitin mediated proteolysis; cellular protein half life;
KM ubiquitination inhibitor; p53; cyclin; cell cycle regulator;

```

KM	myc deregulation; human papillomavirus; HPV-18 E6 protein;
KW	cervical cancer; skin cancer; epidermal hyperplasia; epidermal neoplasia;
KW	papillaris; connective tissue disorder; wound healing; cytostatic;
KX	antiproliferative; anticancer; antipsoriatic; ss.
OS	Human papillomavirus; 18.
XX	
FT	Key Location/Qualifiers
FT	1..474
FT	/tag= a
FT	/partial
FT	/product= "HPV-18 E6 protein"
FT	/note= "No stop codon given in the specification"
PN	US606982-A.
PD	
PD	30-MAY-2000.
XX	
PF	17-DEC-1996; 96US-00767942.
XX	
PR	04-JAN-1994; 94US-00176937.
PR	23-MAY-1994; 94US-00242904.
PR	27-MAY-1994; 94US-00250795.
PR	13-SEP-1994; 94US-00305520.
PR	07-JUN-1995; 95US-00486663.
PA	(MITO-) MITOTIX INC.
XI	
P1	Chiu MT, Cottarel G, Berlin V, Draetta G, Damagnez V, Rolfe M;
DR	WP1; 2000-410854/35.
DR	P-P5DB; AAB03176.
PT	
PT	Identifying an inhibitor of ubiquitin mediated proteolysis of regulatory
PT	protein for treating cancers involves measuring ubiquitination levels of
PT	the protein in the presence of candidate agent in an eukaryotic cell.
PS	
PS	Example 2; Col 97-98; 73pp; English.
XX	
CC	The invention relates to a method of identifying an inhibitor of
CC	ubiquitin-mediated proteolysis of a cell cycle regulatory protein
CC	comprising contacting an engineered eukaryotic cell with a candidate
CC	agent. The eukaryotic cells is engineered to express a recombinant human,
CC	Candida albicans or Schizosaccharomyces pombe ubiquitin-conjugating
CC	enzyme (AAB03169-B03171), a cell cycle regulatory protein (such as p53)
CC	and ubiquitin. The specific action also discloses novel Candida albicans
CC	and Schizosaccharomyces pombe ubiquitin-conjugating enzymes, caUBC and
CC	spUBC (AAB03170, AAB03171), and two novel human ubiquitin-conjugating
CC	enzymes, hUBC and rapUC (AAB03165, AAB03173). The ubiquitin-mediated
CC	proteolysis system is the major pathway for the selective, controlled
CC	degradation of intracellular proteins in eukaryotic cells, and is
CC	important in controlling the half-lives of cellular proteins, and is
CC	progression. Alterations in the levels of proteins involved in cell cycle
CC	therefore play a role in the development of cancers. For example, human
CC	papillomaviruses such as HPV-18 encode a transforming protein, B6
CC	(AAB03176), which combines with a cellular B6-associated protein (B6-AP;
CC	AAB03177) to stimulate the ubiquitination of p53, thus targeting it for
CC	degradation. The ubiquitination inhibitors identified according to the
CC	method of the invention are useful for treatment of cervical cancers and
CC	connective tissue disorders and for controlling the wound healing
CC	process. They are also useful in treatment of hyperplastic epidermal
CC	conditions such as psoriasis, neoplastic epidermal conditions, skin
CC	cancers e.g., basal cell carcinomas, squamous cell carcinomas. The
CC	inhibitors are useful for downregulating myc expression and rendering the
CC	cells sensitive to chemotherapeutic treatment or to upset the balance of
CC	transformed cells and cause apoptosis to occur. Inhibitors of ubiquitin-
CC	mediated degradation of cyclins are useful as antiproliferative agents.
CC	The present sequence represents cDNA encoding HPV-18 E6 protein. Note:
CC	The present sequence is referred to as SEQ ID NO:16 in the examples, but
CC	is given as SEQ ID NO:18 in the sequence listing. (Updated on 15-SEP-2003
XX	to standardise OS field)

XX	SO	Sequence	476 BP; 163 A; 95 C; 100 G; 118 T; 0 U; 0 Other;
XX	QY	Query Match	100.0%; Score 32; DB 3; Length 476;
XX		Best Local Similarity	100.0%; Pred. No. 0.00016;
XX		Matches	32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX	DB	301	TTATTATTAAGTGCCTCGCGGTGCCAAGAACC 332
XX	AAU54443	standard; DNA; 477 BP.	
XX	AAU54443		
XX	AC	03-APR-2003	(first entry)
XX	DE	HPV18 E6 siRNA derived DNA sequence.	
XX	KW	Vitricide; cytosolic; anti-HIV; dermatological; small interfering RNA;	
XX	KM	selective post-translational silencing; siRNA; oncogene; genital wart;	
XX	KX	human papilloma virus; HPV gene; cancer; human cervical cancer; HIV;	
XX	XX	smallpox; flu; common cold; cervical cancer; penile cancer;	
XX	OS	malignant squamous cell carcinoma; verruca vulgaris; gene therapy; ds.	
XX	PA	Human papilloma virus.	
XX	FN	WO2003008573-A2.	
XX	PD	30-JAN-2003.	
XX	PF	17-JUL-2002; 2002MO-GB003300.	
XX	PR	17-JUL-2001; 2001GB-00017358.	
XX	PR	14-JAN-2002; 2002GB-00000688.	
XX	PR	17-JUN-2002; 2002GB-00013855.	
XX	PI	MILNER AJ;	
XX	DR	WPI; 2003-221850/21.	
XX	PT	Selective post-transcriptional silencing of an exogenous viral gene (e.g.	
XX	PT	human papilloma virus (HPV) E6), for treating e.g. cancer, comprises	
XX	PT	using a small interfering RNA (siRNA) construct homologous to an mRNA of	
XX	PS	the gene.	
XX	Claim 11; Fig 11; 44pp; English.		
CC	The invention relates to a novel method for selective post-translational		
CC	silencing in a mammalian cell of the expression of an exogenous gene of		
CC	viral origin. The method comprises introducing into the cell a small		
CC	interfering RNA (siRNA) construct that is homologous to a part of the		
CC	mRNA sequence of the gene. The method is useful for the selective post-		
CC	transcriptional silencing of an exogenous gene of viral origin (e.g. an		
CC	oncogene or human papilloma virus (HPV) gene) in a mammalian cell. The		
CC	method or the siRNA is particularly useful for treating cancer, human		
CC	cervical cancer, human immunodeficiency virus (HIV), smallpox, flu,		
CC	common cold, or a disease caused by a HPV (e.g. genital warts, cervical		
CC	cancer, penile cancer, malignant squamous cell carcinomas or verruca		
CC	vulgaris). An siRNA construct or vector is useful for use as a medicament		
CC	for the diseases mentioned. The polynucleotide sequence of the invention		
CC	can be used to treat disorders by gene therapy. This polynucleotide		
CC	sequence represents the DNA of a HPV siRNA sequence of the invention		
XX	Sequence	477 BP; 163 A; 96 C; 100 G; 118 T; 0 U; 0 Other;	
XX	Query Match	100.0%; Score 32; DB 10; Length 477;	
XX	Best Local Similarity	100.0%; Pred. No. 0.00016;	
XX	Matches	32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	

OY 1 TTATTATAAGTGGCTGCGTCCAGAAACC 32
 DB 301 TTATTATAAGTGGCTGCGTCCAGAAACC 332

RESULT 9
 ADO44101
 ID ADO44101 standard; DNA; 477 BP.
 AC ADO44101;
 XX
 XX 15-JUN-2004 (first entry)
 DT
 XX
 XX Nucleotide sequence of the E6 polypeptide of HPV18.
 DE
 XX E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer;
 KM cervical cancer; immune response; lower gastrointestinal tract cancer;
 KM anal cancer; reproductive system cancer; penile cancer; vulvar cancer;
 KM gene; ss.
 XX
 XX Human papillomavirus type 18.
 OS
 XX
 XX Key Location/Qualifiers
 FH 1. .477
 FT CDS /*tag= a
 FT /product= "E6 polypeptide"
 XX
 XX MO2004030636-A2.
 PN
 XX
 XX 15-APR-2004.
 PD
 XX
 XX 02-OCT-2003; 2003MO-US031726.
 PF
 XX
 XX 03-OCT-2002; 2002US-0415929P.
 PR
 XX (AMHP) WYETH HOLDINGS CORP.
 PA
 XX
 XX Smith L, Cassetti MC;
 PI
 XX WPI; 2004-116328/29.
 DR P-PSDB; ADO44074.
 DR
 XX
 XX
 XX New polypeptide comprising human papillomavirus E6 and E7 polypeptides,
 PT useful for treating or preventing human papillomavirus (HPV)-associated
 PT cancers, e.g. cervical cancer.
 PT
 XX
 XX Disclosure, Page 94; 101pp; English.
 PS
 XX
 XX The present sequence encodes an E6 polypeptides from human papillomavirus
 CC type 18 (HPV18). The specification describes human papillomavirus E6 and
 CC E7 polypeptides, where the E7 polypeptide has mutations at any one or
 CC more of the amino acids corresponding to amino acids 24, 26 or 91 of the
 CC sequence given in ADO44073 and the E6 polypeptide has no mutations or has
 CC mutations at any one or more of the amino acids corresponding to amino
 CC acids 63 or 106 of their sequence given in ADO44072. The polypeptides of
 CC the invention are useful for treating or preventing human papillomavirus
 CC (HPV)-associated cancers, such as cervical cancer. The fusion proteins
 CC and nucleic acids encoding the fusion proteins are useful for generating
 CC immune responses against HPV. They are also useful for treating lower
 CC gastrointestinal tract cancers, e.g. anal cancer, and other cancers of
 CC the reproductive system, including penile and vulvar cancer.
 CC
 CC
 CC Sequence 477 BP; 164 A; 96 C; 99 G; 118 T; 0 U; 0 Other;

Query Match 100.0%; Score 32; DB 12; Length 477;
 Best Local Similarity 100.0%; Pred. No. 0.00016;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTATTATAAGTGGCTGCGTCCAGAAACC 32
 DB 301 TTATTATAAGTGGCTGCGTCCAGAAACC 332

RESULT 10
 ID AEA51111
 XX AEA51111 standard; DNA; 477 BP.
 AC AEA51111;
 XX
 XX 11-AUG-2005 (first entry)
 DT
 XX
 XX Human papillomavirus type 18 E6/E7 gene fragment. SEQ ID NO: 15.
 DE
 XX
 XX Delivery mechanism; gene therapy; cytostatic; vulnery; virucide;
 KM injury; infection; cancer; gastrointestinal disease;
 KM gynecology and obstetrics; tumor; colorectal tumor;
 KM uterine cervix tumor; squamous cell carcinoma; neoplasia; E7 gene; ds;
 KM E6 gene.
 XX
 XX Human papillomavirus.
 OS
 XX
 XX MO2005051431-A1.
 PN
 XX
 XX 09-JUN-2005.
 PD
 XX
 XX 25-NOV-2004; 2004MO-GB04979.
 PF
 XX
 XX 25-NOV-2003; 2003GB-00027409.
 PR 05-MAR-2004; 2004US-0549919P.
 PR
 XX (MILN/) MILNER A J.
 PA
 XX
 XX Milner AJ;
 PI
 XX
 XX WPI; 2005-405310/41.
 DR
 XX
 XX
 XX Composition useful for delivering an agent into a cell comprises the
 PT agent, a transfer agent and a solid or colloidal carrier medium.
 PT
 XX
 XX Disclosure; SEQ ID NO 15; 56pp; English.
 PS
 XX
 XX The present invention relates to a method and composition comprising a
 CC transfer agent and a solid or colloidal carrier medium for delivering a
 CC biological agents into cells. The invention is useful for the treatment
 CC of cancer, tumor, carcinoma of cutaneous, squamous or cervical epithelia
 CC and colorectal carcinoma, wounds, burns and scars. The invention is also
 CC useful in gene therapy. The present sequence is the human papillomavirus
 CC type 18 E6/E7 gene fragment. This sequence is useful in a method for
 CC treating carcinomas.
 CC
 CC
 CC Sequence 477 BP; 164 A; 95 C; 100 G; 118 T; 0 U; 0 Other;

Query Match 100.0%; Score 32; DB 14; Length 477;
 Best Local Similarity 100.0%; Pred. No. 0.00016;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTATTATAAGTGGCTGCGTCCAGAAACC 32
 DB 301 TTATTATAAGTGGCTGCGTCCAGAAACC 332

RESULT 11
 ID AAO75471
 XX AAO75471 standard; DNA; 483 BP.
 AC AAO75471;
 XX
 XX 16-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 28-JUN-1995 (first entry)
 DT
 XX
 XX HPV18 E6/E7 proteins.
 DE
 XX HPV; HPV18; E6 protein; E7 protein; diagnosis; cervical dysplasia;
 KM cervix cancer; ss.

```

XX OS Human papillomavirus; strain 18.
XX PH Key Location/Qualifiers
XX FT CDS 1..480
XX FT /*tag= a
XX PN WO9426934-A2.
XX PD 24-NOV-1994.
XX PF 06-MAY-1994; 94MO-US005085.
XX PR 06-MAY-1993; 93US-00058920.
XX PA (BAKT ) BAXTER DIAGNOSTICS INC.
XX PI Brown JT;
XX DR WPI; 1995-006821/01.
XX DR P-PSDB; AAR63866.
XX PT Human papilloma virus detection assay - by amplification using self
XX PT sustained sequence replication and hybridisation with a detector probe.
XX PS Disclosure; Page 27-28; 79pp; English.
XX CC The sequences of the E6 and E7 polypeptide-encoding regions of human
XX CC papillomavirus (HPV) 16 and 18 are given in AAQ75470-71 and the encoded
XX CC proteins in AAR63865-66, respectively. Probes and primers based on these
XX CC sequences were used for HPV infection diagnosis; expression of E6 and E7
XX CC is diagnostic for cervical cancer or pre-malignant states. (Updated on
XX CC 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-2003 to standardise
XX CC OS field)
XX SQ Sequence 483 BP; 167 A; 95 C; 100 G; 121 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 32; DB 2; Length 483;
XX Best Local Similarity 100.0%; Pred. No. 0.00016;
XX Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TTATTATAAGTGCCTGCGTCCGACGAAAC 32
XX DB 301 TTATTATAAGTGCCTGCGTCCGACGAAAC 332
XX
RESULT 12
XX ID AAN91786
XX ID AAN91786 standard; DNA; 802 BP.
XX AC AAN91786;
XX XX
XX DT 27-AUG-2003 (revised)
XX DT 25-MAR-2003 (revised)
XX DT 16-MAR-1990 (first entry)
XX XX
XX DE DNA probe complementary to human papilloma virus type 18.
XX KM Cervical cancer.
XX XX
XX OS Human papillomavirus type 18.
XX PN WO8909940-A.
XX PD 19-OCT-1989.
XX PF 04-APR-1989; 89WO-US001318.
XX PR 04-APR-1988; 88US-00177404.
XX PR 31-MAR-1989; 89US-00330381.
XX PA (ONCO-) ONCOR INC.
XX XX

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PI George AL, Groff DE;
XX DR WPI; 1989-324314/44.
XX PH Rapid detection of specific human papilloma virus genotypes - by
XX PT hybridisation of DNA digest with new labelled nucleic acid probes.
XX PS Claim 46; Page 48; 81pp; English.
XX CC Obt'd. by cutting HPV18 with BamH and Sau3A. The patent describes probes
XX CC (DNA or RNA) and their complements capable of detecting one or a
XX CC combination of HPV types 6, 11, 16, 18, 31, 33 and 35. (Updated on 25-MAR
XX CC -2003 to correct PR field.) (Updated on 27-AUG-2003 to correct OS field.)
XX SQ Sequence 802 BP; 269 A; 158 C; 182 G; 193 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 32; DB 1; Length 802;
XX Best Local Similarity 100.0%; Pred. No. 0.00018;
XX Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TTATTATAAGTGCCTGCGTCCGACGAAAC 32
XX DB 287 TTATTATAAGTGCCTGCGTCCGACGAAAC 318
XX
RESULT 13
XX ID AAQ29390
XX ID AAQ29390 standard; DNA; 817 BP.
XX AC AAQ29390;
XX XX
XX DT 24-OCT-2003 (revised)
XX DT 25-MAR-2003 (revised)
XX DT 09-MAR-1993 (first entry)
XX XX
XX DE DNA encoding HPV 18 E6/E7 proteins obt'd. by PCR.
XX KM Virus vector; vaccinia virus; papillomavirus; HPV; human; amplification;
XX KW immunotherapeutic; 88.
XX OS Human papillomavirus; 18.
XX PH Key Location/Qualifiers
XX FT CDS 1..816
XX FT /*tag= a
XX FT /note= "reading frame 1"
XX FT 2..815
XX FT /*tag= b
XX FT /note= "reading frame 2"
XX FT 3..814
XX FT /*tag= d
XX FT /note= "reading frame 3"
XX FT 6..482
XX FT /*tag= e
XX FT /note= "third reading frame encoding HPV 18 E6"
XX FT 491..808
XX FT /*tag= c
XX FT /note= "second reading frame encoding HPV 18 E7"
XX
XX PN WO9216636-A1.
XX PD 01-OCT-1992.
XX PF 10-MAR-1992; 92WO-GB000424.
XX PR 14-MAR-1991; 91GB-00005383.
XX PA (IMMU ) IMMUNOLOGY LTD.
XX XX
XX PI Bourneill MEG, Inglis SC, Munro AJ;
XX DR WPI; 1992-349219/42.
XX DR P-PSDB; AAR27726, AAR27727, AAR27728.

```

XX Recombinant virus vectors encoding human papillomavirus proteins - for
 PT treating and vaccinating against HPV infections and conditions caused by
 PT chem, such as cervical cancer.
 XX Disclosure, Fig 1b; 83pp; English.
 CC The fragment of DNA contg. the HPV-18 E6/E7 coding region was prep'd. by
 CC PCR from plasmid pBR322/HPV18 (Boshart et al., EMBO J. 3: 1151) using
 CC oligonucleotide S01 and S02. The DNA prod. has a site for NcoI at the
 CC beginning of the E6 gene and a SmaI site immediately downstream of the
 CC termination codon for E7. The E6 and E7 ORFs are fused together to form a
 CC single continuous ORF via site directed mutagenesis and the immortalising
 CC potential of E7 is removed by altering two key codons of the HPV E7
 CC sequence. The single ORF of HPV-18 E6/E7 may be inserted into vaccinia
 CC virus DNA at neutral sites (pref. by inserting two sets of the DNA in
 CC opposite orientations to overcome the problem of intertypic
 CC recombination) to make a recombinant virus vector for use
 CC immunotherapeutically to activate cells of the immune system against HPV.
 CC See also AAO29385-400 and AAO29450-69. (Updated on 25-MAR-2003 to correct
 CC P1 field.) (Updated on 24-OCT-2003 to standardise OS field)
 CC
 SQ Sequence 817 BP; 266 A; 173 C; 177 G; 201 T; 0 U; 0 Other;
 Query Match 100.0%; Score 32; DB 2; Length 817;
 Best Local Similarity 100.0%; Pred. No. 0.00018;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTATTAATAGGTCCTGCGTCCAGAAACC 32
 Db 306 TTATTAATAGGTCCTGCGTCCAGAAACC 337
 RESULT 14
 ID AAX78800 standard; DNA; 837 BP.
 AC AAX78800;
 XX 06-SEP-1999 (first entry)
 DT
 XX HPV fusion protein D1/3-E6-His/HPV18 DNA.
 DE
 XX Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour;
 KM immunological fusion partner; CpG oligonucleotide; immune response;
 KM HPV antigen; prevention; treatment; ss.
 XX
 OS Synthetic.
 OS Human papillomavirus.
 XX
 PN WO9933868-A2.
 XX
 XX 08-JUL-1999.
 PD
 XX 18-DEC-1998; 98WO-EP008563.
 PF
 XX 24-DEC-1997; 97GB-00027262.
 PR
 XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 PA
 PI Dalemans WJ, Gerard CMG;
 XX
 XX WPI; 1999-405485/34.
 DR P-PSDB; AAY25385.
 XX
 XX Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to
 PT induce immune response to HPV.
 PT
 XX Example XI; Page 59; 62pp; English.
 PS
 XX AAX78791-X78801 represent nucleic acid sequences which encode novel
 CC constructs comprising an E6 or E7 protein or E6/E7 fusion protein from
 CC HPV (represented in AAY25375-Y25386). These constructs are optionally

CC linked to an immunological fusion partner and an immunomodulatory CpG
 CC oligonucleotide. The products of the invention can be used to induce an
 CC immune response in a patient to an HPV antigen. They can also be used for
 CC preventing or treating HPV induced tumours
 CC
 SQ Sequence 837 BP; 283 A; 169 C; 167 G; 218 T; 0 U; 0 Other;
 Query Match 100.0%; Score 32; DB 2; Length 837;
 Best Local Similarity 100.0%; Pred. No. 0.00018;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTATTAATAGGTCCTGCGTCCAGAAACC 32
 Db 634 TTATTAATAGGTCCTGCGTCCAGAAACC 665
 RESULT 15
 ID AAX29789 standard; DNA; 837 BP.
 AC AAX29789;
 XX 17-OCT-2003 (revised)
 DT 22-JUN-1999 (first entry)
 XX
 XX Prot.D1/3-E6-His/HPV18 coding sequence.
 DE
 XX Chimeric; E6; E7; fusion protein; protein D; vaccine; immunotherapy;
 KM tumour; lesion; benign; malignant; virus; infection; ss.
 KM
 XX Human papillomavirus.
 OS Haemophilus influenzae.
 OS Chimeric.
 XX
 PN WO9910375-A2.
 PD
 XX 04-MAR-1999.
 PD
 XX 17-AUG-1998; 98WO-BP005285.
 PF
 XX 22-AUG-1997; 97GB-00017953.
 PR
 XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 PA
 PI Bruck C, Cabezon Silva T, Delisse ABF, Gerard CMG;
 PI Lombardo-Bencheikh A;
 DR WPI; 1999-190587/16.
 DR P-PSDB; AAY02641.
 XX
 XX Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for
 PT treatment or prophylaxis of HPV induced lesions.
 PT
 XX Disclosure, Fig 22; 95pp; English.
 PS
 XX This sequence represents the coding region for a chimeric E6 or E7
 CC protein or E6/E7 fusion protein from human papillomavirus (HPV) linked to
 CC an immunological fusion partner. In this case, a fragment of the
 CC Haemophilus influenzae B protein D. The sequence also contains a
 CC histidine tag at the C-terminus of the encoded protein. The protein can
 CC be used in a vaccine, for immuno-therapeutically treating HPV induced
 CC tumour lesions (benign or malignant) and preventing HPV viral infection.
 CC (Updated on 17-OCT-2003 to standardise OS field)
 CC
 SQ Sequence 837 BP; 283 A; 169 C; 167 G; 218 T; 0 U; 0 Other;
 Query Match 100.0%; Score 32; DB 2; Length 837;
 Best Local Similarity 100.0%; Pred. No. 0.00018;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTATTAATAGGTCCTGCGTCCAGAAACC 32
 Db 634 TTATTAATAGGTCCTGCGTCCAGAAACC 665

```
RESULT 16
AED52652
ID AED52652 standard; DNA; 837 BP.
XX
XX AED52652;
AC
XX 29-DEC-2005 (first entry)
DT
XX
XX Fusion protein D1/3-E6-His (HPV18), DNA.
DE
XX
XX Fusion protein; vaccine; papilloma; cytosolic; papillomavirus infection;
XX virucide; uterine cervix tumor; E6; ds; gene; D protein.
XX
XX Haemophilus influenzae; strain 772.
OS
XX Human papillomavirus type 18.
OS Synthetic.
OS Chimeric.
XX
XX Key Location/Qualifiers
XX CDS 1..837
XX /*tag= a
XX /product= "Fusion protein D1/3-E6-His (HPV18)"
XX
XX IN9801903-14.
XX
XX 04-MAR-2005.
XX
XX 24-AUG-1998; 98IN-CH001903.
XX
XX 22-AUG-1997; 97EP-00179535.
XX
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX Tyrell AMR;
XX
XX WPI; 2005-557648/57.
XX
XX P-PSDB; AED52653.
XX
XX Vaccine.
XX
XX Example 16; Fig 22; 96pp; English.
XX
XX The invention relates to human Papilloma virus (HPV) fusion proteins,
XX linked to an immunological fusion partner that provides T helper epitopes
XX to the HPV antigen. Vaccine formulations comprising the fusion proteins
XX are useful in the treatment or prophylaxis of HPV induced lesions
XX (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7
XX proteins (singly, as an E6-E7 fusion or mutated) were fused to either
XX Haemophilus influenzae D protein (20-127), the C-terminus of
XX Streptococcus pneumoniae Lyta protein (cLYCA) or chlorodoxin. The present
XX sequence encodes an HPV-H. influenzae D protein, fusion protein of the
XX invention.
XX
XX Sequence 837 BP; 283 A; 169 C; 167 G; 218 T; 0 U; 0 Other;
SQ
XX
XX Query Match 100.0%; Score 32; DB 14; Length 837;
XX Best Local Similarity 100.0%; Pred. No. 0.00018;
XX Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTATTATTAAGGTGCTGCGGTGCCAGAAACC 32
DB 634 TTATTATTAAGGTGCTGCGGTGCCAGAAACC 665
```

```
XX
DE Human papillomavirus E6 and E7 coding sequence, SEQ ID 29.
XX
XX Cytostatic; Virucide; Antibacterial; Antiparasitic; Vaccine; infection;
XX cancer; gene; ds; antigen.
XX
XX Human papillomavirus.
XX
XX Key Location/Qualifiers
XX CDS 40..516
XX /*tag= a
XX /product= "E6 protein"
XX CDS 525..842
XX /*tag= b
XX /product= "E7 protein"
XX
XX US2004258688-A1.
XX
XX 23-DEC-2004.
XX
XX 12-MAR-2004; 2004US-00800023.
XX
XX 31-JAN-1995; 95US-00381528.
XX 31-JAN-1996; 96WO-US001383.
XX 05-JUN-2000; 2000US-00586704.
XX 09-AUG-2001; 2001US-00925284.
XX
XX (HAWI/) HAWIGER D.
XX (NUSZ/) NUSSENZWEIG M.
XX (STEI/) STEINMAN R M.
XX (BONI/) BONIFAZ L.
XX
XX Hawiger D, Nussenzweig M, Steinman RM, Bonifaz L;
XX
XX WPI; 2005-078933/09.
XX
XX P-PSDB; ADV85646, ADV85647.
XX
XX Promoting antigen presentation comprises targeting antigen to dendritic
XX cells using an anti-DEC-205 antibody.
XX
XX Disclosure; SEQ ID NO 29; 116pp; English.
XX
XX The present invention relates to a method (M1) for promoting highly
XX efficient antigen presentation in a mammal, by targeting a preselected
XX antigen to an endocytic receptor on an antigen-presenting cell, e.g. a
XX dendritic cell. An example of a dendritic cell is the cell endocytic
XX receptor DEC-205. The method comprises exposing dendritic cells from the
XX mammal to either: a conjugate comprising a preselected antigen covalently
XX bound to an antibody; a conjugate comprising a preselected anti-DEC-205 antibody
XX genetically engineered to contain at least one preselected antigen on at
XX least one preselected site on the antibody molecule; and promoting
XX maturation of the dendritic cells. The sequence encoding an anti-DEC-205
XX antibody (fragment) is preferably selected from ADV85632 and ADV85633,
XX which encode the heavy or light chain variable region of an anti-DEC-205
XX antibody. The antigen is targeted to antigen presenting cells through the
XX inclusion of the anti-DEC-205 antibody, making antigen presentation
XX highly efficient. The immunity induced is robust and long lasting, even
XX from a single dose at low concentration. The method of the invention is
XX useful for immunizing a mammal to prevent or treat a disease such as a
XX viral, bacterial or other infection or cancer. The immunization
XX preferably results in induction of long term T cell, B cell or mucosal
XX immunity. The present sequence is a HPV DNA sequence which encodes the E6
XX and E7 proteins. The present sequence can be used as a vaccine antigen.
XX
XX Sequence 843 BP; 283 A; 170 C; 183 G; 207 T; 0 U; 0 Other;
SQ
XX
XX Query Match 100.0%; Score 32; DB 14; Length 843;
XX Best Local Similarity 100.0%; Pred. No. 0.00018;
XX Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTATTATTAAGGTGCTGCGGTGCCAGAAACC 32
DB 340 TTATTATTAAGGTGCTGCGGTGCCAGAAACC 371
```

```

RESULT 18
AAQ08623
ID AAQ08623 standard; DNA; 1000 BP.
XX
AC AAQ08623;
XX
DT 24-OCT-2003 (revised)
DT 21-APR-1994 (first entry)
XX
DE HPV-18 fragment.
XX
KM HPV-18; HPV-16; amplification; primer; polymerase chain reaction; PCR;
KM 88.
XX
OS Human papillomavirus; 18.
XX
FH Key Location/Qualifiers
FH misc_binding 167..186
FT /*tag= a
FT /note= "primer (AAQ08624) binding site"
FT 647..666
FT /*tag= c
FT /note= "primer (AAQ08626) binding site"
FT 667..686
FT /*tag= b
FT /note= "primer (AAQ08625) binding site"
XX
PN DE3838269-A.
XX
PD 17-MAY-1990.
XX
PF 11-NOV-1988; 88DE-03838269.
XX
PR 11-NOV-1988; 88DE-03838269.
XX
PA (BEHW ) BEHRINGERWERKE AG.
XX
PI Cerutti P, Whitcomb J, Ziflstra J, Devillers EM;
XX WPI, 1990-156905/21.
XX
PT Detection of human papilloma virus - by DNA amplification and analysis.
XX
PS Example 4a; Page 4; 11pp; German.
XX
CC Example 4a describes the results of the amplification of HPV-18 DNA by
CC PCR using primers. (Updated on 24-OCT-2003 to standardise OS field)
XX
SQ Sequence 1000 BP; 341 A; 198 C; 221 G; 240 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 32; DB 2; Length 1000;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TTATTATAAGTGCTGCGTGCAGAAACC 32
Db 405 TTATTATAAGTGCTGCGTGCAGAAACC 436

RESULT 19
AAK78801
ID AAK78801 standard; DNA; 1152 BP.
XX
AC AAK78801;
XX
DT 06-SEP-1999 (first entry)
XX
DE HPV fusion protein D1/3-E6/E7-His/HPV18 DNA.
XX
KM Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour;
KM immunological fusion partner; Cpg oligonucleotide; immune response;

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KM HPV antigen; prevention; treatment; ss.
XX
OS Synthetic.
OS Human papillomavirus.
XX
PN WO9933868-A2.
XX
PD 08-JUL-1999.
XX
PF 18-DEC-1998; 98MO-EP008563.
XX
PR 24-DEC-1997; 97GB-00027262.
XX
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Dalemans WLJ, Gerard CMG;
XX
DR WPI, 1999-405485/34.
DR P-PSDB; AAY25386.
XX
PT Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to
PT induce immune response to HPV.
XX
PS Example XII; Page 60-61; 62pp; English.
XX
AAK78791-X78801 represent nucleic acid sequences which encode novel
CC constructs comprising an E6 or E7 protein or E6/E7 fusion protein from
CC HPV (represented in AAY25375-Y25386). These constructs are optionally
CC linked to an immunological fusion partner and an immunomodulatory Cpg
CC oligonucleotide. The products of the invention can be used to induce an
CC immune response in a patient to an HPV antigen. They can also be used for
CC preventing or treating HPV induced tumours
XX
SQ Sequence 1152 BP; 378 A; 240 C; 240 G; 294 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 32; DB 2; Length 1152;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TTATTATAAGTGCTGCGTGCAGAAACC 32
Db 634 TTATTATAAGTGCTGCGTGCAGAAACC 665

RESULT 20
AAK29790
ID AAK29790 standard; DNA; 1152 BP.
XX
AC AAK29790;
XX
DT 17-OCT-2003 (revised)
DT 22-JUN-1999 (first entry)
XX
DE Prot. D1/3-E6-E7-His/HPV18 coding sequence.
XX
KM Chimeric; E6; E7; fusion protein; protein D; vaccine; immunotherapy;
KM tumour; lesion; benign; malignant; virus; infection; ss.
XX
OS Human papillomavirus.
OS Haemophilus influenzae.
OS Chimeric.
XX
PN WO9910375-A2.
XX
PD 04-MAR-1999.
XX
PF 17-AUG-1998; 98MO-EP005285.
XX
PR 22-AUG-1997; 97GB-00017953.
XX
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Bruck C, Caberon Silva T, Delisse ABF, Gerard CMG;

```

PI Lombardo-Bencheikh A;
XX WPI; 1999-190587/16.
DR P-PSDB; AAY02642.
XX
PT Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for
XX treatment or prophylaxis of HPV induced lesions.
PS Disclosure; Fig 25; 95pp; English.
XX
CC This sequence represents the coding region for a chimeric E6 or E7
CC protein or E6/E7 fusion protein from Human Papillomavirus (HPV) linked to
CC an immunological fusion partner, in this case, a fragment of the
CC Haemophilus influenzae B protein D. The sequence also contains a
CC histidine tag at the C-terminus of the encoded protein. The protein can
CC be used in a vaccine, for immuno-therapeutically treating HPV induced
CC tumour lesions (benign or malignant) and preventing HPV viral infection.
CC (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 1152 BP; 378 A; 240 C; 240 G; 294 T; 0 U; 0 Other;
Query Match 100.0%; Score 32; DB 2; Length 1152;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTATTAATAAGTGCCTGCGGTGCCAGAAACC 32
DB 634 TTATTAATAAGTGCCTGCGGTGCCAGAAACC 665
RESULT 21
ID AED52656 standard; DNA; 1152 BP.
XX
AC AED52656;
XX
DT 29-DEC-2005 (first entry)
XX
DE Fusion protein D1/3-E6-E7-His/HPV18, DNA.
XX
KM Fusion protein; vaccine; papilloma; cytostatic; papillomavirus infection;
KM virucide; uterine cervix tumor; E7; E6; ds; gene; D protein.
XX
OS Haemophilus influenzae; strain 772.
OS Human Papillomavirus type 18.
OS Synthetic.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT CDS 1..1152
FT /*tag= a
FT /product= "Fusion protein D1/3-E6-E7-His/HPV18"
XX
PN IN9801903-14.
XX
PD 04-MAR-2005.
XX
PE 24-AUG-1998; 98IN-CH001903.
XX
PR 22-AUG-1997; 97BP-00179535.
XX
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Tyrell AMR;
XX
XX WPI; 2005-557648/57.
DR P-PSDB; AED52657.
XX
PT Vaccine.
XX
PS Example 17; Fig 25; 96pp; English.
XX
CC The invention relates to human Papilloma virus (HPV) fusion proteins,

CC linked to an immunological fusion partner that provides T helper epitopes
CC to the HPV antigen. Vaccine formulations comprising the fusion proteins
CC are useful in the treatment or prophylaxis of HPV induced lesions
CC (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7
CC proteins (singly, as an E6-E7 fusion or mutated) were fused to either
CC Haemophilus influenzae D protein (20-127), the C-terminus of
CC Streptococcus pneumoniae LytA protein (cLytA) or thioredoxin. The present
CC sequence encodes an HPV-H. influenzae D protein, fusion protein of the
CC invention.
XX
SQ Sequence 1152 BP; 378 A; 240 C; 240 G; 294 T; 0 U; 0 Other;
Query Match 100.0%; Score 32; DB 14; Length 1152;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTATTAATAAGTGCCTGCGGTGCCAGAAACC 32
DB 634 TTATTAATAAGTGCCTGCGGTGCCAGAAACC 665
RESULT 22
ID AAN80161 standard; DNA; 1731 BP.
XX
AC AAN80161;
XX
DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 10-MAR-2003 (revised)
DT 19-OCT-1990 (first entry)
XX
DE Human papilloma virus 18 protein.
XX
XX Human papilloma virus; HPV16; HPV18; malignant genital tumours; ss.
XX
OS Human papillomavirus.
XX
FH Key Location/Qualifiers
FT CDS 99..572
FT /*tag= a
FT /label= HPV18 E6 protein
FT 584..898
FT /*tag= b
FT /label= HPV 18 E7 protein
FT 908..729
FT /*tag= c
FT /label= HPV 18 B1 protein
XX
PN DE3625257-A.
XX
PD 04-FEB-1988.
XX
PE 25-JUL-1986; 86DE-03625257.
XX
PR 23-JUL-1986; 86DE-03624786.
XX
PA (BEHM) BEHRINGWERKE AG.
XX
PI Schwarz B, Oltersdorf T, Rowekamp W, Schneiderg A, Seedorf K;
XX Durt M;
XX WPI; 1988-037095/06.
DR P-PSDB; AAP82076.
XX
PT Expression prods. of human papilloma viruses type 16 and 18 - used for
PT the prodn. of diagnostics for HPV16 and HPV18 infections.
XX
PS Disclosure; Page 7; 7pp; German.
XX
XX The expression prods. of HPV18, contained in this sequence, are used to
CC produce antibodies to detect these. HPV16 expression prods are also used
CC for antibody prodn. See also AAN80155-59. (Updated on 10-MAR-2003 to add

CC missing OS field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated
CC on 25-MAR-2003 to correct PI field.) (Updated on 27-AUG-2003 to correct
CC OS field.)

XX Sequence 1731 BP; 610 A; 313 C; 403 G; 405 T; 0 U; 0 Other;

Query Match 100.0%; Score 32; DB 1; Length 1731;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTATTAATAGGTCCTGGCGTCCAGAAACC 32
DB 399 TTATTAATAGGTCCTGGCGTCCAGAAACC 430

RESULT 23

ADZ45648
ID ADZ45648 standard; DNA; 7857 BP.

AC ADZ45648;

XX 30-JUN-2005 (first entry)

DE Human papillomavirus type 18 full length genomic clone - SEQ ID 2.

XX tumor marker; genome; diagnosis; cancer; uterine cervix tumor;

KM rectal tumor; colon tumor; ds.

XX Human papillomavirus type 18.

XX WO200503333-A2.

PD 14-APR-2005.

PF 04-OCT-2004; 2004WO-DK000670.

XX 07-OCT-2003; 2003DK-00001474.

PR 07-OCT-2003; 2003US-0509205P.

PR 13-FEB-2004; 2004US-0543925P.

XX (DAKO-) DAKOCYTOMATION DENMARK AS.

XX Chau MF, Bisgaard-Franzen K, Lin J, Raemussen OF, Wang Z, Lusk J;
PI Lindberg M, Yeast S;
XX WPI; 2005-285441/29.

XX New composition having a nucleic acid molecule identical to genomic clone
PT of human papilloma virus 16, 18 or 51, useful in diagnosing cancer or the
PT risk of developing cancer, in particular cervical, anal, colon and HPV-
related cancer.

PS Claim 1; SEQ ID NO 2; 169pp; English.

XX The invention comprises a composition for the detection of cancer
CC markers, the composition contains a nucleic acid molecule which is
CC substantially identical to a full length genomic clone of a human
CC papilloma virus (type 11, 16, 18, 51, 56, 58, 66, 70, or 73). The
CC composition of the invention is useful for diagnosing cancer or the risk
CC of developing cancer, in particular cervical, anal, colon and HPV-related
CC cancer. The present DNA sequence represents a human papilloma virus full
CC length genomic clone of the invention.

XX Sequence 7857 BP; 2365 A; 1497 C; 1680 G; 2315 T; 0 U; 0 Other;

Query Match 100.0%; Score 32; DB 14; Length 7857;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTATTAATAGGTCCTGGCGTCCAGAAACC 32
DB 405 TTATTAATAGGTCCTGGCGTCCAGAAACC 436

RESULT 24

ADO44106
ID ADO44106 standard; DNA; 477 BP.

AC ADO44106;

XX 15-JUL-2004 (first entry)

DE Nucleotide sequence of the E6 polypeptide of HPV45.

XX E6 protein; E7 protein; fusion protein; HPV45; HPV-associated cancer;
KM cervical cancer; immune response; lower gastrointestinal tract cancer;
KM anal cancer; reproductive system cancer; penile cancer; vulvar cancer;
KM gene; ss.

XX Human papillomavirus type 45.

XX Key Location/Qualifiers

FT CDS 1..477

FT /product= "E6 polypeptide"

XX WO2004030636-A2.

XX 15-APR-2004.

PF 02-OCT-2003; 2003WO-US031726.

XX 03-OCT-2002; 2002US-0415929P.

XX (AMHP) WYETH HOLDINGS CORP.

PI Smith L, Cassetti MC;

XX WPI; 2004-316328/29.

DR P-PSDB; ADO44079.

XX New polypeptide comprising human papillomavirus E6 and E7 polypeptides,
PT useful for treating or preventing human papillomavirus (HPV)-associated
PT cancers, e.g. cervical cancer.

XX Disclosure; Page 96; 101pp; English.

XX The present sequence encodes an E6 polypeptides from human papillomavirus
CC type 45 (HPV45). The specification describes human papillomavirus E6 and
CC E7 polypeptides, where the E7 polypeptide has mutations at any one or
CC more of the amino acids corresponding to amino acids 24, 26 or 91 of the
CC sequence given in ADO44073 and the E6 polypeptide has no mutations or has
CC mutations at any one or more of the amino acids corresponding to amino
CC acids 63 or 106 of the sequence given in ADO44072. The polypeptides of
CC the invention are useful for treating or preventing human papillomavirus
CC (HPV)-associated cancers, such as cervical cancer. The fusion proteins
CC and nucleic acids encoding the fusion proteins are useful for generating
CC immune responses against HPV. They are also useful for treating lower
CC gastrointestinal tract cancers, e.g. anal cancer, and other cancers of
CC the reproductive system, including penile and vulvar cancer.

XX Sequence 477 BP; 171 A; 86 C; 101 G; 119 T; 0 U; 0 Other;

Query Match 95.0%; Score 30.4; DB 12; Length 477;
Best Local Similarity 96.9%; Pred. No. 0.00089;
Matches 31; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTATTAATAGGTCCTGGCGTCCAGAAACC 32
DB 301 TTATTAATAGGTCCTGGCGTCCAGAAACC 332

RESULT 25

ADO44105
ID ADO44105 standard; DNA; 477 BP.

XX

```

AC ADO44105;
XX
XX 15-JUL-2004 (first entry)
XX
DE Nucleotide sequence of the E6 polypeptide of HPV39.
XX
XX E6 protein; E7 protein; fusion protein; HPV39; HPV-associated cancer;
KM cervical cancer; immune response; lower gastrointestinal tract cancer;
KM anal cancer; reproductive system cancer; penile cancer; vulvar cancer;
XX gene; ss.
XX
OS Human papillomavirus type 39.
XX
XX
XX Key Location/Qualifiers
XX CDS 1..477
XX /tag= a
XX /product= "E6 polypeptide"
XX
XX MO2004030636-A2.
XX
XX 15-APR-2004.
XX
XX 02-OCT-2003; 2003MO-US031726.
XX
XX 03-OCT-2002; 2002US-0415929P.
XX
XX (AMHP ) WYETH HOLDINGS CORP.
XX
XX Smith L, Cassetti MC;
XX
XX WPI; 2004-316328/29.
XX
XX P-PSDB; ADO44078.
XX
XX New polypeptide comprising human papillomavirus E6 and E7 polypeptides,
XX useful for treating or preventing human papillomavirus (HPV)-associated
XX cancers, e.g. cervical cancer.
XX
XX
XX Disclosure; Page 95-96; 101pp; English.
XX
XX
XX The present sequence encodes an E6 polypeptides from human papillomavirus
XX type 39 (HPV39). The specification describes human papillomavirus E6 and
XX E7 polypeptides, where the E7 polypeptide has mutations at any one or
XX more of the amino acids corresponding to amino acids 24, 26 or 91 of the
XX sequence given in ADO44073 and the E6 polypeptide has no mutations or has
XX mutations at any one or more of the amino acids corresponding to amino
XX acids 63 or 106 of the sequence given in ADO44072. The polypeptides of
XX the invention are useful for treating or preventing human papillomavirus
XX (HPV)-associated cancers, such as cervical cancer. The fusion proteins
XX and nucleic acids encoding the fusion proteins are useful for generating
XX immune responses against HPV. They are also useful for treating lower
XX gastrointestinal tract cancers, e.g. anal cancer, and other cancers of
XX the reproductive system, including penile and vulvar cancer.
XX
XX Sequence 477 BP; 170 A; 96 C; 100 G; 111 T; 0 U; 0 Other;
XX
XX Query Match 75.0%; Score 24; DB 12; Length 477;
XX Best Local Similarity 84.4%; Pred. No. 0.84;
XX Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
XX 1 TTATTATAAGGCTGCGGTGCGAGAAACC 32
XX 301 TTATTATAAGGCTGCGGTGCGAGAAACC 332
XX
XX
XX RESULT 26
XX ADO44112
XX ID ADO44112 standard; DNA; 477 BP.
XX
XX ADO44112;
XX
XX 15-JUL-2004 (first entry)
XX
XX Nucleotide sequence of the E6 polypeptide of HPV68.
XX

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XX
XX E6 protein; E7 protein; fusion protein; HPV68; HPV-associated cancer;
KM cervical cancer; immune response; lower gastrointestinal tract cancer;
KM anal cancer; reproductive system cancer; penile cancer; vulvar cancer;
XX gene; ss.
XX
XX Human papillomavirus type 68.
XX
XX
XX Key Location/Qualifiers
XX CDS 1..477
XX /tag= a
XX /product= "E6 polypeptide"
XX
XX MO2004030636-A2.
XX
XX 15-APR-2004.
XX
XX 02-OCT-2003; 2003MO-US031726.
XX
XX 03-OCT-2002; 2002US-0415929P.
XX
XX (AMHP ) WYETH HOLDINGS CORP.
XX
XX Smith L, Cassetti MC;
XX
XX WPI; 2004-316328/29.
XX
XX P-PSDB; ADO44085.
XX
XX New polypeptide comprising human papillomavirus E6 and E7 polypeptides,
XX useful for treating or preventing human papillomavirus (HPV)-associated
XX cancers, e.g. cervical cancer.
XX
XX
XX Disclosure; Page 98; 101pp; English.
XX
XX
XX The present sequence encodes an E6 polypeptides from human papillomavirus
XX type 68 (HPV68). The specification describes human papillomavirus E6 and
XX E7 polypeptides, where the E7 polypeptide has mutations at any one or
XX more of the amino acids corresponding to amino acids 24, 26 or 91 of the
XX sequence given in ADO44073 and the E6 polypeptide has no mutations or has
XX mutations at any one or more of the amino acids corresponding to amino
XX acids 63 or 106 of the sequence given in ADO44072. The polypeptides of
XX the invention are useful for treating or preventing human papillomavirus
XX (HPV)-associated cancers, such as cervical cancer. The fusion proteins
XX and nucleic acids encoding the fusion proteins are useful for generating
XX immune responses against HPV. They are also useful for treating lower
XX gastrointestinal tract cancers, e.g. anal cancer, and other cancers of
XX the reproductive system, including penile and vulvar cancer.
XX
XX Sequence 477 BP; 167 A; 93 C; 102 G; 115 T; 0 U; 0 Other;
XX
XX Query Match 75.0%; Score 24; DB 12; Length 477;
XX Best Local Similarity 84.4%; Pred. No. 0.84;
XX Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
XX 1 TTATTATAAGGCTGCGGTGCGAGAAACC 32
XX 301 TTATTATAAGGCTGCGGTGCGAGAAACC 332
XX
XX
XX RESULT 27
XX AA231781
XX ID AA231781 standard; DNA; 1095 BP.
XX
XX AA231781;
XX
XX 21-JAN-2000 (first entry)
XX
XX HPV68 DNA sequence.
XX
XX HPV68, human papillomavirus 68; detection; immunisation; infection; ss.
XX
XX Human papillomavirus.
XX

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PN US5981173-A.
XX
XX 09-NOV-1999.
XX
XX 11-FEB-1997; 97US-00815667.
XX
XX 14-FEB-1996; 96US-0011650P.
XX
XX 15-FEB-1996; 96US-0020458P.
XX
XX (INSP ) INST PASTEUR.
XX (INRM ) INST NAT SANTE & RECH MEDICALE.
XX
XX Longuet M, Orth G, Beaudenon S;
XX WPI; 1999-633305/54.
XX
XX New human papillomavirus (HPV) 68 and 70 DNA sequences, useful in the
XX treatment of HPV infections.
XX
XX Claim 2; Fig 5a; 25pp; English.
XX
XX This sequence represents a human papillomavirus (HPV) 68 DNA sequence.
XX The invention relates to a purified HPV68 DNA (I) deposited at C.N.C.M.
XX (Collection Nationale de Culture de Microorganismes) under Accession No. I
XX -1540, and a HPV70 DNA (II) sequence. Fragments of the HPV68 and HPV70
XX DNA may be useful as primers or probes in the detection of HPV68 or HPV70
XX infections. Proteins produced by the HPV DNA's can be used to immunise
XX animals against HPV68 or HPV70 infections
XX
XX Sequence 1095 BP; 370 A; 220 C; 231 G; 274 T; 0 U; 0 Other;
XX
XX Query Match 75.0%; Score 24; DB 2; Length 1095;
XX Best Local Similarity 84.4%; Pred. No. 0.99;
XX Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
XX 1 TTATTATAAGTGCTGCGGTCGCGAACC 32
XX ||||| ||||| ||||| ||||| |||||
XX 580 TTATTGATAGTGATGATGCTGCGAACC 611
XX
XX RESULT 28
XX AAZ31783
XX ID AAZ31783 standard; DNA; 1108 BP.
XX
XX AAZ31783;
XX
XX 21-JAN-2000 (first entry)
XX
XX HPV68 E6 and E7 protein coding sequence.
XX
XX HPV68; human papillomavirus 68; detection; immunisation; infection;
XX E6 protein; E7 protein; ss.
XX
XX Human papillomavirus.
XX
XX US5981173-A.
XX
XX 09-NOV-1999.
XX
XX 11-FEB-1997; 97US-00815667.
XX
XX 14-FEB-1996; 96US-0011650P.
XX
XX 15-FEB-1996; 96US-0020458P.
XX
XX (INSP ) INST PASTEUR.
XX (INRM ) INST NAT SANTE & RECH MEDICALE.
XX
XX Longuet M, Orth G, Beaudenon S;
XX WPI; 1999-633305/54.
XX
XX New human papillomavirus (HPV) 68 and 70 DNA sequences, useful in the
XX treatment of HPV infections.
XX
XX

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XX
XX Claim 4; Fig 3a; 25pp; English.
XX
XX This sequence encodes the E6 and E7 proteins of human papillomavirus
XX (HPV) 68. The invention relates to a purified HPV68 DNA (I) deposited at
XX C.N.C.M. (Collection Nationale de Culture de Microorganismes) under
XX Accession No. I-1540, and a HPV70 DNA (II) sequence. Fragments of the
XX HPV68 and HPV70 DNA may be useful as primers or probes in the detection
XX of HPV68 or HPV70 infections. Proteins produced by the HPV DNA's can be
XX used to immunise animals against HPV68 or HPV70 infections
XX
XX Sequence 1108 BP; 375 A; 223 C; 231 G; 279 T; 0 U; 0 Other;
XX
XX Query Match 75.0%; Score 24; DB 2; Length 1108;
XX Best Local Similarity 84.4%; Pred. No. 1;
XX Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
XX 1 TTATTATAAGTGCTGCGGTCGCGAACC 32
XX ||||| ||||| ||||| ||||| |||||
XX 593 TTATTGATAGTGATGATGCTGCGAACC 624
XX
XX RESULT 29
XX AAZ31789
XX ID AAZ31789 standard; DNA; 3283 BP.
XX
XX AAZ31789;
XX
XX 21-JAN-2000 (first entry)
XX
XX HPV70 DNA sequence.
XX
XX HPV68; human papillomavirus 68; detection; immunisation; infection;
XX HPV70; ss.
XX
XX Human papillomavirus.
XX
XX US5981173-A.
XX
XX 09-NOV-1999.
XX
XX 11-FEB-1997; 97US-00815667.
XX
XX 14-FEB-1996; 96US-0011650P.
XX
XX 15-FEB-1996; 96US-0020458P.
XX
XX (INSP ) INST PASTEUR.
XX (INRM ) INST NAT SANTE & RECH MEDICALE.
XX
XX Longuet M, Orth G, Beaudenon S;
XX WPI; 1999-633305/54.
XX
XX New human papillomavirus (HPV) 68 and 70 DNA sequences, useful in the
XX treatment of HPV infections.
XX
XX Disclosure; Fig 6; 25pp; English.
XX
XX This sequence represents a human papillomavirus (HPV) 70 DNA sequence.
XX The invention relates to a purified HPV68 DNA (I) deposited at C.N.C.M.
XX (Collection Nationale de Culture de Microorganismes) under Accession No. I
XX -1540, and a HPV70 DNA (II) sequence. Fragments of the HPV68 and HPV70
XX DNA may be useful as primers or probes in the detection of HPV68 or HPV70
XX infections. Proteins produced by the HPV DNA's can be used to immunise
XX animals against HPV68 or HPV70 infections
XX
XX Sequence 3283 BP; 945 A; 640 C; 699 G; 999 T; 0 U; 0 Other;
XX
XX Query Match 75.0%; Score 24; DB 2; Length 3283;
XX Best Local Similarity 84.4%; Pred. No. 1.2;
XX Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
XX 1 TTATTATAAGTGCTGCGGTCGCGAACC 32
XX

```

Db 2754 TTATCATTAAGTGCATGAGTGTGCTGAAACC 2785

|||||

RESULT 30

AAQ25937

AAQ25937 standard; DNA; 7833 BP.

XX

AC AAQ25937;

XX

DT 24-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 18-JAN-1993 (first entry)

XX

DE Human papilloma virus HPV39 genome.

XX

KW HPV39 infection; cancer; glucocorticoid response element; GRE; enhancer;

KM 88.

XX

OS Human papillomavirus; 39.

XX

XX Key Location/Qualifiers

FT repeat_unit 43..53

FT /*tag= f

FT /function= "enhancer"

FT /note= "papillomavirus-specific palindrome"

FT 58..70

FT /*tag= g

FT /function= "enhancer"

FT /note= "papillomavirus-specific palindrome"

FT complement(406..411)

FT /*tag= c

FT complement(424..427)

FT /*tag= d

FT complement(776..2050)

FT /*tag= a

FT complement(1861..1871)

FT /*tag= e

FT /standard_name= "splice_acceptor_site"

FT /note= "potential"

FT complement(3875..4204)

FT /*tag= b

FT 7456..7467

FT /*tag= h

FT /function= "enhancer"

FT /note= "papillomavirus-specific palindrome"

XX

XX MO9211369-A1.

XX

XX 09-JUL-1992.

XX

XX 20-DEC-1991; 91WO-FR001053.

XX

XX 20-DEC-1990; 90PR-00016044.

XX

XX (INSP) INST PASTEUR.

XX (INRM) INSERM INST NAT SANTE & RECH MED.

XX

XX Orth G, Volpers C, Strecek RE;

XX

XX WPI; 1992-250090/30.

XX

XX DNA sequences of the HPV39 Papilloma:virus genome - used as a probe for

XX in-vitro diagnosis of Papilloma:virus infections in cervical, vulvar and

XX penile cancer.

XX

XX Claim 1; Fig 1; 33pp; French.

XX

XX DNA was isolated from a previously identified HPV39 clone (Virology 161,

XX 374-384, 1987), subcloned and sequenced. The HPV39 genome was found to

XX comprise 7833bp and have a G/C content of 40%. The genome comprises open

XX reading frames conserved among all the known HPV's; the ORFs are

XX postulated to code for the early proteins and capsid components of the

CC virus. In addition, two ORFs have been found on the complementary strand

CC of the genome (see features table). The non-coding regions contain three

CC complete copies of an HPV enhancer as well as two degenerate versions of

CC the consensus palindrome (location not given). Other putative features

CC which are described in the specification as being present within the

CC regulatory region but whose positions are not given include: 4 nuclear

CC factor-1 binding sites, 2 activation protein-1 binding sites, a

CC papillomavirus enhancer associated factor binding site and a

CC glucocorticoid response element. The HPV39 sequence has most homology

CC with HPV18. The HPV39 is thought to belong to a sub-group of genital HPV's

CC (with HPV18, HPV45 and a new type cloned from carcinoma ME180 cell line)

CC representing a potential oncogene. (Updated on 25-MAR-2003 to correct PN

CC field.) (Updated on 24-OCT-2003 to standardise OS field)

XX

SQ Sequence 7833 BP; 2423 A; 1486 C; 1662 G; 2262 T; 0 U; 0 Other;

Query Match 75.0%; Score 24; DB 2; Length 7833;

Best Local Similarity 84.4%; Pred. No. 1.5;

Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TTATTAATTAAGTGCATGAGTGTGCTGAAACC 32

Db 407 TTATTAATTAAGTGCATGAGTGTGCTGAAACC 438

|||||

RESULT 31

AD245655

ID AD245655 standard; DNA; 7905 BP.

XX

AC AD245655;

XX

DT 30-JUN-2005 (first entry)

XX

DE Human papillomavirus type 70 full length genomic clone - SEQ ID 9.

XX

KW tumor marker; genome; diagnosis; cancer; uterine cervix tumor;

KM rectal tumor; colon tumor; de.

XX

OS Human papillomavirus type 70.

XX

XX WO2005033333-A2.

XX

XX 14-APR-2005.

XX

XX 04-OCT-2004; 2004MO-DX000670.

XX

XX 07-OCT-2003; 2003DK-00001474.

XX

XX 07-OCT-2003; 2003US-0509205P.

XX

XX 13-FEB-2004; 2004US-0543925P.

XX

XX (DAKO-) DAKOCYTOMATION DENMARK AS.

XX

XX Chau MF, Bisgaard-Franzen K, Lin J, Raemussen OF, Wang Z, Lusk J;

XX Lindberg M, Yoast S;

XX

XX WPI; 2005-285441/29.

XX

XX New composition having a nucleic acid molecule identical to genomic clone

XX of human papilloma virus 16, 18 or 51, useful in diagnosing cancer or the

XX risk of developing cancer, in particular cervical, anal, colon and HPV-

XX related cancer.

XX

XX Claim 2; SEQ ID NO 9; 169pp; English.

XX

XX The invention comprises a composition for the detection of cancer

XX markers, the composition contains a nucleic acid molecule which is

XX substantially identical to a full length genomic clone of a human

XX papilloma virus (type 11, 16, 18, 51, 56, 58, 66, 70, or 73). The

XX composition of the invention is useful for diagnosing cancer or the risk

XX of developing cancer, in particular cervical, anal, colon and HPV-related

XX cancer. The present DNA sequence represents a human papilloma virus full

XX length genomic clone of the invention.

SQ Sequence 7905 BP; 2425 A; 1495 C; 1693 G; 2292 T; 0 U; 0 Other;
Query Match 75.0%; Score 24; DB 14; Length 7905;
Best Local Similarity 84.4%; Pred. No. 1.5;
Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 TTATTAATAAGTGCTGCGGTCCGACGAAACC 32
DB 407 TTATCATATAAGTGCTGACGAGTCTGCGAAACC 438
RESULT 32
ACCA6617
ID ACCA6617 standard; cDNA; 627 BP.
XX
AC ACCA6617;
XX
DT 02-JUN-2003 (first entry)
XX
DE Human dltbp ribosomal protein-encoding cDNA.
XX
KM Human; dltbp; diagnostic and therapeutic polynucleotide; diagnosis;
KM cancer; cell proliferative disorder; autoimmune disorder;
KM inflammatory disorder; infection; hormonal disorder; metabolic disorder;
KM neurological disorder; gastrointestinal disorder; transport disorder;
KM connective tissue disorder; drug screening; proteome analysis;
KM gene therapy; antisense therapy; genotyping; transgenic animal; knock in;
KM disease model; toxicological testing; transcript imaging;
KM ribosomal protein; gene; ss.
XX
OS Homo sapiens.
XX
PN MO200297031-A2.
XX
PD 05-DEC-2002.
XX
PF 27-MAR-2002; 2002MO-US010056.
XX
PR 28-MAR-2001; 2001US-0279619P.
PR 29-MAR-2001; 2001US-0280067P.
PR 29-MAR-2001; 2001US-0280068P.
PR 16-MAY-2001; 2001US-0291280P.
PR 17-MAY-2001; 2001US-0291829P.
PR 17-MAY-2001; 2001US-0291849P.
PR 19-JUN-2001; 2001US-0299428P.
PR 20-JUN-2001; 2001US-0299776P.
PR 20-JUN-2001; 2001US-0300001P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
PI Dufour GB, Hillman JL, Yu JY, Tuason O, Yap PE, Ameshey SR;
PI Daughtery SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstein EH;
PI Peralta CH, David WH, Lewis SA, Chen AL, Panzer SR, Harris B;
PI Flores V, Marwaha R, Lo A, Lan RX, Urashka ME;
XX
XX WPI; 2003-129518/12.
DR P-PSDB; ABR41680.
XX
PT Novel human diagnostic and therapeutic polypeptide useful for identifying
XX test compound which specifically binds to a polypeptide encoded by human
XX diagnostic and therapeutic polynucleotide, and to induce antibodies.
PS Claim 2; SEQ ID NO 538; 591bp; English.
XX
XX The invention relates to novel human diagnostic and therapeutic
XX polynucleotides designated dltbp (ACCA6080-ACCA6749) and to their encoded
XX proteins (DITHP; ABR41136-ABR41812). The invention also relates to
XX polynucleotide sequences at least 90% identical to the dltbp cDNA
XX sequences of the invention; recombinant vectors, host cells and
XX transgenic organisms comprising a dltbp nucleic acid sequence; the
XX recombinant production of DITHP proteins; antibodies specific for DITHP
XX proteins; microarrays comprising dltbp nucleic acid sequences; methods of

CC detecting dltbp nucleotide and protein sequences; methods of screening
CC for compounds which specifically bind a DITHP protein; and methods of
CC assessing the toxicity of test compounds using a dltbp hybridisation
CC probe. dltbp nucleic acid sequences and DITHP proteins may be used in the
CC diagnosis of a wide variety of conditions including cancer and other cell
CC proliferative disorders; autoimmune or inflammatory disorders; bacterial,
CC viral, fungal or parasitic infections; hormonal disorders; metabolic
CC disorders; neurological disorders; gastrointestinal disorders; transport
CC disorders; and connective tissue disorders. They may also be used to
CC screen for modulators of protein activity or gene expression. DITHP
CC proteins can additionally be used in analysis of the proteome of a tissue
CC or cell type and to induce antibodies. The dltbp nucleic acids are
CC additionally useful in somatic or germ-line gene therapy of the disorders
CC mentioned above, as a source of antisense sequences, as a source of
CC probes and primers, in genotyping and identification of individuals, in
CC the generation of transgenic animal models of human disease or knock in
CC humanised animals, in toxicological testing, and in transcript imaging.
CC The present sequence represents a dltbp cDNA encoding a DITHP protein
CC which is a ribosomal protein. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 627 BP; 192 A; 139 C; 169 G; 127 T; 0 U; 0 Other;
Query Match 74.4%; Score 23.8; DB 8; Length 627;
Best Local Similarity 92.6%; Pred. No. 1.1;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6 AATAAGTGCTGCGGTCCGACGAAACC 32
DB 69 AATAAGTGCTGCGGTCCGACGAAACC 95
RESULT 33
ABK62613
ID ABK62613 standard; cDNA; 630 BP.
XX
AC ABK62613;
XX
DT 18-JUN-2002 (first entry)
XX
DE Rat sequence differentially expressed in response to a hepatocoxin #520.
XX
XX Rat; ss; hepatocoxin; expressed sequence tag; EST; drug screening;
KM differential expression; centrilobular necrosis; steatosis.
XX
XX Rattus norvegicus.
XX
OS
XX
PN MO200210453-A2.
XX
PD 07-FEB-2002.
XX
PF 30-JUL-2001; 2001MO-US023872.
XX
PR 31-JUL-2000; 2000US-0222040P.
PR 02-NOV-2000; 2000US-0244880P.
PR 11-MAY-2001; 2001US-0290029P.
PR 15-MAY-2001; 2001US-0290645P.
PR 22-MAY-2001; 2001US-0292336P.
PR 06-JUN-2001; 2001US-0295798P.
PR 13-JUN-2001; 2001US-0297457P.
PR 19-JUN-2001; 2001US-0298849P.
PR 09-JUL-2001; 2001US-0303459P.
XX
XX (GENE-) GENE LOGIC INC.
XX
XX Mendrick D, Porter WM, Johnson KR, Castle AL, Elashoff MR;
XX WPI; 2002-241625/29.
XX
XX Predicting toxic effects of compounds or the progression of these toxic
XX effects by determining the changes in gene expression in tissues or cells

XX 30-AUG-2001.
 PD
 XX
 PF 21-FEB-2001; 2001MO-US006059.
 XX
 XX 24-FEB-2000; 2000US-0184693P.
 PR 24-FEB-2000; 2000US-0184697P.
 PR 24-FEB-2000; 2000US-0184698P.
 PR 24-FEB-2000; 2000US-0184768P.
 PR 24-FEB-2000; 2000US-0184769P.
 PR 24-FEB-2000; 2000US-0184770P.
 PR 24-FEB-2000; 2000US-0184771P.
 PR 24-FEB-2000; 2000US-0184772P.
 PR 24-FEB-2000; 2000US-0184773P.
 PR 24-FEB-2000; 2000US-0184774P.
 PR 24-FEB-2000; 2000US-0184776P.
 PR 24-FEB-2000; 2000US-0184777P.
 PR 24-FEB-2000; 2000US-0184779P.
 PR 24-FEB-2000; 2000US-0184813P.
 PR 24-FEB-2000; 2000US-0184837P.
 PR 24-FEB-2000; 2000US-0185213P.
 PR 24-FEB-2000; 2000US-0185216P.
 PR 12-MAY-2000; 2000US-0203785P.
 PR 15-MAY-2000; 2000US-0204226P.
 PR 16-MAY-2000; 2000US-0204525P.
 PR 16-MAY-2000; 2000US-0204821P.
 PR 16-MAY-2000; 2000US-0204908P.
 PR 16-MAY-2000; 2000US-0205232P.
 PR 17-MAY-2000; 2000US-0204815P.
 PR 17-MAY-2000; 2000US-0204863P.
 PR 17-MAY-2000; 2000US-0205221P.
 PR 17-MAY-2000; 2000US-0205285P.
 PR 17-MAY-2000; 2000US-0205286P.
 PR 17-MAY-2000; 2000US-0205287P.
 PR 17-MAY-2000; 2000US-0205323P.
 PR 17-MAY-2000; 2000US-0205324P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Panzer SR, Spiro PA, Banville SC, Shah P, Chalup MS, Chang SC,
 PI Chen A, D'sa SA, Amshay S, Dahl CR, Dam TC, Daniels SE, Dutoir GE,
 PI Flores V, Fong WT, Greenwalt LB, Hillman JL, Jones AL, Liu TF,
 PI Roseberry AM, Rosen BH, Russo FD, Stockreiner TK, Dafio A,
 PI Wright RJ, Yap PR, Yu JY, Bradley DL, Bratcher SR, Chen W,
 PI Cohen HJ, Hodgson DM, Lincoln SE, Jackson S;
 XX
 XX WPI, 2001-502867/55.
 DR P-PSDB; AAU19582.
 XX
 PT Polynucleotides encoding diagnostic and therapeutic proteins, e.g.
 PT enzymes, hormones and receptors, useful in diagnostics and therapeutics.
 XX
 PS Claim 1, Page 378; 522pp; English.
 XX
 CC The invention relates to polynucleotides (I) encoding diagnostic and
 CC therapeutic (DTRP) polypeptides (II), which include e.g. enzymes, and
 CC proteins involved in growth and development and receptors. (I) and (II)
 CC may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate DTRP expression. For example, (I) and (II)
 CC may be used to treat disorders associated with decreased polypeptide
 CC expression by rectifying mutations or deletions in a patient's genome,
 CC that affect the activity of the DTRPs, by expressing inactive proteins
 CC or supplementing the patient's own production of them. (I) and (II) may
 CC be used to treat diseases, for example, cell proliferative disorder,
 CC Crohn's disease, acquired immune deficiency syndrome (AIDS), lymphoma,
 CC leukemia, autoimmune disorders, and respiratory disorders. Additionally,
 CC (I) may be used to produce the DTRPs, by inserting the nucleic acids
 CC into a host cell and culturing the cell to express the protein. (I) and
 CC its complementary sequences may also be used as DNA probes in diagnostic
 CC assays to detect and quantitate the presence of similar nucleic acids in
 CC samples, and therefore which patients may be in need of restorative
 CC therapy. (II) may also be used as antigens in the production of

CC antibodies against DTRPs and in assays to identify modulators of DTRP
 CC expression and activity. The anti-DTRP antibodies and antagonists may
 CC also be used to down regulate expression and activity. The anti-DTRP
 CC antibodies may also be used as diagnostic agents for detecting the
 CC presence of DTRPs in samples (e.g. by enzyme linked immunosorbent assay
 CC (ELISA)). AAS30986-AAS31196 represent human diagnostic and therapeutic
 CC (DTRP) polynucleotides of the invention
 XX
 SQ Sequence 885 BP; 284 A; 181 C; 229 G; 187 T; 0 U; 4 Other;
 Query Match 74.4%; Score 23.8; DB 4; Length 885;
 Best Local Similarity 92.6%; Pred. No. 1.2;
 Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 6 AATAGAGTGCTGCGGTGCGAAGAC 32
 Db 69 AAAAGGTTCTCTCGGTGCGAAGAC 95
 RESULT 36
 ID AAT71196 standard; DNA; 40 BP.
 XX
 AC AAT71196;
 XX
 DT 25-MAR-2003 (revised)
 DT 20-AUG-1997 (first entry)
 XX
 DE HPV type 18 exon-specific probe, binds to spliced B6 region.
 XX
 KW Human papillomavirus; HPV; cervical cancer; cervix; neoplasia; tumour;
 KM probe; detection; diagnosis; hybridisation; ss.
 XX
 OS Synthetic.
 XX
 EN US5580970-A.
 XX
 PD 03-DEC-1996.
 PD
 PF 04-MAR-1994; 94US-00207226.
 XX
 PR 01-DEC-1989; 89US-00444526.
 PR 05-DEC-1990; 90US-00622742.
 XX
 PA (STAD) AMOCO CORP.
 XX
 PI Parodos K, Rigby S, Lane DJ, Hendricks DA;
 XX
 DR WPI, 1997-033604/03.
 XX
 PT Nucleic acid probes specific for human papilloma virus - for prognosis of
 PT cervical neoplasias and cancers.
 XX
 PS Example 1; Fig 4; 18pp; English.
 XX
 CC AAT71194-T71199 are probes used for the detection of spliced exons of
 CC human papillomavirus (HPV) types 16, 18, 31, 33 and 35. The probes
 CC specifically hybridise to B6 region exons at the splice junction of the
 CC spliced HPV genome. The probes are used for accurate and reliable
 CC prognosis of HPV-induced cancers, in particular cervical cancer. (Updated
 CC on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 40 BP; 8 A; 12 C; 9 G; 11 T; 0 U; 0 Other;
 Query Match 72.5%; Score 23.2; DB 2; Length 40;
 Best Local Similarity 89.3%; Pred. No. 1.2;
 Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 4 TTATAGAGTGCTGCGGTGCGAAGAC 31
 Db 28 TTACAGAGTGCTGCGGTGCGAAGAC 1

```
RESULT 37
AAQ44290/c
ID AAQ44290 standard; DNA, 30 BP.
XX
AC AAQ44290;
XX
DT 25-MAR-2003 (revised)
DT 02-DEC-1993 (first entry)
XX
DE Sequence of primer 2PV18 5' (C6, NH2) for human papilloma virus (HPV)
DE directed to the E6 region (19).
XX
XX Primer; exponential amplification; PCR; human papilloma virus; HPV18; ss.
XX
OS Synthetic.
XX
PN WO9312245-A1.
XX
PD 24-JUN-1993.
XX
PF 07-DEC-1992; 92MO-US010524.
XX
PR 11-DEC-1991; 91US-00804951.
XX
PA (IGEN-) IGEN INC.
XX
PI Kenten JH, Link JR;
XX
XX WPI; 1993-214186/26.
XX
PT Amplifying nucleic acid sequences of interest - using single primer to
PT provide exponential amplification in polymerase reaction.
XX
PS Example; Page 32; 54pp; English.
XX
CC The invention is in a process for exponentially amplifying a nucleic acid
CC sequence by a single unpaired primer. It includes a method for modifying
CC a putative primer to improve its ability to prime a single primer
CC exponential amplification process. Oligo amino modifications to the 5'
CC end occurred at the last coupling step. The resulting 5' modified oligos
CC all contained a six carbon spacer arm to the amino gp., designated (C6,
CC NH2). Oligo Ru(II) modifications to the 5' end occurred at the last
CC coupling step and the oligo is designated Ru(II) (Updated on 25-MAR-2003
CC to correct RN field.)
XX
SQ Sequence 30 BP; 10 A; 7 C; 4 G; 9 T; 0 U; 0 Other;
XX
Query Match 71.9%; Score 23; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 23; Conservative 0; Mismatches 0; Gaps 0;
Indels 0;

OY 1 TTATTAATAGTGCTCGCGTG 23
Db 23 TTATTAATAGTGCTCGCGTG 1

RESULT 38
AAZ07822/c
ID AAZ07822 standard; DNA, 30 BP.
XX
AC AAZ07822;
XX
DT 03-DEC-1999 (first entry)
XX
DE Oligo 2PV18 directed to HPV E6 region.
XX
XX Binding assay; electrochemiluminescence; luminescence; HPV; E6 region;
XX PCR primer; ss.
XX
OS Synthetic.
XX
PN US5962218-A.
XX
```

```
PD 05-OCT-1999.
XX
XX 24-NOV-1993; 93US-00160063.
XX
PR 03-NOV-1988; 88US-00266882.
PR 18-JUN-1990; 90US-00539389.
PR 06-FEB-1991; 91US-00652427.
PR 03-FEB-1992; 92US-00827270.
PR 12-JUL-1993; 93US-00090467.
PR 24-NOV-1993; 93US-00158193.
XX
XX (IGEN-) IGEN INT INC.
XX
PI Shah HP, Kenten JH, Goodman JE, Blackburn GF, Maesey RJ;
PI Lowke GE, Leland JK;
XX
XX WPI; 1999-579609/49.
XX
PT Binding assay based on detection of electrochemiluminescence.
XX
XX Example 20; Col 30; 43pp; English.
XX
PS The invention provides a binding assay based on measuring
XX CC electrochemiluminescence from a luminescent component concentrated in an
XX CC assay composition which is collected at an electrode for detection. The
XX CC binding assay is used to measure luminescence emitted by one or more
XX CC labeled components of the assay system. The assay can be used to measure
XX CC e.g. antigen-antibody, ligand-receptor, RNA and DNA interactions. The
XX CC sample may be derived from cells, water, feces, saliva, tissue, hair,
XX CC sweat or urine and the analyte of interest may be e.g. a whole cell,
XX CC surface antigen, subcellular particle, virus, antibody, antigen, hapten,
XX CC polysaccharide, hormone, nucleic acid, vitamin, amino acid, sugar,
XX CC recombinant protein, pharmacological agent, steroid or inorganic
XX CC molecule. The assay has improved sensitivity, faster assay time, greater
XX CC specificity, lower detection limits and greater precision than previous
XX CC methods. Sequences AAZ07818-823 represent PCR oligos directed to the HPV
XX CC E6 region, used during the course of the invention
XX
SQ Sequence 30 BP; 10 A; 7 C; 4 G; 9 T; 0 U; 0 Other;
XX
Query Match 71.9%; Score 23; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 23; Conservative 0; Mismatches 0; Gaps 0;
Indels 0;

OY 1 TTATTAATAGTGCTCGCGTG 23
Db 23 TTATTAATAGTGCTCGCGTG 1

RESULT 39
ADZ64772/c
ID ADZ64772 standard; DNA, 30 BP.
XX
AC ADZ64772;
XX
DT 30-JUN-2005 (first entry)
XX
DE HPV 18 E6 region specific PCR primer, 2PV18.
XX
XX Analyte detection; luminescence; PCR; primer; ss.
XX
XX Human papillomavirus type 18.
XX
XX Key Location/Qualifiers
XX FH modified_base 1
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "linked to a six carbon spacer arm designated (C6,
XX FT NH2)"
XX FT modified_base 30
XX FT /*tag= b
XX FT /mod_base= OTHER
XX FT /note= "linked to a three carbon spacer"
XX
```

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XX US6881589-BI.
XX
XX 19-APR-2005.
XX
XX 05-JUN-1995; 95US-00465443.
XX
XX 30-APR-1987; 87MO-US000987.
XX
XX 03-NOV-1988; 88US-00266882.
XX
XX 21-JUL-1989; 89US-00369560.
XX
XX 18-JUN-1990; 90US-00539389.
XX
XX 06-FEB-1991; 91US-00652427.
XX
XX 24-NOV-1993; 93US-00158193.
XX
XX 30-NOV-1994; 94US-00346832.
XX
XX 30-APR-1996; 96US-00858354.
XX
XX (BIOV-) BIOVERIS CORP.
XX
XX Ireland UK, Shah HP, Kenten JH, Goodman JE, Lowke GE, Namba Y,
XX Blackburn GF, Massey RJ;
XX
XX WPI; 2005-312301/32.
XX
XX
XX Electroluminescent composition useful in assay for analyte e.g.,
XX virus, comprises electroluminescent label, first and second binding
XX reagents having binding partners of analyte, collectable magnetic
XX particles and electrolyte.
XX
XX Example 20; Col 29; 48pp; English.
XX
XX
XX The present invention relates to an electroluminescent (EL)
XX composition suitable for use in electroluminescent assay for analyte
XX of interest which comprises electroluminescent label binding
XX reagents, collectable magnetic particles and an electrolyte. The present
XX composition is the human papillomavirus (HPV) E6 region specific PCR primer.
XX This sequence was used in a binding assay for an analyte of interest
XX present in a sample based upon electroluminescence.
XX
XX Sequence 30 BP; 10 A; 7 C; 4 G; 9 T; 0 U; 0 Other;
XX
XX
XX Query Match 71.9%; Score 23; DB 14; Length 30;
XX Best Local Similarity 100.0%; Pred. No. 1.4;
XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
XX 1 TTATTATAAGTGGCTGCGGTG 23
XX | ||||| ||||| ||||| |||||
XX 23 TTATTATAAGTGGCTGCGGTG 1
XX
XX
XX RESULT 40
XX ABV07997
XX ID ABV07997 standard; cDNA; 167 BP.
XX
XX
XX ABV07997;
XX
XX 13-SBP-2002 (first entry)
XX
XX Human prostate expression marker cDNA 7988.
XX
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenomic marker; gene; ss.
XX
XX Homo sapiens.
XX
XX MO200160860-A2.
XX
XX 23-AUG-2001.
XX
XX 20-FEB-2001; 2001MO-US005171.
XX
XX 17-FEB-2000; 2000US-0183319P.
XX
XX 16-MAR-2000; 2000US-0189862P.
XX
XX 25-MAY-2000; 2000US-0207454P.
XX
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```
PR 09-JUN-2000; 2000US-0211314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-025281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Schlegel R, Endege WO, Monahan JR;
XX
XX WPI; 2001-662795/76.
XX
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
XX prostate cells and correlating with presence of prostate cancer, useful
XX for detecting presence of prostate cancer, stage of prostate cancer.
XX
XX Claim 1; Page 1279; 11750pp; English.
XX
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
XX a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the
XX specification or its complement. (I) is useful for: (a) assessing whether
XX a patient is afflicted with prostate cancer; (b) monitoring the
XX progression of prostate cancer in a patient; (c) assessing the efficacy
XX of a test compound to inhibit prostate cancer in a patient; (d) assessing
XX the efficacy of a therapy for inhibiting prostate cancer in a patient;
XX (e) selecting a composition for inhibiting prostate cancer in a patient;
XX (f) assessing the prostate cell carcinogenic potential of a compound; (g)
XX determining whether prostate cancer has metastasized in a patient; (h)
XX assessing the aggressiveness or indolence of prostate cancer in a patient
XX ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
XX
XX Sequence 167 BP; 48 A; 33 C; 48 G; 37 T; 0 U; 1 Other;
XX
XX
XX Query Match 70.6%; Score 22.6; DB 5; Length 167;
XX Best Local Similarity 83.3%; Pred. No. 3;
XX Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
XX
XX 3 ATTATTAAGTGGCTGCGGTGCCGAAACC 32
XX | ||||| ||||| ||||| |||||
XX 88 AANAGAGAGGTCTCTGTGCCAGAAACC 117
XX
XX
XX RESULT 41
XX ACH89313/C
XX ID ACH89313 standard; DNA; 159 BP.
XX
XX
XX ACH89313;
XX
XX 29-JUL-2004 (first entry)
XX
XX Human genome derived single exon probe #22508.
XX
XX Human; probe; ss; gene expression; single exon probe; microarray;
XX alternative splicing event; genomic alteration.
XX
XX Homo sapiens.
XX
XX US2003194704-A1.
XX
XX 16-OCT-2003.
XX
XX 03-APR-2002; 2002US-00029386.
XX
XX 03-APR-2002; 2002US-00029386.
XX
XX (PENN/) PENN S G.
XX (RANK/) RANK D R.
XX (HANZ/) HANZEL D K.
XX
XX Penn SG, Rank DR, Hanzel DK;
XX
XX WPI; 2004-119264/12.
XX
XX New human genome-derived single exon nucleic acid probes useful for human
XX gene expression analysis, for identifying or characterizing alternative
XX
```

PT applying events, for assessing genomic alterations or as tools for
PT surveying tissues.
XX
PS Claim 1, SEQ ID NO 22508, 80bp; English.
XX
CC The invention relates to a nucleic acid probe for measuring human gene
CC expression, comprising any of the 27,400 fully defined nucleotide
CC sequences in the specification, or their complements or fragments, and
CC encoding at least 8 amino acids of any of the 6888 amino acid sequences
CC fully defined in the specification. The probe is a single exon probe that
CC hybridizes under high stringency conditions to a nucleic acid molecule
CC expressed in human cells or tissues. Also included are a spatially-
CC addressable set of single exon nucleic acid probes for measuring human
CC gene expression (comprising a plurality of single exon nucleic acid
CC probes cited above, where each of the plurality of probes is separately
CC and addressably isolatable or amplifiable from the plurality), a single
CC exon microarray for measuring human gene expression, a method of
CC measuring human gene expression, a vector comprising the single exon
CC probe cited above, an ORF-encoded peptide comprising at least 8
CC contiguous amino acids of any of the above-mentioned amino acid
CC sequences (optionally with conservative amino acid substitutions), an
CC isolated antibody that binds specifically to a peptide cited above,
CC methods of selling and/or licensing single exon probes or microarrays to
CC a customer desiring to measure gene expression, a method of providing
CC human gene expression data by subsequence, and a computer-readable
CC storage medium which contains a database having a plurality of records
CC (each record including data on the expression of a single exon probe
CC cited above). The probe, methods and apparatus are useful in gene
CC expression analysis. The probes may be used as tools for surveying
CC tissues to detect the presence of expressed messages that contain their
CC specific exon, or in constructing genome-derived single exon microarrays.
CC In addition, the probes are used in identifying and characterizing
CC alternative splicing events, in detecting and characterizing gross
CC alterations in the genomic locus that includes their exon, in assessing
CC smaller genomic alterations, in priming the synthesis of nucleic acids,
CC or in expressing the ORF-encoded peptide. Note: The sequence data for this
CC single exon probe of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docID=20030194704
XX
SQ Sequence 159 BP; 30 A; 40 C; 26 G; 63 T; 0 U; 0 Other;
XX
Query Match 69.4%; Score 22.2; DB 12; Length 159;
Best Local Similarity 88.9%; Pred. No. 4.6;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 6 AATTAAGGTGCTGCGTGCCGAGAAACC 32
Db 127 AAGAAAGTTCCTGCTGTGCCAGAAACC 101
XX
RESULT 42
AAS78228
ID AAS78228 standard; cDNA; 297 BP.
XX
AC AAS78228;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #14032.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KM food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN M0200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX

PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
DR P-PSDB; ABG14041.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 1, SEQ ID NO 14032, 103bp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridization probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping.
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 297 BP; 98 A; 57 C; 66 G; 76 T; 0 U; 0 Other;
XX
Query Match 69.4%; Score 22.2; DB 5; Length 297;
Best Local Similarity 88.9%; Pred. No. 5.2;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 6 AATTAAGGTGCTGCGTGCCGAGAAACC 32
Db 59 AAGAAAGTTCCTGCTGTGCCAGAAACC 85
XX
RESULT 43
ABX40477
ID ABX40477 standard; cDNA; 421 BP.
XX
AC ABX40477;
XX
DT 20-FEB-2003 (first entry)
XX
DE Bovine EST associated with lactation/muscle/fat deposition #5642.
XX
XX Bovine; ss; EST; expressed sequence tag; lactation; LMPD;
KM muscle deposition; fat deposition; genome mapping; gene identification;
XX gene analysis; cattle breeding.
XX
OS Bos Taurus.
XX
PN US2002137139-A1.
XX
PD 26-SEP-2002.
XX
PF 24-SEP-2001; 2001US-00960352.
XX
XX 12-JAN-1999; 99US-0115707P.
PR

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PR 11-JAN-2000; 2000US-00480902.
XX
XX (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
XX
XX Byatt JC, Mathialagan N, Tao N, Warren WC;
XX WPI; 2003-110599/10.
XX
XX New nucleic acid associated with lactation, and muscle and fat
PT deposition, useful for genome mapping, gene identification and analysis,
PT cattle breeding, or for genetically improving cattle.
XX
XX Claim 2; SEQ ID NO 5642; 245bp; English.
XX
XX The invention relates to a purified nucleic acid molecule associated with
CC lactation or muscle and fat deposition (designated LMPD), derived from
CC cattle, and the LMPD nucleic acid can specifically hybridize to a second
CC nucleic acid molecule comprising any of 1512 nucleotide sequences,
CC appearing as ABX34836-ABX49947, or complements of them. Also included are
CC (1) a transformed cell having a nucleic acid comprising an LMPD nucleic
CC acid linked to a promoter and a 3' non-translated sequence that
CC functions in the cell to cause termination of transcription and addition
CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
CC (2) determining a level or pattern of a molecule in a bovine cell or
CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
CC of the 1512 nucleic acid sequences or its complement or fragment) with a
CC complementary nucleic acid molecule obtained from the bovine cell or
CC tissue, where hybridization between the marker nucleic acid and the
CC complementary nucleic acid permits the detection of the molecule; and (b)
CC detecting the level or pattern of the complementary nucleic acid, where
CC the detection of the complementary nucleic acid is predictive of the
CC level or pattern of the molecule. The LMPD nucleic acid is used for
CC determining a level or pattern of a molecule in a bovine cell or tissue.
CC It is useful for genome mapping, gene identification and analysis, cattle
CC breeding, preparation of constructs for use in cattle gene expression, or
CC for genetically improving cattle. The present sequence is one of the
CC 1512 bovine LMPD BST (expressed sequence tag) nucleic acids. Note: The
CC present sequence was not shown in the specification but was obtained in
CC electronic format from the USPTO web site:
CC seqdata.uspto.gov/sequence.html?DocID=20020137139
XX
XX Sequence 421 BP; 142 A; 85 C; 111 G; 83 T; 0 U; 0 Other;
SQ
XX
XX Query Match 69.4%; Score 22.2; DB 8; Length 421;
XX Best Local Similarity 88.9%; Pred. No. 5.6;
XX Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 6 AATAAGTGCTCGGTCGCGAACC 32
DB 30 AAGAAGTCTCTCTGTGCGAACC 56

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XX
XX 30-JAN-2001; 2001WO-US000670.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488901/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human cervical epithelial cells.
XX
XX Claim 25; SEQ ID NO 62; 487bp; English.
XX
XX The present invention relates to human single exon nucleic acid probes
CC (SENPs). The present sequence is one such probe. The SENPs are derived
CC from human HeLa cells. The SENPs can be used to produce a single exon
CC microarray, which can be used for measuring human gene expression in a
CC sample derived from human cervical epithelial cells. By measuring gene
CC expression, the probes are therefore useful in grading and/or staging of
CC diseases of the cervix, notably cervical cancer. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 460 BP; 163 A; 87 C; 112 G; 98 T; 0 U; 0 Other;
SQ
XX
XX Query Match 69.4%; Score 22.2; DB 4; Length 460;
XX Best Local Similarity 88.9%; Pred. No. 5.7;
XX Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 6 AATAAGTGCTCGGTCGCGAACC 32
DB 38 AAGAAGTCTCTCTGTGCGAACC 64

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XX
XX 30-JAN-2001; 2001WO-US000669.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX ABA51759
XX ABA51759;
XX
XX 01-FEB-2002 (first entry)
XX
XX Human foetal liver single exon nucleic acid probe #64.
XX
XX Human, foetal liver; gene expression; single exon nucleic acid probe; ss.
XX Homo sapiens.
XX
XX WO200157277-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000669.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX

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XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI WPI; 2001-483447/52.
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human fetal liver.
XX
PS Claim 1; SEQ ID NO 64; 639pp + Sequence listing; English.
XX
XX The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and
CC displaying gene expression in samples derived from human fetal liver. The
CC present sequence is a single exon nucleic acid probe of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 460 BP; 163 A; 87 C; 112 G; 98 T; 0 U; 0 Other;
XX
Query Match 69.4%; Score 22.2; DB 4; Length 460;
Best Local Similarity 88.9%; Pred. No. 5.7;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 6 AATTAAGTGCCTGCGTCCGCAAAACC 32
DB 38 AAGAAGTCTCTGCTGCGCAAAACC 64
RESULT 46
AA131375
ID AA131375 standard; DNA; 460 BP.
XX
AC AA131375;
XX
DT 17-OCT-2001 (first entry)
XX
DE Probe #61 used to measure gene expression in human placenta sample.
XX
KM Probe; microarray; human; placenta; antenatal diagnosis;
KM genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200157272-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000663.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488897/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.
XX
PS Claim 25; SEQ ID NO 61; 654pp; English.
XX
XX The present invention relates to single exon nucleic acid probes (SENP).
CC The present sequence is one such probe. The probes are useful for
CC producing a microarray for predicting, measuring and displaying gene

CC expression in samples derived from human placenta. The probes are useful
CC for antenatal diagnosis of human genetic disorders
XX
SQ Sequence 460 BP; 163 A; 87 C; 112 G; 98 T; 0 U; 0 Other;
XX
Query Match 69.4%; Score 22.2; DB 4; Length 460;
Best Local Similarity 88.9%; Pred. No. 5.7;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 6 AATTAAGTGCCTGCGTCCGCAAAACC 32
DB 38 AAGAAGTCTCTGCTGCGCAAAACC 64
RESULT 47
ABA21587
ID ABA21587 standard; DNA; 460 BP.
XX
AC ABA21587;
XX
DT 23-JAN-2002 (first entry)
XX
DE Probe #53 for gene expression analysis in human heart cell sample.
XX
KM Human; gene expression; heart; microarray; vascular system; probe;
KM cardiovascular disease; hypertension; cardiac arrhythmia;
KM congenital heart disease; ss.
XX
OS Homo sapiens.
XX
PN WO200157274-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000666.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488897/53.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT hearts.
XX
PS Claim 1; SEQ ID NO 53; 530pp; English.
XX
XX The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart. The
CC present sequence is one such probe. The probes may be used for
CC predicting, measuring and displaying gene expression in samples derived
CC from the human heart via microarray. By measuring gene expression, the
CC probes are useful for predicting, diagnosing, grading, staging,
CC monitoring and prognostating diseases of the human heart and vascular system
CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC congenital heart disease. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 460 BP; 163 A; 87 C; 112 G; 98 T; 0 U; 0 Other;
XX
Query Match 69.4%; Score 22.2; DB 4; Length 460;
Best Local Similarity 88.9%; Pred. No. 5.7;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX

PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX

DR WPI; 2001-488898/53.
 XX

PT Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human adult liver.

PS Claim 1; SEQ ID NO 63; 658bp; English.

XX
 CC The invention relates to a single exon nucleic acid probe (SENP) (I) for
 CC measuring human gene expression in a sample derived from human adult
 CC liver, comprising one of 13109 defined nucleotide sequences given in the
 CC specification (or complements/ fragments). The probe hybridises at high
 CC stringency to a nucleic acid molecule expressed in the human adult liver.
 CC (I) may be used for predicting, measuring and displaying gene expression
 CC in samples derived from human adult liver. The genes identified may be
 CC involved in genetic liver diseases such as cirrhosis,
 CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
 CC associated with coronary heart disease. ABS25011-ABS51005 represent human
 CC liver single exon nucleic acid probes of the invention. Note: The
 CC sequence information for this patent does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

SQ Sequence 460 BP; 163 A; 87 C; 112 G; 98 T; 0 U; 0 Other;

Query Match 69.4%; Score 22.2; DB 4; Length 460;

Best Local Similarity 88.9%; Pred. No. 5.7;

Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 AATAGGTGCTGCGGTGCCAGAAACC 32

DB 38 AAGAGGTGCTGCTGCGGTGCCAGAAACC 64

Search completed: May 24, 2006, 05:55:19
 Job time : 382.899 secs

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OM nucleic - nucleic search, using sw model

Run on: May 24, 2006, 05:47:01 ; Search time 2208.88 Seconds
(without alignments)
810.102 Million cell updates/sec

Title: US-10-601-913-121

Perfect score: 32
Sequence: 1 TTTATATAGTGCTGCGGTGCCAGAAC 32

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 2795965780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1000 summaries

Database :

EST: *
1: gb_est1: *
2: gb_est3: *
3: gb_est4: *
4: gb_est5: *
5: gb_est6: *
6: gb_est7: *
7: gb_est8: *
8: gb_est9: *
9: gb_est10: *
10: gb_est11: *
11: gb_est12: *
12: gb_est13: *
13: gb_est14: *
14: gb_est15: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	100.0	316	10	DM414483 HHAGB0152
2	32	100.0	549	9	DA567416
3	32	100.0	890	7	BE543005
4	25.6	80.0	443	10	BE911801
5	24.2	75.6	219	10	DM445957
6	24.2	75.6	229	10	DM443699
7	24.2	75.6	287	10	DM442480
8	24.2	75.6	289	10	DM442488
9	24.2	75.6	294	10	DM442532
10	24.2	75.6	312	10	DM415682
11	24.2	75.6	405	2	BE912441
12	24.2	75.6	405	2	BE912537
13	24.2	75.6	407	10	DM419176
14	24.2	75.6	410	2	BE912279
15	24.2	75.6	420	7	AM675319
16	24.2	75.6	509	7	BE018031
17	24.2	75.6	742	2	BI260198
18	24.2	75.6	748	2	BI333226
19	24.2	75.6	758	2	BI222960

20	24.2	75.6	827	2	BI255152
21	24.2	75.6	833	2	BI223045
22	24.2	75.6	833	4	BX400902
23	24.2	75.6	856	7	BE54557
24	24.2	75.6	922	7	BE544755
25	24.2	75.6	1043	2	BI256241
26	24.2	75.6	1114	2	BI257598
27	24	74.4	554	1	AI747399
28	23.8	74.4	202	1	AA68665
29	23.8	74.4	212	1	AA686627
30	23.8	74.4	289	10	DM320563
31	23.8	74.4	299	1	AA685796
32	23.8	74.4	323	10	DM300318
33	23.8	74.4	341	1	AA685923
34	23.8	74.4	344	7	BE127031
35	23.8	74.4	346	1	AI229881
36	23.8	74.4	346	10	H35039
37	23.8	74.4	347	10	DM311724
38	23.8	74.4	350	10	DM380853
39	23.8	74.4	359	1	AJ647449
40	23.8	74.4	367	7	BE128703
41	23.8	74.4	386	8	CV971013
42	23.8	74.4	386	10	DM383713
43	23.8	74.4	387	10	DM383827
44	23.8	74.4	398	10	DM385499
45	23.8	74.4	401	10	DM386589
46	23.8	74.4	415	1	AA956776
47	23.8	74.4	418	5	CF273504
48	23.8	74.4	490	1	AA944687
49	23.8	74.4	498	1	AJ647149
50	23.8	74.4	502	1	AJ650336
51	23.8	74.4	509	4	CB784201
52	23.8	74.4	507	5	CD373031
53	23.8	74.4	523	4	CB718681
54	23.8	74.4	529	7	BE408050
55	23.8	74.4	571	4	CB608193
56	23.8	74.4	575	4	CB608193
57	23.8	74.4	592	5	CD372858
58	23.8	74.4	605	4	CA339837
59	23.8	74.4	607	5	CF273502
60	23.8	74.4	618	3	BE949183
61	23.8	74.4	620	10	DV216610
62	23.8	74.4	621	4	BE578714
63	23.8	74.4	621	4	BE578714
64	23.8	74.4	624	7	AM914081
65	23.8	74.4	630	1	AI009096
66	23.8	74.4	632	5	CD372845
67	23.8	74.4	632	4	CB576783
68	23.8	74.4	637	5	BE500480
69	23.8	74.4	651	5	CD372782
70	23.8	74.4	654	10	DT901616
71	23.8	74.4	666	4	CB557077
72	23.8	74.4	668	2	BM388719
73	23.8	74.4	671	5	CF977555
74	23.8	74.4	702	5	CK366084
75	23.8	74.4	706	10	DT897178
76	23.8	74.4	712	5	CK365811
77	23.8	74.4	739	3	BU491662
78	23.8	74.4	739	8	CV120816
79	23.8	74.4	741	8	CO562425
80	23.8	74.4	744	3	BU492327
81	23.8	74.4	761	5	CD373397
82	23.8	74.4	768	10	DT900112
83	23.8	74.4	788	4	CB316334
84	23.8	74.4	808	4	CB316171
85	23.8	74.4	824	4	CB314729
86	23.8	74.4	824	8	CO388606
87	23.8	74.4	846	8	CO398822
88	23.8	74.4	846	8	CO388172
89	23.8	74.4	855	8	CO388172
90	23.8	74.4	875	5	CF111188
91	23.6	73.8	216	5	CF527423
92	23.6	73.8	708	9	DM886035

BI255152	60297434
BI223045	602943381
BX400902	601076564
BE54557	601076564
BE544755	601076520
BI256241	602975055
BI257598	60297170
AI747399	u105h08.y
AA68665	EST110976
AA686627	EST110842
DM320563	LRAGEB0453
AA685796	EST108189
DM300318	LRAGEB0621
AA685923	EST108644
BE127031	DEPA0780
AI229881	EST126576
H35039	EST109541.R
DM311724	LRAGEB0725
DM380853	LRAGEB0255
AJ647449	AJ647449
BE128703	DEPA2453
CV971013	LRAGEB0101
DM383713	LRAGEB0287
DM383827	LRAGEB0288
DM385499	LRAGEB0296
DM386589	LRAGEB0299
AA956776	UI-R-B1-f
CF273504	IGAM8.Rac
AA944687	EST920186
AJ647149	AJ647149
AJ650336	AJ650336
CB784201	AMGNNUC.C
CD373031	UI-R-GRO-
CB718681	AMGNNUC.C
BE408050	UI-R-BJ2-
CB615525	AMGNNUC.N
CB608193	AMGNNUC.N
CD372858	UI-R-GRO-
CA339837	NISC.1y08
CF273502	IGAT368.R
BE949183	BP494183
DV216610	gx25e06.y
BE578714	AMGNNUC.U
BE578714	AMGNNUC.U
AM914081	EST745398
AI009096	EST703547
DM398288	LRAGEB0406
CD372845	UI-R-GRO-
CB576783	AMGNNUC.C
BE500480	BP500480
CD372782	UI-R-GRO-
DT901616	1480859.M
CB557077	AMGNNUC.N
BM388719	UI-R-DZ0-
CF977555	FAR1281.R
CK366084	AGENCOURT
DT897178	1459354.M
CK365811	AGENCOURT
BU491662	604129275
CV120816	AGENCOURT
CO562425	AGENCOURT
BU492327	604129172
CD373397	UI-R-GRO-
DT900112	1479196.M
CB316334	AGENCOURT
CB316171	AGENCOURT
CB314729	AGENCOURT
CO388606	AGENCOURT
CO398822	AGENCOURT
CO388172	AGENCOURT
CF111188	Shultzomi
CF527423	tu-C--21
DM886035	na54a02.

93	23.6	73.8	834	9	DN882440	DN882440 naef07g06.	166	22.2	69.4	441	10	DY073827	DY073827 000227BSP
94	23.6	73.8	851	9	DN886755	DN886755 naef39a12.	167	22.2	69.4	445	2	BM433882	BM433882 10m10c02
95	23.2	72.5	277	10	DM427931	DM427931 HJAGE0276	168	22.2	69.4	448	7	BE484970	BE484970 171811 BA
96	23	71.9	197	10	DY141347	DY141347 001122BPM	169	22.2	69.4	452	2	BM434009	BM434009 10m16D05
97	23	71.9	579	1	AA098831	AA098831 zmf5a06.r	170	22.2	69.4	452	10	DV842825	DV842825 1801212 C
98	22.8	71.2	147	1	AA108307	AA108307 EST0050.r	171	22.2	69.4	456	4	CB144715	CB144715 K-EST0199
99	22.8	71.2	306	10	DM289857	DM289857 LEAGE0526	172	22.2	69.4	462	1	AV596893	AV596893 AV596893
100	22.6	70.6	415	10	DM418838	DM418838 HJAGE0015	173	22.2	69.4	464	10	DY189000	DY189000 000203BCX
101	22.6	70.6	649	13	DU243786	DU243786 109857422	174	22.2	69.4	467	7	DV800388	DV800388 1801313.C
102	22.4	70.0	193	7	BB562912	BB562912 BB562912	175	22.2	69.4	470	7	BE588312	BE588312 194172 BA
103	22.4	70.0	341	4	BY052503	BY052503 BY052503	176	22.2	69.4	481	2	BM326951	BM326951 AR071E051
104	22.4	70.0	414	5	CJ053554	CJ053554 CJ053554	177	22.2	69.4	483	2	BM430474	BM430474 18034H11
105	22.4	70.0	463	2	BF726799	BF726799 by12b05.y	178	22.2	69.4	497	2	BG223675	BG223675 180006E03
106	22.4	70.0	1282	2	BM456712	BM456712 AGENC02RT	179	22.2	69.4	497	10	DV812780	DV812780 F23112
107	22.2	69.4	109	10	DY182402	DY182402 001023BUT	180	22.2	69.4	508	10	F23112	F23112 SSC22E03 Po
108	22.2	69.4	143	5	CK968119	CK968119 4083335 B	181	22.2	69.4	510	7	BE481387	BE481387 166811 BA
109	22.2	69.4	153	7	BE476901	BE476901 160352 BA	182	22.2	69.4	512	7	BE478596	BE478596 162920 BA
110	22.2	69.4	201	10	DY107203	DY107203 000308BSP	183	22.2	69.4	513	7	BE485272	BE485272 172250 BA
111	22.2	69.4	205	14	DQ031010	DQ031010 Pan trogl	184	22.2	69.4	517	7	AM411470	AM411470 EH12e06.x
112	22.2	69.4	207	14	DQ031009	DQ031009 Homo sapi	185	22.2	69.4	517	7	BE483880	BE483880 170226 BA
113	22.2	69.4	211	10	DY205215	DY205215 000727BPM	186	22.2	69.4	520	1	AV668063	AV668063 AV668063
114	22.2	69.4	212	10	DY110059	DY110059 0000714BTS	187	22.2	69.4	530	7	BE482154	BE482154 167831 BA
115	22.2	69.4	221	8	CO953375	CO953375 UMC-Pfeto	188	22.2	69.4	530	8	CX050330	CX050330 PDTC#2044
116	22.2	69.4	224	7	BE846115	BE846115 232259 BA	189	22.2	69.4	535	8	CN433269	CN433269 BR030001A
117	22.2	69.4	249	1	AJ747524	AJ747524 AJ747524	190	22.2	69.4	536	8	CN434893	CN434893 BR030010A
118	22.2	69.4	249	10	DV846885	DV846885 LB01229.C	191	22.2	69.4	543	2	BM429129	BM429129 AV592129
119	22.2	69.4	253	10	DY149492	DY149492 001030BMU	192	22.2	69.4	543	2	BM429193	BM429193 1A15C11 B
120	22.2	69.4	266	10	DY051828	DY051828 000218BOV	193	22.2	69.4	546	1	AV591542	AV591542 AV591542
121	22.2	69.4	267	10	DY117206	DY117206 000802BAP	194	22.2	69.4	548	10	DV805861	DV805861 LB0137.CR
122	22.2	69.4	267	10	DY197959	DY197959 000803BML	195	22.2	69.4	553	10	DY039978	DY039978 001019BUT
123	22.2	69.4	269	10	DY152333	DY152333 001009BUT	196	22.2	69.4	556	1	AV664344	AV664344 AV664344
124	22.2	69.4	272	10	DY111603	DY111603 000218BOV	197	22.2	69.4	557	2	B1326995	B1326995 AR072D121
125	22.2	69.4	274	10	DY141132	DY141132 001013BMP	198	22.2	69.4	558	8	CX058901	CX058901 PDTC#2029
126	22.2	69.4	284	7	BR477427	BR477427 161114 BA	199	22.2	69.4	558	9	DB195996	DB195996 DB195996
127	22.2	69.4	297	10	DY138281	DY138281 000803BML	200	22.2	69.4	559	1	AV594595	AV594595 AV594595
128	22.2	69.4	300	10	DV842878	DV842878 LB01213.C	201	22.2	69.4	563	1	AV599885	AV599885 AV599885
129	22.2	69.4	301	10	DT831240	DT831240 LB00410.C	202	22.2	69.4	564	1	AV597152	AV597152 AV597152
130	22.2	69.4	301	10	DY143342	DY143342 000403BMV	203	22.2	69.4	554	9	DN884268	DN884268 naE21D04.C
131	22.2	69.4	314	10	DY044136	DY044136 000207BCR	204	22.2	69.4	555	8	CX060994	CX060994 PDTC#2052
132	22.2	69.4	314	10	DY165102	DY165102 000727BPM	205	22.2	69.4	566	1	AV591474	AV591474 AV591474
133	22.2	69.4	316	10	DY063793	DY063793 001013BMP	206	22.2	69.4	570	9	DB077192	DB077192 DB077192
134	22.2	69.4	317	10	DY186529	DY186529 001007BMP	207	22.2	69.4	571	8	CX060440	CX060440 PDTC#2046
135	22.2	69.4	319	10	DY089295	DY089295 000210BCR	208	22.2	69.4	571	10	DY070611	DY070611 991221BTL
136	22.2	69.4	320	10	DY123760	DY123760 000314BSP	209	22.2	69.4	572	3	BU917276	BU917276 EST218 Bo
137	22.2	69.4	323	10	DY068346	DY068346 000209BCR	210	22.2	69.4	573	14	CR806533	CR806533 GRO9AA28C
138	22.2	69.4	324	10	DY154757	DY154757 000308BSP	211	22.2	69.4	574	1	AV593978	AV593978 AV593978
139	22.2	69.4	327	10	DY124409	DY124409 001011BMP	212	22.2	69.4	577	8	CN435140	CN435140 BR030011B
140	22.2	69.4	328	10	DV802844	DV802844 LB01322.C	213	22.2	69.4	578	10	DY111448	DY111448 000416BSV
141	22.2	69.4	333	10	DY058909	DY058909 001009BMP	214	22.2	69.4	579	8	CN435433	CN435433 BR030010B
142	22.2	69.4	352	10	DY202803	DY202803 000204BCX	215	22.2	69.4	580	1	AV597438	AV597438 AV597438
143	22.2	69.4	354	10	DY135659	DY135659 000124BLI	216	22.2	69.4	582	8	CN435381	CN435381 BR030012B
144	22.2	69.4	359	10	DY188107	DY188107 000207BCR	217	22.2	69.4	582	10	DY153512	DY153512 000807BMV
145	22.2	69.4	360	10	DY056362	DY056362 000405BPP	218	22.2	69.4	583	1	AV599592	AV599592 AV599592
146	22.2	69.4	368	10	DY126431	DY126431 991201BOV	219	22.2	69.4	584	5	CD288440	CD288440 4.H1.bd
147	22.2	69.4	370	10	DY073689	DY073689 000312BSP	220	22.2	69.4	586	7	BE589991	BE589991 156749 BA
148	22.2	69.4	384	10	DY136414	DY136414 9911127BCM	221	22.2	69.4	586	10	DV836965	DV836965 LB01114.C
149	22.2	69.4	387	10	DY126754	DY126754 000405BPP	222	22.2	69.4	589	4	CB288075	CB288075 CMD73.D10
150	22.2	69.4	388	10	DY101488	DY101488 000229BOV	223	22.2	69.4	589	8	CV876053	CV876053 PDTC#1147
151	22.2	69.4	391	10	DY077573	DY077573 000130BLI	224	22.2	69.4	590	1	AV592533	AV592533 AV592533
152	22.2	69.4	407	10	DY069960	DY069960 991117BCM	225	22.2	69.4	590	1	AV597402	AV597402 AV597402
153	22.2	69.4	410	4	CB223764	CB223764 1JEJ27D6	226	22.2	69.4	590	8	CN435148	CN435148 BR030011B
154	22.2	69.4	410	10	DY076935	DY076935 000330BMP	227	22.2	69.4	590	8	DN885544	DN885544 naE30D05.
155	22.2	69.4	412	10	DY111059	DY111059 000220BOV	228	22.2	69.4	591	1	AV595211	AV595211 AV595211
156	22.2	69.4	415	1	AM005067	AM005067 AM005067	229	22.2	69.4	592	1	AV597314	AV597314 AV597314
157	22.2	69.4	418	1	AM004540	AM004540 AM004540	230	22.2	69.4	593	1	AV652922	AV652922 AV652922
158	22.2	69.4	420	9	DN824009	DN824009 LB0011.C2	231	22.2	69.4	593	4	CB223491	CB223491 1JES2248
159	22.2	69.4	420	9	DN824382	DN824382 LB0012.C2	232	22.2	69.4	593	10	DV803780	DV803780 AV608291
160	22.2	69.4	420	9	DN824811	DN824811 LB0013.C2	233	22.2	69.4	594	1	AV608291	AV608291 AV608291
161	22.2	69.4	420	9	DN825066	DN825066 LB0014.C2	234	22.2	69.4	594	4	CB465785	CB465785 727850 MA
162	22.2	69.4	425	1	AA983028	AA983028 vF58a05.r	235	22.2	69.4	594	5	CF765705	CF765705 C88001443
163	22.2	69.4	435	10	DY050600	DY050600 000223BSP	236	22.2	69.4	595	1	AV616915	AV616915 AV616915
164	22.2	69.4	435	10	DY056571	DY056571 000403BMV	237	22.2	69.4	596	10	DV835984	DV835984 LB01110.C
165	22.2	69.4	435	10	DY058351	DY058351 000405BTV	238	22.2	69.4	596	10	DV846593	DV846593 LB01228.C

239	22.2	69.4	597	5	CK961984	CK961984 4076421 B	312	22.2	69.4	691	9	DN883192	DN883192 nat13b10.
240	22.2	69.4	597	10	DV823311	DV823311 LB02012.C	313	22.2	69.4	691	10	DV829689	DV829689 LB01912.C
241	22.2	69.4	598	1	AV618112	AV618112 AV618112	314	22.2	69.4	692	1	AJ945999	AJ945999 AJ945999
242	22.2	69.4	598	5	CF765204	CF765204 CES002425	315	22.2	69.4	692	10	DV802586	DV802586 LB01332.C
243	22.2	69.4	599	1	AV596443	AV596443 AV596443	316	22.2	69.4	694	10	DN892899	DN892899 1475367 M
244	22.2	69.4	599	5	CF768594	CF768594 CES002415	317	22.2	69.4	695	10	DV837051	DV837051 LB01115.C
245	22.2	69.4	600	1	AV616147	AV616147 AV616147	318	22.2	69.4	696	10	DV830823	DV830823 LB01917.C
246	22.2	69.4	600	4	CB468908	CB468908 cd01 B12.	319	22.2	69.4	697	9	DN886142	DN886142 nat13a901.
247	22.2	69.4	603	10	DV840144	DV840144 LB01127.C	320	22.2	69.4	697	10	DV802003	DV802003 LB01319.C
248	22.2	69.4	606	1	AV665738	AV665738 AV665738	321	22.2	69.4	699	10	DV801945	DV801945 LB01319.C
249	22.2	69.4	606	8	CN435523	CN435523 BE030013B	322	22.2	69.4	701	10	DV801002	DV801002 LB01315.C
250	22.2	69.4	607	7	BE589183	BE589183 194889 BA	323	22.2	69.4	701	10	DV841361	DV841361 LB0117.C
251	22.2	69.4	607	8	CK062917	CK062917 PDUE2073	324	22.2	69.4	702	10	DV836082	DV836082 LB01111.C
252	22.2	69.4	607	10	DT859165	DT859165 LB00539.C	325	22.2	69.4	703	8	CY548000	CY548000 EST416 Bo
253	22.2	69.4	609	1	AV594566	AV594566 AV594566	326	22.2	69.4	703	10	DV801112	DV801112 LB01316.C
254	22.2	69.4	609	1	AV601067	AV601067 AV601067	327	22.2	69.4	704	10	DV809959	DV809959 LB01423.C
255	22.2	69.4	612	8	CN435087	CN435087 BE030011B	328	22.2	69.4	705	10	DT847613	DT847613 LB00478.C
256	22.2	69.4	612	10	DV809250	DV809250 LB01420.C	329	22.2	69.4	706	10	DV830532	DV830532 LB01915.C
257	22.2	69.4	616	10	DV835589	DV835589 LB0199.CR	330	22.2	69.4	706	10	DV833278	DV833278 LB01926.C
258	22.2	69.4	619	10	DT844871	DT844871 LB004105.C	331	22.2	69.4	709	5	CK830829	CK830829 4054186 B
259	22.2	69.4	621	10	DV804231	DV804231 LB01328.C	332	22.2	69.4	709	10	DV805837	DV805837 LB0137.CR
260	22.2	69.4	621	10	DV809669	DV809669 LB01422.C	333	22.2	69.4	710	10	DV805526	DV805526 LB0136.CR
261	22.2	69.4	624	8	CN432964	CN432964 BE030005A	334	22.2	69.4	713	10	DT849455	DT849455 LB00487.C
262	22.2	69.4	624	10	DV801018	DV801018 LB01315.C	335	22.2	69.4	720	10	DV801874	DV801874 LB01319.C
263	22.2	69.4	629	10	DV800541	DV800541 LB01314.C	336	22.2	69.4	720	10	DV804649	DV804649 LB01329.C
264	22.2	69.4	633	5	CF765055	CF765055 CES002916	337	22.2	69.4	721	10	DT722512	DT722512 LB0134.CR
265	22.2	69.4	635	5	CF977554	CF977554 PAR1983.R	338	22.2	69.4	721	10	DV835375	DV835375 LB0198.CR
266	22.2	69.4	637	5	CF613542	CF613542 CES008097	339	22.2	69.4	722	5	CF763459	CF763459 CES006037
267	22.2	69.4	637	5	CF766852	CF766852 CES002610	340	22.2	69.4	722	10	DT720249	DT720249 LB0114.CR
268	22.2	69.4	643	8	CR766441	CR766441 DXP2469A	341	22.2	69.4	722	10	DV808541	DV808541 LB01417.C
269	22.2	69.4	644	10	DV824969	DV824969 LB02021.C	342	22.2	69.4	724	10	DV824970	DV824970 LB02021.C
270	22.2	69.4	645	10	DV800740	DV800740 LB01314.C	343	22.2	69.4	724	10	DV829295	DV829295 LB01911.C
271	22.2	69.4	645	10	DV836905	DV836905 LB01114.C	344	22.2	69.4	725	10	DV811320	DV811320 LB01428.C
272	22.2	69.4	649	5	CK831251	CK831251 4054789 B	345	22.2	69.4	725	10	DV833090	DV833090 LB01926.C
273	22.2	69.4	651	5	CF766367	CF766367 CES006755	346	22.2	69.4	726	10	DT896704	DT896704 1458829 M
274	22.2	69.4	654	5	CF615283	CF615283 CES008848	347	22.2	69.4	726	10	DV906251	DV906251 LB0183.CR
275	22.2	69.4	655	8	CK058506	CK058506 PDUE2025	348	22.2	69.4	727	4	CB309887	CB309887 AGENCOURT
276	22.2	69.4	655	5	CK970128	CK970128 4085436 B	349	22.2	69.4	727	10	DV826934	DV826934 LB02031.C
277	22.2	69.4	659	10	DV830613	DV830613 LB01915.C	350	22.2	69.4	728	10	DT888016	DT888016 1464750 M
278	22.2	69.4	660	9	DN884038	DN884038 nat19c08.	351	22.2	69.4	728	10	DV800967	DV800967 LB01315.C
279	22.2	69.4	660	10	DV805126	DV805126 LB0135.CR	352	22.2	69.4	729	1	AJ944912	AJ944912 AJ944912
280	22.2	69.4	661	10	DV807435	DV807435 LB01412.C	353	22.2	69.4	729	10	DR713095	DR713095 LB0054.CR
281	22.2	69.4	663	10	DV829531	DV829531 LB01911.C	354	22.2	69.4	729	10	DV829732	DV829732 LB01912.C
282	22.2	69.4	664	4	BM959074	BM959074 BM959074	355	22.2	69.4	730	10	DT721847	DT721847 LB01133.CR
283	22.2	69.4	664	10	DV840641	DV840641 LB01129.C	356	22.2	69.4	730	10	DT893979	DT893979 1476546 M
284	22.2	69.4	665	5	CK835870	CK835870 4060519 B	357	22.2	69.4	730	10	DV800223	DV800223 LB01313.C
285	22.2	69.4	665	9	CK969861	CK969861 4085469 B	358	22.2	69.4	730	10	DV800950	DV800950 LB01315.C
286	22.2	69.4	666	10	DT721826	DT721826 LB0132.CR	359	22.2	69.4	731	4	CB311057	CB311057 AGENCOURT
287	22.2	69.4	666	10	DV843225	DV843225 LB01214.C	360	22.2	69.4	731	10	DT848473	DT848473 LB00482.C
288	22.2	69.4	667	5	CK949083	CK949083 4074179 B	361	22.2	69.4	731	10	DV824679	DV824679 LB02019.C
289	22.2	69.4	667	8	CK982689	CK982689 4115187 B	362	22.2	69.4	732	10	DV906858	DV906858 LB02016.C
290	22.2	69.4	668	5	CK942179	CK942179 4065755 B	363	22.2	69.4	734	10	DV823974	DV823974 LB02016.C
291	22.2	69.4	668	5	CK963347	CK963347 4077824 B	364	22.2	69.4	734	10	DR769360	DR769360 ILLUMIGEN
292	22.2	69.4	668	5	CK963347	CK963347 4077824 B	365	22.2	69.4	735	10	DT722959	DT722959 LB0142.CR
293	22.2	69.4	668	10	DV803800	DV803800 LB01326.C	366	22.2	69.4	735	10	DV801132	DV801132 LB01316.C
294	22.2	69.4	669	5	CD768115	CD768115 AGENCOURT	367	22.2	69.4	736	10	DV825208	DV825208 LB02022.C
295	22.2	69.4	670	10	DT820469	DT820469 LB00214.C	368	22.2	69.4	738	10	DT847613	DT847613 LB00478.C
296	22.2	69.4	671	10	DV806207	DV806207 LB0139.CR	369	22.2	69.4	738	10	DT847045	DT847045 LB02023.C
297	22.2	69.4	674	10	DV801955	DV801955 LB01319.C	370	22.2	69.4	739	10	DT860206	DT860206 LB00545.C
298	22.2	69.4	675	4	BM957376	BM957376 BM957376	371	22.2	69.4	740	4	CB308991	CB308991 AGENCOURT
299	22.2	69.4	675	8	CK975201	CK975201 4106278 B	372	22.2	69.4	741	10	DT719488	DT719488 LB0111.CR
300	22.2	69.4	676	4	CD052020	CD052020 PL1235 CA	373	22.2	69.4	741	10	DV800210	DV800210 LB01311.C
301	22.2	69.4	680	10	DV844560	DV844560 LB01219.C	374	22.2	69.4	741	10	DV836736	DV836736 LB01113.C
302	22.2	69.4	681	10	DV800891	DV800891 LB01315.C	375	22.2	69.4	742	10	DT720332	DT720332 LB0114.CR
303	22.2	69.4	682	10	DT828323	DT828323 LB00256.C	376	22.2	69.4	743	10	DV832371	DV832371 LB01922.C
304	22.2	69.4	683	5	CK954788	CK954788 4094950 B	377	22.2	69.4	744	14	DO034072	DO034072 Homo sap1
305	22.2	69.4	683	5	CK954788	CK954788 4094950 B	378	22.2	69.4	745	10	DV841201	DV841201 LB011201
306	22.2	69.4	683	10	DT722496	DT722496 LB0134.CR	379	22.2	69.4	747	10	DV839015	DV839015 LB01123.C
307	22.2	69.4	686	10	DT722496	DT722496 LB0134.CR	380	22.2	69.4	747	10	DT850331	DT850331 LB00480.C
308	22.2	69.4	687	10	DV805654	DV805654 LB0137.CR	381	22.2	69.4	748	9	DN884660	DN884660 nat124b01.
309	22.2	69.4	689	10	DV831742	DV831742 LB01920.C	382	22.2	69.4	749	9	DN884552	DN884552 nat123c03.
310	22.2	69.4	689	10	DV836323	DV836323 LB01112.C	383	22.2	69.4	750	9	DR767177	DR767177 ILLUMIGEN
311	22.2	69.4	690	5	CK965211	CK965211 4080059 B	384	22.2	69.4	750	10	DR767177	DR767177 ILLUMIGEN

385	22.2	69.4	750	10	DT721137	DT721137 LB0123.CR	C	458	22.2	69.4	787	9	DN537127	DN537127 1373287 M
386	22.2	69.4	752	10	DV225056	DV225056 EST-AR116	459	22.2	69.4	787	10	DV802317	DV802317 LB01321.C	
387	22.2	69.4	752	10	DV822583	DV822583 LB0202.CR	460	22.2	69.4	787	10	DV904905	DV904905 LB02111.CR	
388	22.2	69.4	753	10	DV824166	DV824166 LB02017.C	461	22.2	69.4	788	4	CB230068	CB230068 AGENCOURT	
389	22.2	69.4	753	10	DT720028	DT720028 LB0113.CR	462	22.2	69.4	788	4	CB2311739	CB2311739 AGENCOURT	
390	22.2	69.4	753	10	DT833302	DT833302 LB00420.C	C	463	22.2	69.4	788	9	DN640162	DN640162 UMC-bend_
391	22.2	69.4	753	10	DV842970	DV842970 LB01213.C	464	22.2	69.4	788	10	DT857371	DT857371 LB00531.C	
392	22.2	69.4	754	10	DT826188	DT826188 LB00242.C	465	22.2	69.4	788	10	DV840293	DV840293 LB01128.C	
393	22.2	69.4	754	10	DV838298	DV838298 LB01120.C	466	22.2	69.4	789	10	DV840493	DV840493 LB01129.C	
394	22.2	69.4	755	1	AJ943555	AJ943555 LB013555	467	22.2	69.4	789	10	DV851765	DV851765 LB00231.CR	
395	22.2	69.4	756	10	DR767635	DR767635 ILLUMIGEN	468	22.2	69.4	789	10	DV852539	DV852539 LB0234.CR	
396	22.2	69.4	758	10	DT859720	DT859720 LB00542.C	469	22.2	69.4	790	4	CB230445	CB230445 AGENCOURT	
397	22.2	69.4	760	9	DN885308	DN885308 natf28g06.	470	22.2	69.4	790	10	DV852722	DV852722 LB0234.CR	
398	22.2	69.4	761	10	DV805848	DV805848 LB0137.CR	471	22.2	69.4	791	4	CB308230	CB308230 AGENCOURT	
399	22.2	69.4	761	10	DV824228	DV824228 LB02017.C	472	22.2	69.4	791	10	DT858656	DT858656 LB00537.C	
400	22.2	69.4	761	10	DV827489	DV827489 LB0208.CR	473	22.2	69.4	791	10	DV827194	DV827194 LB0206.CR	
401	22.2	69.4	762	4	CB310504	CB310504 AGENCOURT	C	474	22.2	69.4	792	9	DN742812	DN742812 1405231 M
402	22.2	69.4	764	10	DV833778	DV833778 LB0128.C	475	22.2	69.4	793	9	DN549614	DN549614 1407919 M	
403	22.2	69.4	764	10	DV835254	DV835254 LB0198.CR	476	22.2	69.4	793	10	DV9222580	DV9222580 LB02328.C	
404	22.2	69.4	765	10	DR768715	DR768715 ILLUMIGEN	477	22.2	69.4	794	5	CJ455059	CJ455059 CJ455059	
405	22.2	69.4	766	10	DT826028	DT826028 LB00241.C	478	22.2	69.4	794	10	DN533710	DN533710 1371751 M	
406	22.2	69.4	766	10	DT857570	DT857570 LB00532.C	479	22.2	69.4	794	10	DT837536	DT837536 LB00439.C	
407	22.2	69.4	767	9	DN882232	DN882232 natf06c11.	480	22.2	69.4	795	4	CB229029	CB229029 AGENCOURT	
408	22.2	69.4	768	10	DT721316	DT721316 LB0124.CR	481	22.2	69.4	795	4	CB308635	CB308635 AGENCOURT	
409	22.2	69.4	768	10	DV831370	DV831370 LB01919.C	482	22.2	69.4	796	5	CJ446769	CJ446769 CJ446769	
410	22.2	69.4	769	10	DR768952	DR768952 ILLUMIGEN	483	22.2	69.4	796	10	DT722208	DT722208 LB01331.CR	
411	22.2	69.4	769	10	DV830228	DV830228 LB01914.C	484	22.2	69.4	796	10	DV831610	DV831610 LB01920.C	
412	22.2	69.4	770	4	CB230151	CB230151 AGENCOURT	485	22.2	69.4	797	10	DT810665	DT810665 LB01612.C	
413	22.2	69.4	770	4	CB308737	CB308737 AGENCOURT	486	22.2	69.4	797	10	DV802870	DV802870 LB01323.C	
414	22.2	69.4	770	4	CB311620	CB311620 AGENCOURT	487	22.2	69.4	798	4	CB311120	CB311120 AGENCOURT	
415	22.2	69.4	771	4	CB229097	CB229097 AGENCOURT	488	22.2	69.4	798	10	DT820693	DT820693 LB00215.C	
416	22.2	69.4	771	4	CB308021	CB308021 AGENCOURT	489	22.2	69.4	798	10	DT838351	DT838351 LB00443.C	
417	22.2	69.4	771	5	CJ478816	CJ478816 CJ478816	490	22.2	69.4	798	10	DV837736	DV837736 LB01117.C	
418	22.2	69.4	771	5	DT721879	DT721879 LB01321.CR	491	22.2	69.4	798	10	DV841977	DV841977 LB01191.CR	
419	22.2	69.4	773	4	CB309547	CB309547 AGENCOURT	492	22.2	69.4	798	10	DV851617	DV851617 LB02311.CR	
420	22.2	69.4	773	4	CB311624	CB311624 AGENCOURT	493	22.2	69.4	799	4	CB308642	CB308642 AGENCOURT	
421	22.2	69.4	774	4	CB229102	CB229102 AGENCOURT	494	22.2	69.4	799	4	CB310018	CB310018 AGENCOURT	
422	22.2	69.4	775	8	CV982301	CV982301 UMC-bm1x	495	22.2	69.4	799	10	DV852464	DV852464 LB02341.CR	
423	22.2	69.4	775	10	DR769738	DR769738 ILLUMIGEN	496	22.2	69.4	799	10	DV906124	DV906124 LB01821.CR	
424	22.2	69.4	775	10	DT721555	DT721555 LB01311.CR	497	22.2	69.4	800	9	DN742645	DN742645 1412157 M	
425	22.2	69.4	776	10	DV815974	DV815974 LB01718.C	498	22.2	69.4	800	10	DR766783	DR766783 ILLUMIGEN	
426	22.2	69.4	776	10	DV827728	DV827728 LB02091.CR	499	22.2	69.4	800	10	DT720772	DT720772 LB01221.CR	
427	22.2	69.4	776	10	DV840427	DV840427 LB01128.C	500	22.2	69.4	800	10	DT848185	DT848185 LB00481.C	
428	22.2	69.4	777	1	AJ945947	AJ945947 AJ945947	501	22.2	69.4	800	10	DV828323	DV828323 LB01921.CR	
429	22.2	69.4	777	5	CJ461049	CJ461049 AGENCOURT	502	22.2	69.4	800	10	DN644162	DN644162 UMC-bocf_0	
430	22.2	69.4	777	5	DT845319	DT845319 LB0041071.	503	22.2	69.4	801	9	DN6442675	DN6442675 UMC-boef_0	
431	22.2	69.4	777	10	DT849140	DT849140 LB004851.C	504	22.2	69.4	801	10	DV904903	DV904903 LB02111.CR	
432	22.2	69.4	777	10	DT849140	DT849140 LB004851.C	505	22.2	69.4	802	10	DV906694	DV906694 LB01851.CR	
433	22.2	69.4	777	10	DT855267	DT855267 LB005201.C	506	22.2	69.4	802	8	CN436523	CN436523 BE04009A2	
434	22.2	69.4	777	10	DV827242	DV827242 LB02071.CR	507	22.2	69.4	804	10	DT829081	DT829081 AGENCOURT	
435	22.2	69.4	777	10	DV904929	DV904929 LB02111.CR	508	22.2	69.4	805	4	CB229081	CB229081 AGENCOURT	
436	22.2	69.4	778	4	CB228526	CB228526 AGENCOURT	C	509	22.2	69.4	805	9	DN742644	DN742644 1403941 M
437	22.2	69.4	778	10	DT844344	DT844344 LB0041021.	510	22.2	69.4	805	10	DT842901	DT842901 LB004661.C	
438	22.2	69.4	778	10	DV799903	DV799903 LB013101.C	511	22.2	69.4	805	10	DV835380	DV835380 LB01981.CR	
439	22.2	69.4	780	4	CB229436	CB229436 AGENCOURT	512	22.2	69.4	806	4	CB229762	CB229762 AGENCOURT	
440	22.2	69.4	780	4	CB311755	CB311755 AGENCOURT	513	22.2	69.4	806	4	DV822764	DV822764 LB020101.C	
441	22.2	69.4	781	12	BZ883639	BZ883639 CH240_243	514	22.2	69.4	807	9	CX950295	CX950295 UMC-bc1_0	
442	22.2	69.4	781	4	CB311908	CB311908 AGENCOURT	C	515	22.2	69.4	807	10	DV825096	DV825096 LB02021.C
443	22.2	69.4	781	10	DV804420	DV804420 LB019141.C	516	22.2	69.4	808	1	AJ944328	AJ944328 AJ944328	
444	22.2	69.4	782	4	CB312026	CB312026 AGENCOURT	517	22.2	69.4	808	10	DT841022	DT841022 LB004571.C	
445	22.2	69.4	782	4	DV804925	DV804925 LB013301.C	518	22.2	69.4	808	10	DV822568	DV822568 LB02021.CR	
446	22.2	69.4	782	10	DV824292	DV824292 LB020171.C	519	22.2	69.4	809	5	CJ449084	CJ449084 CJ449084	
447	22.2	69.4	783	10	CB228953	CB228953 AGENCOURT	520	22.2	69.4	809	10	DT722116	DT722116 LB013311.CR	
448	22.2	69.4	783	4	CB311897	CB311897 AGENCOURT	521	22.2	69.4	810	9	DN882781	DN882781 natf10a08.	
449	22.2	69.4	783	4	CB312312	CB312312 AGENCOURT	522	22.2	69.4	810	10	DV821801	DV821801 LB02011.CR	
450	22.2	69.4	783	10	DV823390	DV823390 LB020131.C	523	22.2	69.4	811	10	DT849866	DT849866 LB004881.C	
451	22.2	69.4	784	9	DN882828	DN882828 natf10d041.	524	22.2	69.4	812	10	DT841324	DT841324 LB004591.C	
452	22.2	69.4	784	9	CB303497	CB303497 AGENCOURT	525	22.2	69.4	813	10	DT838802	DT838802 LB004451.C	
453	22.2	69.4	785	4	CB309497	CB309497 AGENCOURT	526	22.2	69.4	813	10	DT849798	DT849798 LB004881.C	
454	22.2	69.4	785	5	CJ033556	CJ033556 CJ033556	527	22.2	69.4	813	10	DV846115	DV846115 LB012261.C	
455	22.2	69.4	786	9	DN883188	DN883188 natf13b071.	528	22.2	69.4	814	10	DT830921	DT830921 LB004921.CR	
456	22.2	69.4	786	9	DT838280	DT838280 LB004431.C	529	22.2	69.4	814	10	DT848516	DT848516 LB004821.C	
457	22.2	69.4	787	4	CB230640	CB230640 AGENCOURT	530	22.2	69.4	814	10	DT848516	DT848516 LB004821.C	

531	22.2	69.4	814	10	DV826803	DV826803 LB02030.C	604	22.2	69.4	835	10	DV846201	DV846201 LB01226.C
532	22.2	69.4	814	10	DV834661	DV834661 LB0195.CR	605	22.2	69.4	836	10	DV852511	DV852511 LB0234.C
533	22.2	69.4	815	1	AJ943393	AJ943393 AJ943393	606	22.2	69.4	836	5	CJ493505	CJ493505 CJ493505
534	22.2	69.4	815	9	DN281660	DN281660 1162872 M	607	22.2	69.4	836	10	DT839559	DT839559 DT839559
535	22.2	69.4	815	9	DN517266	DN517266 1257794 M	608	22.2	69.4	837	4	CB311845	CB311845 AGENCOURT
536	22.2	69.4	815	9	DR769704	DR769704 ILLUMIGEN	609	22.2	69.4	837	8	CR938888	CR938888 CR938888
537	22.2	69.4	815	10	DT838129	DT838129 LB00442.C	610	22.2	69.4	837	8	CR938915	CR938915 CR938915
538	22.2	69.4	815	8	CN644382	CN644382 ILLUMIGEN	611	22.2	69.4	837	10	DR770189	DR770189 ILLUMIGEN
539	22.2	69.4	816	8	CN802948	CN802948 ILLUMIGEN	612	22.2	69.4	837	10	DV832086	DV832086 LB01921.C
540	22.2	69.4	816	10	DT827113	DT827113 LB00249.C	613	22.2	69.4	838	10	DV828672	DV828672 LB0192.CR
541	22.2	69.4	816	10	DV921239	DV921239 LB02924.C	614	22.2	69.4	839	10	DV828148	DV828148 LB0192.CR
542	22.2	69.4	817	9	DN547876	DN547876 1405618 M	615	22.2	69.4	839	14	CT180198	CT180198 Sub acrole
543	22.2	69.4	817	9	DN549880	DN549880 1408306 M	616	22.2	69.4	840	10	DV916222	DV916222 LB0291.CR
544	22.2	69.4	817	10	DT849817	DT849817 LB00488.C	617	22.2	69.4	841	4	CB310610	CB310610 AGENCOURT
545	22.2	69.4	818	9	DN519978	DN519978 1252670 M	618	22.2	69.4	841	8	CR938872	CR938872 CR938872
546	22.2	69.4	818	9	DN741985	DN741985 1412011 M	619	22.2	69.4	842	8	CR938891	CR938891 CR938891
547	22.2	69.4	818	10	DR766948	DR766948 ILLUMIGEN	620	22.2	69.4	843	8	CO647806	CO647806 ILLUMIGEN
548	22.2	69.4	818	10	DT820031	DT820031 LB00212.C	621	22.2	69.4	844	8	CO646625	CO646625 ILLUMIGEN
549	22.2	69.4	818	10	DT851767	DT851767 LB00493.C	622	22.2	69.4	844	10	DR713118	DR713118 LB0054.C
550	22.2	69.4	818	10	DV885390	DV885390 LB0267.CR	623	22.2	69.4	844	10	DV804604	DV804604 LB01329.C
551	22.2	69.4	819	5	CJ473829	CJ473829 CJ473829	624	22.2	69.4	845	8	CO580579	CO580579 ILLUMIGEN
552	22.2	69.4	819	10	DT818720	DT818720 LB0026.CR	625	22.2	69.4	845	8	CR938852	CR938852 CR938852
553	22.2	69.4	819	10	DV821859	DV821859 LB0204.CR	626	22.2	69.4	846	8	CN801804	CN801804 ILLUMIGEN
554	22.2	69.4	819	10	DV828509	DV828509 LB0193.CR	627	22.2	69.4	846	8	CO579687	CO579687 ILLUMIGEN
555	22.2	69.4	820	8	CV981476	CV981476 UMC-bmlx	628	22.2	69.4	846	8	CO580551	CO580551 ILLUMIGEN
556	22.2	69.4	820	10	DR770310	DR770310 ILLUMIGEN	629	22.2	69.4	846	8	CR938859	CR938859 CR938859
557	22.2	69.4	821	10	DT832202	DT832202 LB00415.C	630	22.2	69.4	846	10	DR770474	DR770474 ILLUMIGEN
558	22.2	69.4	821	10	DT840615	DT840615 LB00455.C	631	22.2	69.4	846	10	DT721715	DT721715 LB0131.CR
559	22.2	69.4	821	10	DV909642	DV909642 LB02815.C	632	22.2	69.4	847	5	CJ472559	CJ472559 CJ472559
560	22.2	69.4	822	4	CB228942	CB228942 AGENCOURT	633	22.2	69.4	847	8	CO580167	CO580167 ILLUMIGEN
561	22.2	69.4	822	4	CB311703	CB311703 AGENCOURT	634	22.2	69.4	848	8	CO647726	CO647726 ILLUMIGEN
562	22.2	69.4	822	10	DT857406	DT857406 LB00531.C	635	22.2	69.4	849	8	CO581129	CO581129 ILLUMIGEN
563	22.2	69.4	823	9	DN885779	DN885779 na639c05.	636	22.2	69.4	849	8	CO648345	CO648345 ILLUMIGEN
564	22.2	69.4	824	8	CR938908	CR938908 CR938908	637	22.2	69.4	849	8	CO648861	CO648861 ILLUMIGEN
565	22.2	69.4	824	10	DV821681	DV821681 LB0201.CR	638	22.2	69.4	849	8	CO648924	CO648924 ILLUMIGEN
566	22.2	69.4	825	10	DT819413	DT819413 LB0029.CR	639	22.2	69.4	849	10	DT835319	DT835319 LB00430.C
567	22.2	69.4	826	10	DT818721	DT818721 LB0026.CR	640	22.2	69.4	852	10	DT838486	DT838486 LB00444.C
568	22.2	69.4	827	8	CO580354	CO580354 ILLUMIGEN	641	22.2	69.4	853	8	CO579533	CO579533 ILLUMIGEN
569	22.2	69.4	827	8	CO648993	CO648993 ILLUMIGEN	642	22.2	69.4	854	8	CN646801	CN646801 ILLUMIGEN
570	22.2	69.4	827	8	CR938850	CR938850 CR938850	643	22.2	69.4	854	10	DV837511	DV837511 LB01117.C
571	22.2	69.4	827	9	DN550241	DN550241 1408581 M	644	22.2	69.4	855	10	DV834599	DV834599 LB0195.CR
572	22.2	69.4	827	10	DT847728	DT847728 LB00479.C	645	22.2	69.4	856	10	DT824431	DT824431 LB00233.C
573	22.2	69.4	829	4	CB311382	CB311382 AGENCOURT	646	22.2	69.4	857	5	CF767224	CF767224 CES001503
574	22.2	69.4	829	8	CO774881	CO774881 ILLUMIGEN	647	22.2	69.4	862	10	DT836775	DT836775 LB00436.C
575	22.2	69.4	829	10	DT834534	DT834534 LB00426.C	648	22.2	69.4	864	10	DV820707	DV820707 LB00215.C
576	22.2	69.4	829	10	DV825086	DV825086 LB02021.C	649	22.2	69.4	864	10	DV814275	DV814275 LB01712.C
577	22.2	69.4	830	10	DT826680	DT826680 LB00244.C	650	22.2	69.4	867	10	DT721739	DT721739 LB0131.CR
578	22.2	69.4	830	10	DT852829	DT852829 LB0055.CR	651	22.2	69.4	874	8	CN802301	CN802301 ILLUMIGEN
579	22.2	69.4	830	10	DV803261	DV803261 LB01324.C	652	22.2	69.4	876	8	CO580040	CO580040 ILLUMIGEN
580	22.2	69.4	830	10	DV818951	DV818951 LB01727.C	653	22.2	69.4	876	10	DT849882	DT849882 LB00488.C
581	22.2	69.4	831	10	DT842283	DT842283 LB00463.C	654	22.2	69.4	888	2	BG165124	BG165124 602343947
582	22.2	69.4	831	10	DT853217	DT853217 LB0057.CR	655	22.2	69.4	891	10	DT858685	DT858685 LB00537.C
583	22.2	69.4	832	6	BC109560	BC109560 Bos taunu	656	22.2	69.4	894	8	CN641541	CN641541 ILLUMIGEN
584	22.2	69.4	832	8	CO581862	CO581862 ILLUMIGEN	657	22.2	69.4	907	10	DR771808	DR771808 ILLUMIGEN
585	22.2	69.4	832	8	CO581862	CO581862 ILLUMIGEN	658	22.2	69.4	911	8	CO774625	CO774625 ILLUMIGEN
586	22.2	69.4	832	10	DN548136	DN548136 1405893 M	659	22.2	69.4	912	10	DT832998	DT832998 LB00419.C
587	22.2	69.4	832	10	DT848733	DT848733 LB00463.C	660	22.2	69.4	913	10	CO774659	CO774659 ILLUMIGEN
588	22.2	69.4	832	10	DV803285	DV803285 LB01324.C	661	22.2	69.4	918	10	DR772523	DR772523 ILLUMIGEN
589	22.2	69.4	833	8	CR938909	CR938909 CR938909	662	22.2	69.4	938	4	CB231013	CB231013 AGENCOURT
590	22.2	69.4	833	10	CR938916	CR938916 CR938916	663	22.2	69.4	952	2	BG180869	BG180869 602327321
591	22.2	69.4	833	10	DT840168	DT840168 LB00453.C	664	22.2	69.4	1021	1	AJ927344	AJ927344 AJ927344
592	22.2	69.4	833	10	DT841755	DT841755 LB00461.C	665	22.2	69.4	1055	4	CB228635	CB228635 AGENCOURT
593	22.2	69.4	833	10	DT848007	DT848007 LB00480.C	666	22.2	69.4	1105	5	CK231605	CK231605 ILLUMIGEN
594	22.2	69.4	833	10	DT848732	DT848732 LB00463.C	667	22.2	69.4	1105	5	CR552705	CR552705 ILLUMIGEN
595	22.2	69.4	833	10	DV821769	DV821769 LB0201.CR	668	22.2	69.4	1116	6	CR859318	CR859318 Porogo pyg
596	22.2	69.4	833	10	DV827626	DV827626 LB0208.CR	669	22.2	69.4	1195	4	CB230296	CB230296 AGENCOURT
597	22.2	69.4	833	10	DV831788	DV831788 LB01920.C	670	22.2	69.4	1332	10	DV799013	DV799013 HW join_3
598	22.2	69.4	834	9	DN884276	DN884276 na621b11.	671	22.2	69.4	1332	10	DV797486	DV797486 HW join_3
599	22.2	69.4	834	9	DN884982	DN884982 na626e08.	672	22.2	69.4	1332	10	CK675615	CK675615 UCRCS08_6
600	22.2	69.4	834	10	DT841980	DT841980 LB00462.C	673	22.2	69.4	471	9	CK675615	CK675615 UCRCS08_6
601	22.2	69.4	834	10	DV806484	DV806484 LB01312.C	674	22.2	69.4	639	4	CA262559	CA262559 SCBFLB202
602	22.2	69.4	834	10	DV827792	DV827792 LB0209.CR	675	22.2	69.4	641	4	CA245659	CA245659 SCBFL508
603	22.2	69.4	835	10	DV839199	DV839199 LB01124.C	676	22.2	69.4	641	4	CA245659	CA245659 SCBFL508

677	22	68.8	941.2	BI758228	BI758228 603029873	750	20.8	65.0	297.4	BY783761	BY783761 BY783761
678	22	68.8	974.4	BX342147	BX342147 BX342147	751	20.8	65.0	298.7	BE192736	BE192736 EST331465
679	22	68.8	1547.3	BM926884	BM926884 AGENCOURT	752	20.8	65.0	299.4	BY113439	BY113439 BY113439
680	21.8	68.1	406.10	DY164885	DY164885 0001148M	753	20.8	65.0	300.7	AM647032	AM647032 EST325622
681	21.8	68.1	409.10	DM328338	DM328338 LRAGE0881	754	20.8	65.0	302.1	AI8469574	AI8469574 UT-M-AH1-
682	21.6	67.5	678.10	DR421867	DR421867 NAV05A05.	755	20.8	65.0	302.9	D77896	D77896 MUSB1H05 mo
683	21.4	66.9	153.9	DN911367	DN911367 UST EST-0	756	20.8	65.0	303.7	BB585398	BB585398 BB585398
684	21.4	66.9	593.7	AM619343	AM619343 717 MARC	757	20.8	65.0	306.4	BY052068	BY052068 BY052068
685	21.4	66.9	715.2	Bj642124	Bj642124 Bf642124	758	20.8	65.0	307.4	BY779928	BY779928 BY779928
686	21.4	66.9	784.11	B2153935	B2153935 CH230-442	759	20.8	65.0	307.4	BY783614	BY783614 BY783614
687	21.4	66.9	932.2	BU185996	BU185996 AGENCOURT	760	20.8	65.0	307.5	BY076528	BY076528 C1097628
688	21.4	66.9	1060.2	BM465253	BM465253 AGENCOURT	761	20.8	65.0	309.4	BY350352	BY350352 BY350352
689	21.2	66.2	294.10	DY089705	DY089705 001119BAM	762	20.8	65.0	310.4	BY035689	BY035689 BY035689
690	21.2	66.2	354.14	DO030246	DO030246 Homo sap1	763	20.8	65.0	311.4	BY327141	BY327141 BY327141
691	21.2	66.2	355.10	DY062079	DY062079 000316BAG	764	20.8	65.0	313.4	BY070128	BY070128 BY070128
692	21.2	66.2	375.4	BY299543	BY299543 BY299543	765	20.8	65.0	316.4	BY028099	BY028099 BY028099
693	21.2	66.2	394.1	AV618350	AV618350 AV618350	766	20.8	65.0	317.4	BY114156	BY114156 BY114156
694	21.2	66.2	611.10	DY142872	DY142872 001011BMP	767	20.8	65.0	317.4	BY119597	BY119597 BY119597
695	21.2	66.2	788.9	CX950445	CX950445 UMC-bcl.0	768	20.8	65.0	317.4	BY347627	BY347627 BY347627
696	21.2	66.2	806.8	CO740422	CO740422 SILL07a27	769	20.8	65.0	317.5	CJ132416	CJ132416 CJ132416
697	21.2	66.2	811.10	DV830030	DV830030 LB01913.C	770	20.8	65.0	319.4	BY121106	BY121106 BY121106
698	21.2	66.2	828.8	CM646269	CM646269 ILLDMTGM	771	20.8	65.0	319.4	BY131948	BY131948 BY131948
699	21.2	66.2	838.9	DN883461	DN883461 na115a05.	772	20.8	65.0	320.4	BY109443	BY109443 BY109443
700	21.2	66.2	839.5	CJ455666	CJ455666 CJ455666	773	20.8	65.0	321.4	BY794440	BY794440 BY794440
701	21.2	66.2	1197.3	BM809428	BM809428 AGENCOURT	774	20.8	65.0	323.4	BY110429	BY110429 BY110429
702	21	65.6	278.1	AA356281	AA356281 EST64803	775	20.8	65.0	324.4	BY114400	BY114400 BY114400
703	21	65.6	282.14	AG025446	AG025446 Oryza sat	776	20.8	65.0	324.4	BY120253	BY120253 BY120253
704	21	65.6	300.14	AG213486	AG213486 Oryza sat	777	20.8	65.0	324.4	BY121577	BY121577 BY121577
705	21	65.6	400.1	AL362489	AL362489 AL362489	778	20.8	65.0	324.4	BY149833	BY149833 BY149833
706	21	65.6	586.13	CL622362	CL622362 OR_BBA001	779	20.8	65.0	324.4	BY331926	BY331926 BY331926
707	21	65.6	646.14	DU571886	DU571886 OO_Ba005	780	20.8	65.0	325.4	BY352138	BY352138 BY352138
708	21	65.6	654.13	CM972787	CM972787 A1AA-aa5	781	20.8	65.0	326.4	BY113878	BY113878 BY113878
709	21	65.6	662.13	CM697636	CM697636 CG_BBA006	782	20.8	65.0	326.5	CJ098269	CJ098269 CJ098269
710	21	65.6	678.13	CL807253	CL807253 OR_CBA002	783	20.8	65.0	327.4	BY120341	BY120341 BY120341
711	21	65.6	686.13	CZ141784	CZ141784 OA_BBA003	784	20.8	65.0	327.4	BY139702	BY139702 BY139702
712	21	65.6	730.14	AU128873	AU128873 AU128873	785	20.8	65.0	327.4	BY140121	BY140121 BY140121
713	21	65.6	739.14	AG584606	AG584606 Mus muscu	786	20.8	65.0	327.4	BY144269	BY144269 BY144269
714	21	65.6	742.13	CL757926	CL757926 OR_BBA012	787	20.8	65.0	327.4	BY151633	BY151633 BY151633
715	21	65.6	768.13	CM771664	CM771664 OG_BBA004	788	20.8	65.0	327.4	BY328542	BY328542 BY328542
716	21	65.6	781.13	CM509094	CM509094 OA_BBA012	789	20.8	65.0	327.4	BY782614	BY782614 BY782614
717	21	65.6	802.9	CX567193	CX567193 UT-N-HK0-	790	20.8	65.0	328.4	BY111074	BY111074 BY111074
718	21	65.6	809.11	AQ687570	AQ687570 ndxb0075M	791	20.8	65.0	328.4	BY113275	BY113275 BY113275
719	21	65.6	2472.13	CL960339	CL960339 OaIFCC004	792	20.8	65.0	328.4	BY113884	BY113884 BY113884
720	20.8	65.0	158.4	BY043357	BY043357 BY043357	793	20.8	65.0	328.4	BY324733	BY324733 BY324733
721	20.8	65.0	159.1	AA790581	AA790581 vx71G05.x	794	20.8	65.0	328.4	BY780184	BY780184 BY780184
722	20.8	65.0	159.1	AA562499	AA562499 v143d04.x	795	20.8	65.0	329.4	BY150156	BY150156 BY150156
723	20.8	65.0	179.4	BY347534	BY347534 MMS34449	796	20.8	65.0	329.4	BY144261	BY144261 BY144261
724	20.8	65.0	182.8	CX219406	CX219406 MMS34449	797	20.8	65.0	329.4	BY330992	BY330992 BY330992
725	20.8	65.0	185.7	BF585301	BF585301 602101967	798	20.8	65.0	330.4	BY784678	BY784678 BY784678
726	20.8	65.0	214.5	CJ054879	CJ054879 CJ054879	799	20.8	65.0	331.4	BY115678	BY115678 BY115678
727	20.8	65.0	214.7	BB568296	BB568296 BB568296	800	20.8	65.0	332.4	BY120215	BY120215 BY120215
728	20.8	65.0	216.7	BB584137	BB584137 BB584137	801	20.8	65.0	332.4	BY350903	BY350903 BY350903
729	20.8	65.0	219.1	AA073048	AA073048 mm78C08.x	802	20.8	65.0	333.4	BY108471	BY108471 BY108471
730	20.8	65.0	223.7	BB588547	BB588547 BB588547	803	20.8	65.0	333.4	BY147751	BY147751 BY147751
731	20.8	65.0	227.7	BB583633	BB583633 BB583633	804	20.8	65.0	333.4	BY150150	BY150150 BY150150
732	20.8	65.0	230.9	D77833	D77833 MUSB9E09 mo	805	20.8	65.0	333.4	BY349120	BY349120 BY349120
733	20.8	65.0	262.4	BY039912	BY039912 BY039912	806	20.8	65.0	333.4	BY779082	BY779082 BY779082
734	20.8	65.0	265.7	BB567043	BB567043 BB567043	807	20.8	65.0	333.7	BF452187	BF452187 u85f07.y
735	20.8	65.0	266.4	BY050952	BY050952 BY050952	808	20.8	65.0	334.4	BY110765	BY110765 BY110765
736	20.8	65.0	267.4	BY004830	BY004830 BY004830	809	20.8	65.0	334.4	BY139727	BY139727 BY139727
737	20.8	65.0	269.9	D77865	D77865 MUSB9G09 mo	810	20.8	65.0	334.4	BY350946	BY350946 BY350946
738	20.8	65.0	272.2	BB599220	BB599220 BB599220	811	20.8	65.0	334.4	BY792559	BY792559 BY792559
739	20.8	65.0	276.9	D76483	D76483 MUSB6H07 mo	812	20.8	65.0	335.4	BY120325	BY120325 BY120325
740	20.8	65.0	278.5	CJ188425	CJ188425 CJ188425	813	20.8	65.0	335.4	BY323433	BY323433 BY323433
741	20.8	65.0	279.7	BY120438	BY120438 BY120438	814	20.8	65.0	335.4	BY327835	BY327835 BY327835
742	20.8	65.0	279.7	BB579145	BB579145 BB579145	815	20.8	65.0	336.4	BY111977	BY111977 BY111977
743	20.8	65.0	281.4	BY120537	BY120537 BY120537	816	20.8	65.0	336.4	BY149814	BY149814 BY149814
744	20.8	65.0	285.5	CJ169232	CJ169232 CJ169232	817	20.8	65.0	336.4	BY150358	BY150358 BY150358
745	20.8	65.0	286.7	BE192933	BE192933 EST331578	818	20.8	65.0	336.4	BY778366	BY778366 BY778366
746	20.8	65.0	294.4	BY142263	BY142263 BY142263	819	20.8	65.0	336.4	BY788063	BY788063 BY788063
747	20.8	65.0	295.4	BY113449	BY113449 BY113449	820	20.8	65.0	336.4	BY792764	BY792764 BY792764
748	20.8	65.0	296.4	BY148363	BY148363 BY148363	821	20.8	65.0	337.4	BY115707	BY115707 BY115707
749	20.8	65.0	297.4	BY334051	BY334051 BY334051	822	20.8	65.0	337.4	BY149473	BY149473 BY149473

823	20.8	65.0	338	4	BY103994	BY103994	BY103994	896	20.8	65.0	351	4	BY774100	BY774100
824	20.8	65.0	338	4	BY110045	BY110045	BY110045	897	20.8	65.0	352	4	BY049164	BY049164
825	20.8	65.0	338	4	BY111903	BY111903	BY111903	898	20.8	65.0	352	4	BY137392	BY137392
826	20.8	65.0	338	4	BY145407	BY145407	BY145407	899	20.8	65.0	352	4	BY133083	BY143083
827	20.8	65.0	338	4	BY331335	BY331335	BY331335	900	20.8	65.0	352	4	BY148206	BY148206
828	20.8	65.0	338	4	BY350862	BY350862	BY350862	901	20.8	65.0	352	4	BY150610	BY150610
829	20.8	65.0	338	4	BY794193	BY794193	BY794193	902	20.8	65.0	352	4	BY164504	BY164504
830	20.8	65.0	339	1	AA896692	Vx54f04.r	AA896692	903	20.8	65.0	352	4	BY772702	BY772702
831	20.8	65.0	339	4	BY120749	BY120749	BY120749	904	20.8	65.0	353	4	BY305729	BY305729
832	20.8	65.0	339	4	BY301480	BY301480	BY301480	905	20.8	65.0	354	4	BY106603	BY106603
833	20.8	65.0	339	4	BY790300	BY790300	BY790300	906	20.8	65.0	354	4	BY335073	BY335073
834	20.8	65.0	340	4	BY108801	BY108801	BY108801	907	20.8	65.0	354	4	BY351282	BY351282
835	20.8	65.0	340	4	BY112882	BY112882	BY112882	908	20.8	65.0	355	4	BY099860	BY099860
836	20.8	65.0	340	4	BY120126	BY120126	BY120126	909	20.8	65.0	355	4	BY104931	BY104931
837	20.8	65.0	340	4	BY328493	BY328493	BY328493	910	20.8	65.0	355	4	BY125877	BY125877
838	20.8	65.0	340	4	BY352169	BY352169	BY352169	911	20.8	65.0	355	4	BY770090	BY770090
839	20.8	65.0	340	4	BY784256	BY784256	BY784256	912	20.8	65.0	356	4	BY037628	BY037628
840	20.8	65.0	340	4	BY790957	BY790957	BY790957	913	20.8	65.0	356	4	BY056170	BY056170
841	20.8	65.0	341	4	BY106443	BY106443	BY106443	914	20.8	65.0	356	4	BY119311	BY119311
842	20.8	65.0	341	4	BY118269	BY118269	BY118269	915	20.8	65.0	356	4	BY351250	BY351250
843	20.8	65.0	341	4	BY119818	BY119818	BY119818	916	20.8	65.0	356	4	BY768703	BY768703
844	20.8	65.0	341	4	BY144413	BY144413	BY144413	917	20.8	65.0	357	1	AL363407	AL363407
845	20.8	65.0	341	4	BY336256	BY336256	BY336256	918	20.8	65.0	357	4	BY045231	BY045231
846	20.8	65.0	341	4	BY349440	BY349440	BY349440	919	20.8	65.0	357	4	BY072042	BY072042
847	20.8	65.0	342	4	BY107708	BY107708	BY107708	920	20.8	65.0	357	4	BY111315	BY111315
848	20.8	65.0	342	4	BY109408	BY109408	BY109408	921	20.8	65.0	357	4	BY782445	BY782445
849	20.8	65.0	342	4	BY110969	BY110969	BY110969	922	20.8	65.0	357	4	BY782501	BY782501
850	20.8	65.0	342	4	BY112375	BY112375	BY112375	923	20.8	65.0	358	4	BY117239	BY117239
851	20.8	65.0	342	4	BY150872	BY150872	BY150872	924	20.8	65.0	358	4	BY140641	BY140641
852	20.8	65.0	342	4	BY151602	BY151602	BY151602	925	20.8	65.0	358	4	BY351274	BY351274
853	20.8	65.0	342	4	BY348220	BY348220	BY348220	926	20.8	65.0	358	4	BY769669	BY769669
854	20.8	65.0	342	4	BY776602	BY776602	BY776602	927	20.8	65.0	359	4	BY043983	BY043983
855	20.8	65.0	342	4	BY784378	BY784378	BY784378	928	20.8	65.0	359	4	BY766378	BY766378
856	20.8	65.0	343	4	BY109041	BY109041	BY109041	929	20.8	65.0	359	4	BY75691	BY75691
857	20.8	65.0	343	4	BY148085	BY148085	BY148085	930	20.8	65.0	359	4	BY757526	BY757526
858	20.8	65.0	343	4	BY151207	BY151207	BY151207	931	20.8	65.0	359	4	BY779229	BY779229
859	20.8	65.0	343	4	BY781349	BY781349	BY781349	932	20.8	65.0	360	4	BY038241	BY038241
860	20.8	65.0	343	5	CJ056943	CJ056943	CJ056943	933	20.8	65.0	360	4	BY073223	BY073223
861	20.8	65.0	344	4	BY104869	BY104869	BY104869	934	20.8	65.0	360	4	BY088875	BY088875
862	20.8	65.0	344	4	BY108727	BY108727	BY108727	935	20.8	65.0	360	4	BY137687	BY137687
863	20.8	65.0	344	4	BY109843	BY109843	BY109843	936	20.8	65.0	360	4	BY143398	BY143398
864	20.8	65.0	344	4	CB692959	AMGNNUC:N	CB692959	937	20.8	65.0	360	4	BY146540	BY146540
865	20.8	65.0	345	1	AA184492	mc49906.r	AA184492	938	20.8	65.0	360	4	BY782568	BY782568
866	20.8	65.0	345	4	BY048693	BY048693	BY048693	939	20.8	65.0	361	4	BY084360	BY084360
867	20.8	65.0	345	4	BY046718	BY046718	BY046718	940	20.8	65.0	361	4	BY139275	BY139275
868	20.8	65.0	345	4	BY349648	BY349648	BY349648	941	20.8	65.0	361	4	BY766562	BY766562
869	20.8	65.0	345	4	BY351573	BY351573	BY351573	942	20.8	65.0	361	5	CJ140843	CJ140843
870	20.8	65.0	345	4	BY775968	BY775968	BY775968	943	20.8	65.0	362	4	BY056819	BY056819
871	20.8	65.0	345	4	BY784758	BY784758	BY784758	944	20.8	65.0	362	4	BY767984	BY767984
872	20.8	65.0	345	4	BY794120	BY794120	BY794120	945	20.8	65.0	362	4	BY769033	BY769033
873	20.8	65.0	346	4	BY049270	BY049270	BY049270	946	20.8	65.0	362	4	BY787901	BY787901
874	20.8	65.0	346	4	BY107001	BY107001	BY107001	947	20.8	65.0	363	4	BY055547	BY055547
875	20.8	65.0	346	4	BY115386	BY115386	BY115386	948	20.8	65.0	363	4	BY196405	BY196405
876	20.8	65.0	346	4	BY118248	BY118248	BY118248	949	20.8	65.0	363	4	BY775306	BY775306
877	20.8	65.0	346	4	BY139109	BY139109	BY139109	950	20.8	65.0	363	4	BY776373	BY776373
878	20.8	65.0	347	4	BY110114	BY110114	BY110114	951	20.8	65.0	364	4	BY045188	BY045188
879	20.8	65.0	347	4	BY145595	BY145595	BY145595	952	20.8	65.0	364	4	BY056914	BY056914
880	20.8	65.0	347	4	BY349758	BY349758	BY349758	953	20.8	65.0	364	4	BY116290	BY116290
881	20.8	65.0	347	4	BY353234	BY353234	BY353234	954	20.8	65.0	364	4	BY171624	BY171624
882	20.8	65.0	348	4	BY137096	BY137096	BY137096	955	20.8	65.0	364	4	BY171934	BY171934
883	20.8	65.0	348	4	BY327309	BY327309	BY327309	956	20.8	65.0	364	4	BY784165	BY784165
884	20.8	65.0	348	4	BY769948	BY769948	BY769948	957	20.8	65.0	364	5	CJ088303	CJ088303
885	20.8	65.0	349	4	BY138042	BY138042	BY138042	958	20.8	65.0	364	5	CJ140857	CJ140857
886	20.8	65.0	349	4	BY142770	BY142770	BY142770	959	20.8	65.0	365	4	BY052888	BY052888
887	20.8	65.0	349	4	BY150589	BY150589	BY150589	960	20.8	65.0	365	4	BY146558	BY146558
888	20.8	65.0	349	4	BY769984	BY769984	BY769984	961	20.8	65.0	365	4	BY153306	BY153306
889	20.8	65.0	349	4	BY775723	BY775723	BY775723	962	20.8	65.0	365	4	BY769426	BY769426
890	20.8	65.0	349	5	CJ041944	CJ041944	CJ041944	963	20.8	65.0	366	4	BY083165	BY083165
891	20.8	65.0	350	4	BY013692	BY013692	BY013692	964	20.8	65.0	366	4	BY099063	BY099063
892	20.8	65.0	350	4	BY106672	BY106672	BY106672	965	20.8	65.0	366	4	BY143366	BY143366
893	20.8	65.0	351	4	BY067623	BY067623	BY067623	966	20.8	65.0	366	4	BY767033	BY767033
894	20.8	65.0	351	4	BY121473	BY121473	BY121473	967	20.8	65.0	367	4	BY770257	BY770257
895	20.8	65.0	351	4	BY770034	BY770034	BY770034	968	20.8	65.0	367	4	BY777627	BY777627

969	20.8	65.0	368	4	BY106970	BY106970
970	20.8	65.0	368	4	BY348791	BY348791
971	20.8	65.0	368	4	BY787722	BY787722
972	20.8	65.0	369	4	BY117245	BY117245
973	20.8	65.0	369	4	BY773233	BY773233
974	20.8	65.0	369	10	DT912883	DT912883
975	20.8	65.0	370	4	BY042099	BY042099
976	20.8	65.0	370	4	BY042810	BY042810
977	20.8	65.0	370	4	BY150531	BY150531
978	20.8	65.0	371	4	BY107183	BY107183
979	20.8	65.0	371	4	BY135639	BY135639
980	20.8	65.0	372	4	BY041240	BY041240
981	20.8	65.0	372	4	BY042811	BY042811
982	20.8	65.0	372	4	BY767654	BY767654
983	20.8	65.0	373	1	AA210569	AA210569
984	20.8	65.0	373	4	BY041249	BY041249
985	20.8	65.0	373	4	BY054024	BY054024
986	20.8	65.0	373	5	CJ087274	CJ087274
987	20.8	65.0	374	4	BY055334	BY055334
988	20.8	65.0	374	4	BY069567	BY069567
989	20.8	65.0	375	4	BY035979	BY035979
990	20.8	65.0	375	4	BY057817	BY057817
991	20.8	65.0	375	4	BY307200	BY307200
992	20.8	65.0	375	4	BY767769	BY767769
993	20.8	65.0	375	5	CJ086829	CJ086829
994	20.8	65.0	376	4	BY038584	BY038584
995	20.8	65.0	376	4	BY132354	BY132354
996	20.8	65.0	376	5	CJ077638	CJ077638
997	20.8	65.0	377	2	BM519390	BM519390
998	20.8	65.0	377	4	BY050397	BY050397
999	20.8	65.0	377	4	BY107145	BY107145
1000	20.8	65.0	377	4	BY352533	BY352533

ALIGNMENTS

RESULT 1
LOCUS DM414483 316 bp mRNA linear EST 14-JAN-2006
DEFINITION HMG015213 Human liver regeneration after partial hepatectomy Homo sapiens cDNA, mRNA sequence.

ACCESSION DM414483
VERSION DM414483.1 GI:84916039

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE 1 (bases 1 to 316)

AUTHORS Xu, C.S.

JOURNAL Liver regeneration after PH

COMMENT Unpublished (2003)

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Email: xucse@263.net.

FEATURES
source location/Qualifiers

1. 316
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="Liver"
/clone_id="Human liver regeneration after partial hepatectomy"

Query Match 100.0%; Score 32; DB 10; Length 316;
Best Local Similarity 100.0%; Pred. No. 0.0055;

Matches	32;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	TTATTATAAGTGCCTGCGTCCGAAACC	32						
Db	51	TTATTATAAGTGCCTGCGTCCGAAACC	82						

RESULT 2
LOCUS DA567416 549 bp mRNA linear EST 08-NOV-2005
DEFINITION DA567416 HELAC1 Homo sapiens cDNA clone HELAC1000051 5', mRNA sequence.

ACCESSION DA567416
VERSION DA567416.1 GI:81180149

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE 1 (bases 1 to 549)

AUTHORS Kimura, K., Wakamatsu, A., Suzuki, Y., Oca, T., Nishikawa, T., Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Maeguchi, H., Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kuehida, N., Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Magatsuna, M., Murakawa, K., Ishida, S., Ishibashi, T., Takahashi, Fujii, A., Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isegai, T., and Sugano, S.

Diversification of Transcriptional Modulation: Large-scale Identification of Human Genes

Promoters of Human Genes

Genome Res. 16 (1), 55-65 (2006)

JOURNAL PUBLISHED 16344560

COMMENT Contact: Takao Isegai

Fuj Project (HRI Team)

Helix Research Institute

2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan

Tel: 81-438-52-3975

Fax: 81-438-52-3986

Email: fuj-cdna@nifty.com

NEDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction;

Helix Research Institute (HRI); 5'-end one pass sequencing; HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing; RAB.

FEATURES
source location/Qualifiers

1. 549
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HELAC1000051"
/cell_type="Hela cells"
/clone_id="HELAC1"
/note="Vector: pME18SFL3"

ORIGIN

Query Match 100.0%; Score 32; DB 9; Length 549;
Best Local Similarity 100.0%; Pred. No. 0.006;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTATTATAAGTGCCTGCGTCCGAAACC 32

|||||

Db 1 TTATTATAAGTGCCTGCGTCCGAAACC 32

|||||

RESULT 3

LOCUS BE543005 890 bp mRNA linear EST 09-AUG-2000

DEFINITION 601068927F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3455214 5', mRNA sequence.

ACCESSION BE543005

VERSION BE543005.1 GI:9771650

KEYWORDS
SOURCE EST.
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
JOURNAL Homiidae; Homo.
COMMENT 1 (bases 1 to 890)
 NIH-MGC http://mgs.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapsb@emall.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/BLMT at:
 http://image.llnl.gov
 Plate: L14M8441 row: e column: 07
 High quality sequence stop: 542.
 Location/Qualifiers
 1. 890
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3455214"
 /tissue_type="cervical carcinoma cell line"
 /lab_host="DH10B"
 /clone_id="NH MGC_12"
 /note="Organ: cervix; Vector: pCMV-Sport6; Site 1: NotI;
 Site 2: SalI; Cloned undirectional. Primer: oligo dt.
 Average insert size 1.4 kb. Library prepared by Life
 Technologies."

FEATURES
source
 1. 890
 /organism="Homo sapiens"
 /mol_type="mRNA"
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 /tissue_type="cervical carcinoma cell line"
 /lab_host="DH10B"
 /clone_id="NH MGC_12"
 /note="Organ: cervix; Vector: pCMV-Sport6; Site 1: NotI;
 Site 2: SalI; Cloned undirectional. Primer: oligo dt.
 Average insert size 1.4 kb. Library prepared by Life
 Technologies."

ORIGIN
 Query Match 100.0%; Score 32; DB 7; Length 890;
 Best Local Similarity 100.0%; Pred. No. 0.0065;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
LOCUS BF911801 443 bp mRNA linear EST 18-JAN-2001
DEFINITION MR4-UT0051-101100-001-a10 UT0051 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF911801
VERSION BF911801.1 GI:12303259
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 443)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H.,
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
 O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 10737800
JOURNAL Contact: Simpson A.J.G.
PUBMED Laboratory of Cancer Genetics
COMMENT Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil

FEATURES
source
 1. 443
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_id="UT0051"
 /note="Organ: uterine tumor; Vector: puc18; Site 1: SmaI;
 Site 2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

ORIGIN
 Query Match 80.0%; Score 25.6; DB 2; Length 443;
 Best Local Similarity 87.5%; Pred. No. 3.8;
 Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

RESULT 5
LOCUS DW445957 219 bp mRNA linear EST 14-JAN-2006
DEFINITION HHAGE043687 Human liver regeneration after partial hepatectomy Homo
 sapiens cDNA, mRNA sequence.
ACCESSION DW445957
VERSION DW445957.1 GI:84947513
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 219)
 Xu,C.S.
 Liver regeneration after PH
 Unpublished (2003)
 Contact: Cun-Shuan Xu
 Henan Bioengineering Key Lab
 Henan Normal University
 No. 148 Jianshe Road, Xinxiang City, P.R.China
 Tel: 0086373328084
 Fax: 0086373326524
 Email: xucs@x263.net.
 Location/Qualifiers
 1. 219
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="liver"
 /clone_id="Human liver regeneration after partial
 hepatectomy"

ORIGIN
 Query Match 75.6%; Score 24.2; DB 10; Length 219;
 Best Local Similarity 89.7%; Pred. No. 14;
 Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy	4	TTAATAAGTGCTCGCGGTGCCAGAAACC	32	
Db	139	TTACAGAGTGCTCGCGGTGCCAGAAACC	167	
RESULT 6				
LOCUS	DM443699		229 bp	mRNA
DEFINITION	HNAGB024530 Human liver regeneration after partial hepatectomy Homo sapiens cDNA, mRNA sequence.			
ACCESSION	DM443699			
VERSION	DM443699.1		GI:84945255	
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.			
	1 (bases 1 to 229)			
REFERENCE	Xu,C.S.			
AUTHORS	Liver regeneration after PH			
TITLE	Unpublished (2003)			
JOURNAL	Contact: Cun-Shuan Xu			
COMMENT	Henan Bioengineering Key Lab Henan Normal University No. 148 Jianshe Road, Xinxiang City, P.R.China Tel: 00863733328084 Fax: 00863733326524 Email: xucsx@263.net.			
FEATURES				
Source	Location/Qualifiers			
	1..229			
	/organism="Homo sapiens"			
	/mol_type="mRNA"			
	/db_xref="taxon:9606"			
	/tissue_type="liver"			
	/clone_lib="Human liver regeneration after partial hepatectomy"			
ORIGIN				
Query Match	75.6%; Score 24.2; DB 10; Length 229;			
Best Local Similarity	89.7%; Pred. No. 14;			
Matches	26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;			
Oy	4	TTAATAAGTGCTCGCGGTGCCAGAAACC	32	
Db	139	TTACAGAGTGCTCGCGGTGCCAGAAACC	167	
RESULT 7				
LOCUS	DM424800		287 bp	mRNA
DEFINITION	HNAGB024530 Human liver regeneration after partial hepatectomy Homo sapiens cDNA, mRNA sequence.			
ACCESSION	DM424800			
VERSION	DM424800.1		GI:84926356	
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.			
	1 (bases 1 to 287)			
REFERENCE	Xu,C.S.			
AUTHORS	Liver regeneration after PH			
TITLE	Unpublished (2003)			
JOURNAL	Contact: Cun-Shuan Xu			
COMMENT	Henan Bioengineering Key Lab Henan Normal University No. 148 Jianshe Road, Xinxiang City, P.R.China Tel: 00863733328084 Fax: 00863733326524 Email: xucsx@263.net.			
FEATURES				
	Location/Qualifiers			

source	1..289	/organism="Homo sapiens"
		/mol_type="mRNA"
		/db_xref="taxon:9606"
		/tissue_type="liver"
		/clone_idb="Human liver regeneration after partial hepatectomy"
ORIGIN		
Query Match	75.6%;	Score 24.2; DB 10; Length 289;
Best Local Similarity	89.7%;	Pred.No.15;
Matches	26; Conservative	0; Mismatches 3; Indels 0; Gaps 0;
Oy	4	TTAATTAAGTGCCTGCGGTGCCAGAAACC 32
Db	140	TTACAGAGTGCTCGCGGTGCCAGAAACC 168
RESULT 8		
LOCUS	DM424288	289 bp mRNA linear EST 14-JAN-2006
DEFINITION	HHAGE024018 Human liver regeneration after partial hepatectomy Homo sapiens cDNA, mRNA sequence.	
ACCESSION	DM424288	
VERSION	DM424288.1	GI:84925844
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE	Xu,C.S.	
AUTHORS	Liver regeneration after PH	
TITLE	Unpublished (2003)	
JOURNAL	Contact: Cun-Shuan Xu	
COMMENT	Henan Bioengineering Key Lab	
	Henan Normal University	
	No. 148 Jianshe Road, Xinxiang City, P.R.China	
	Tel: 0086373328084	
	Fax: 0086373326524	
	Email: xucsx@263.net.	
FEATURES	location/Qualifiers	
source	1..289	
	/organism="Homo sapiens"	
	/mol_type="mRNA"	
	/db_xref="taxon:9606"	
	/tissue_type="liver"	
	/clone_idb="Human liver regeneration after partial hepatectomy"	
ORIGIN		
Query Match	75.6%;	Score 24.2; DB 10; Length 289;
Best Local Similarity	89.7%;	Pred.No.15;
Matches	26; Conservative	0; Mismatches 3; Indels 0; Gaps 0;
Oy	4	TTAATTAAGTGCCTGCGGTGCCAGAAACC 32
Db	142	TTACAGAGTGCTCGCGGTGCCAGAAACC 170
RESULT 9		
LOCUS	DM422532	294 bp mRNA linear EST 14-JAN-2006
DEFINITION	HHAGE022822 Human liver regeneration after partial hepatectomy Homo sapiens cDNA, mRNA sequence.	
ACCESSION	DM422532	
VERSION	DM422532.1	GI:84924088
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	

REFERENCE 1 (bases 1 to 294)
AUTHORS Xu, C.S.
TITLE Liver regeneration after PH
JOURNAL Unpublished (2003)
COMMENT Contact: Cun-Shuan Xu
Henan Bioengineering Key Lab
Henan Normal University
No. 148 Jianshe Road, Xinxiang City, P.R.China
Tel: 0086373328084
Fax: 0086373326524
Email: xucse@263.net.

FEATURES
source
1..294
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="liver"
/clone_lib="Human liver regeneration after partial
hepatectomy"

ORIGIN
Query Match 75.6%; Score 24.2; DB 10; Length 294;
Best Local Similarity 89.7%; Pred. No. 15;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TTATAAGTGCTGCGGTCCAGAAACC 32
|||||
139 TTACAGAGTGCTGCGGTCCAGAAACC 167

RESULT 10
LOCUS DW415682 312 bp mRNA linear EST 14-JAN-2006
DEFINITION HhAGE016412 Human liver regeneration after partial hepatectomy Homo
sapiens cDNA, mRNA sequence.
ACCESSION DW415682
VERSION DW415682.1 GI:84917238
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 312)
XU, C.S.
TITLE Liver regeneration after PH
JOURNAL Unpublished (2003)
COMMENT Contact: Cun-Shuan Xu
Henan Bioengineering Key Lab
Henan Normal University
No. 148 Jianshe Road, Xinxiang City, P.R.China
Tel: 0086373328084
Fax: 0086373326524
Email: xucse@263.net.

FEATURES
source
1..312
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="liver"
/clone_lib="Human liver regeneration after partial
hepatectomy"

ORIGIN
Query Match 75.6%; Score 24.2; DB 10; Length 312;
Best Local Similarity 89.7%; Pred. No. 15;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TTATAAGTGCTGCGGTCCAGAAACC 32
|||||
142 TTACAGAGTGCTGCGGTCCAGAAACC 170

RESULT 11
LOCUS BF912441 405 bp mRNA linear EST 18-JAN-2001
DEFINITION IL2-UT0073-161100-246-G12 UT0073 Homo sapiens cDNA, mRNA sequence.
BF912441
VERSION BF912441.1 GI:12303899
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 405)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.P.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?fil=IL2ct=IL2-UT0073-
161100-246-G12ct3=2000-11-16ct4=1)
Seq primer: puc 18 forward
High quality sequence stop: 404.
Location/Qualifiers
1..405
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="adult"
/clone_lib="UT0073"
/note="Organ: uterus tumor; Vector: puc18; Site 1: Sma1;
Site 2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN
Query Match 75.6%; Score 24.2; DB 2; Length 405;
Best Local Similarity 89.7%; Pred. No. 15;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TTATAAGTGCTGCGGTCCAGAAACC 32
|||||
323 TTACAGAGTGCTGCGGTCCAGAAACC 351

RESULT 12
LOCUS BF912537 405 bp mRNA linear EST 18-JAN-2001
DEFINITION IL2-UT0073-191100-246-G12 UT0073 Homo sapiens cDNA, mRNA sequence.
BF912537
VERSION BF912537.1 GI:12303995
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 405)
Dias Neco,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
JOURNAL
PUBMED
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL:
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=IL2&t2=IL2-UT0073-
191100-246-G12&t3=2000-11-13&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 404.
Location/Qualifiers
1..4105
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="UT0073"
/note="Organ: uterus tumor; Vector: puc18; Site_1: Sma1;
Site_2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
ORIGIN
Query Match 75.6%; Score 24.2; DB 2; Length 405;
Best Local Similarity 89.7%; Pred. No. 15;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4 TTATTAAGTGCTGCGGTGCCGGAAC 32
Db 323 TTACAGAGTGCTGCGGTGCCGGAAC 351
RESULT 13
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL:
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=IL2&t2=IL2-UT0073-
131100-245-G08&t3=2000-11-13&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 409.
Location/Qualifiers
1..410
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="UT0073"
/note="Organ: uterus tumor; Vector: puc18; Site_1: Sma1;
Site_2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

Tel: 0086373328084
Fax: 0086373326524
Email: xucex263.net.
Location/Qualifiers
1..407
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/issue_type="liver"
/clone_lib="Human liver regeneration after partial
hepatectomy"
ORIGIN
Query Match 75.6%; Score 24.2; DB 10; Length 407;
Best Local Similarity 89.7%; Pred. No. 15;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4 TTATTAAGTGCTGCGGTGCCGGAAC 32
Db 140 TTACAGAGTGCTGCGGTGCCGGAAC 168
RESULT 14
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL:
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=IL2&t2=IL2-UT0073-
131100-245-G08&t3=2000-11-13&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 409.
Location/Qualifiers
1..410
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="UT0073"
/note="Organ: uterus tumor; Vector: puc18; Site_1: Sma1;
Site_2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Query Match 75.6%; Score 24.2; DB 2; Length 410;
Best Local Similarity 89.7%; Pred. No. 15;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 TTATAAGTGCTCGCGTGCAGAAACC 32
|||||
324 TTACAGAGTGCTCGCGTGCAGAAACC 352

RESULT 15
AW675319 420 bp mRNA linear EST 11-APR-2000
LOCUS b644c01.y1 NIH_MGC_12 Homo sapiens CDNA clone IMAGE:2986080 5'
DEFINITION b644c01.y1 NIH_MGC_12 Homo sapiens CDNA clone IMAGE:2986080 5'
ACCESSION AM675319
VERSION AM675319.1 GI:7540554
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 420)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strauberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
image.lnl.gov/image/htnl/lresources.shtml
Seq primer: -40RP from Glbco.
Location/Qualifiers

FEATURES
source 1..420
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2986080"
/tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
/clone_lib="NIH_MGC_12"
/note="Organ: cervix; Vector: PCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: oligo dt.
Average insert size 1.4 kb. Library prepared by Life
Technologies."

ORIGIN

Query Match 75.6%; Score 24.2; DB 7; Length 420;
Best Local Similarity 89.7%; Pred. No. 15;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 TTATAAGTGCTCGCGTGCAGAAACC 32
|||||
107 TTACAGAGTGCTCGCGTGCAGAAACC 135

RESULT 16
BE018031 509 bp mRNA linear EST 06-JUN-2000
LOCUS b673c04.y1 NIH_MGC_12 Homo sapiens CDNA clone IMAGE:3048006 5'
DEFINITION b673c04.y1 NIH_MGC_12 Homo sapiens CDNA clone IMAGE:3048006 5'
ACCESSION BE018031
VERSION BE018031.1 GI:8277975
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strauberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
image.lnl.gov/image/htnl/lresources.shtml
Seq primer: -40RP from Glbco
High quality sequence stop: 441.
Location/Qualifiers

FEATURES
source 1..509
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3048006"
/tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
/clone_lib="NIH_MGC_12"
/note="Organ: cervix; Vector: PCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: oligo dt.
Average insert size 1.4 kb. Library prepared by Life
Technologies."

ORIGIN

Query Match 75.6%; Score 24.2; DB 7; Length 509;
Best Local Similarity 89.7%; Pred. No. 16;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 TTATAAGTGCTCGCGTGCAGAAACC 32
|||||
94 TTACAGAGTGCTCGCGTGCAGAAACC 122

RESULT 17
B1260198 742 bp mRNA linear EST 17-JUL-2001
LOCUS 602970244.F1 NIH_MGC_12 Homo sapiens CDNA clone IMAGE:5109562 5'
DEFINITION 602970244.F1 NIH_MGC_12 Homo sapiens CDNA clone IMAGE:5109562 5'
ACCESSION B1260198
VERSION B1260198.1 GI:14818276
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 742)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strauberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: L1AM1265 row: h column: 11
High quality sequence stop: 738.
Location/Qualifiers

FEATURES
source 1..742
/organism="Homo sapiens"
/mol_type="mRNA"

DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/INLNL at:
<http://image.inl.gov>
 Plate: LHM11298 row: d column: 09
 High quality sequence stop: 742.
 Location/Qualifiers

FEATURES

source

1. 827
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5122136"
 /tissue_type="cervical carcinoma cell line"
 /lab_host="DH10B"
 /clone_1lb="NIH_MGC_12"
 /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.4 kb. Library prepared by Life
 Technologies."

ORIGIN

Query Match 75.6%; Score 24.2; DB 2; Length 827;
 Best Local Similarity 89.7%; Pred. No. 17;
 Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 4 TTATAAGTGCCCTGCGGTCAGAAACC 32
 100 TTACAGAGTGCTCGCGTCAGAAACC 128

RESULT 21
 BI223045 833 bp mRNA linear EST 11-JUL-2001
 LOCUS 602943381.F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5106352 5',
 DEFINITION mRNA sequence.
 ACCESSION BI223045
 VERSION BI223045.1 GI:14676489
 SOURCE EST.
 ORGANISM Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE 1 (bases 1 to 833)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: Incyte Genomics, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/INLNL at:
<http://image.inl.gov>
 Plate: LHM11257 row: a column: 21
 High quality sequence stop: 803.
 Location/Qualifiers

FEATURES

source

1. 833
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5106352"
 /tissue_type="cervical carcinoma cell line"
 /lab_host="DH10B"
 /clone_1lb="NIH_MGC_12"
 /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.4 kb. Library prepared by Life
 Technologies."

ORIGIN

Query Match 75.6%; Score 24.2; DB 2; Length 833;
 Best Local Similarity 89.7%; Pred. No. 17;
 Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TTATAAGTGCCCTGCGGTCAGAAACC 32
 DB 33 TTACAGAGTGCTCGCGTCAGAAACC 61

RESULT 22
 BX400902 833 bp mRNA linear EST 28-APR-2004
 LOCUS BX400902 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
 DEFINITION cDNA clone CS0DK004YC04 5-PRIME, mRNA sequence.
 ACCESSION BX400902 GI:46845779
 VERSION BX400902.2
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE 1 (bases 1 to 833)
 AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT On May 13, 2003 this sequence version replaced gi:30614402.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 4578.r

There is a virtual cDNA representing this cluster. For more
 information about this cluster and the virtual cDNA, see
<http://www.genoscope.cns.fr/cdnas=CS0DK004B02QPl&c=4578.r>.

FEATURES

source

1. 833
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DK004YC04"
 /cell_type="HELA CELLS COT 25-NORMALIZED"
 /cell_line="HELA"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 75.6%; Score 24.2; DB 4; Length 833;
 Best Local Similarity 89.7%; Pred. No. 17;
 Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 4 TTATAAGTGCCCTGCGGTCAGAAACC 32
 DB 104 TTACAGAGTGCTCGCGTCAGAAACC 132

RESULT 23
 BE546557 856 bp mRNA linear EST 09-AUG-2000
 LOCUS BE546557 60107656.F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3462758 5',
 DEFINITION mRNA sequence.
 ACCESSION BE546557
 VERSION BE546557.1 GI:9775202
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 856)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LHAM640 row: 0 column: 15
High quality sequence stop: 706.
Location/Qualifiers
1..856
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3462758"
/issue_type="cervical carcinoma cell line"
/lab_host="DH10B"
/clone_1lb="NIH_MGC_12"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.4 kb. Library prepared by Life
Technologies."

ORIGIN
Query Match 75.6%; Score 24.2; DB 7; Length 856;
Best Local Similarity 89.7%; Pred. No. 17;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4 TTATATAGTGCTGCGTCCAGAAACC 32
Db 76 TTACAGAGTGCTGCGTCCAGAAACC 104

RESULT 24
BS544755 922 bp mRNA linear EST 09-AUG-2000
LOCUS 601075520F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3461429 5',
DEFINITION mRNA sequence.
ACCESSION BS544755
VERSION BS544755.1 GI:9773400
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 922)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LHAM6457 row: h column: 06
High quality sequence stop: 717.
Location/Qualifiers
1..922

FEATURES
source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3461429"
/issue_type="cervical carcinoma cell line"
/lab_host="DH10B"
/clone_1lb="NIH_MGC_12"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.4 kb. Library prepared by Life
Technologies."

ORIGIN
Query Match 75.6%; Score 24.2; DB 7; Length 922;
Best Local Similarity 89.7%; Pred. No. 18;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4 TTATATAGTGCTGCGTCCAGAAACC 32
Db 133 TTACAGAGTGCTGCGTCCAGAAACC 161

RESULT 25
BI256241 1043 bp mRNA linear EST 17-JUL-2001
LOCUS 602975055F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5114316 5',
DEFINITION mRNA sequence.
ACCESSION BI256241
VERSION BI256241.1 GI:14810460
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 1043)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LHAM1277 row: n column: 13
High quality sequence stop: 723.
Location/Qualifiers
1..1043
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5114316"
/issue_type="cervical carcinoma cell line"
/lab_host="DH10B"
/clone_1lb="NIH_MGC_12"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.4 kb. Library prepared by Life
Technologies."

ORIGIN
Query Match 75.6%; Score 24.2; DB 2; Length 1043;
Best Local Similarity 89.7%; Pred. No. 18;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4 TTATATAGTGCTGCGTCCAGAAACC 32
Db 96 TTACAGAGTGCTGCGTCCAGAAACC 124

RESULT 26
LOCUS B1257598 1114 bp mRNA linear EST 17-JUL-2001
DEFINITION 602967170F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5106952 5', mRNA sequence.

ACCESSION B1257598
VERSION B1257598
KEYWORDS GI:14813133
SOURCE EST.
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS NIH-MGC
TITLE NIH-MGC
JOURNAL http://mgc.nci.nih.gov/
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bcr-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/BLNT at: http://image.llnl.gov
Plate: L14M1258 row: k column: 17
High quality sequence stop: 610.
Location/Qualifiers
1. 1114
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5106952"
/issue_type="cervical carcinoma cell line"
/lab_host="DH10B"
/clone_lib="NIH_MGC_12"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.4 kb. Library prepared by Life Technologies."

ORIGIN
Query Match 75.6%; Score 24.2; DB 2; Length 1114;
Best Local Similarity 89.7%; Pred. No. 18;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TTAATAGGTCCTGCGCTGCCAGAAACC 32
Db 213 TTACAGAGGTGCTCGCTGCCAGAAACC 241

RESULT 27
LOCUS A1747399 554 bp mRNA linear EST 22-JUN-1999
DEFINITION U105h08.y1 Sugano mouse kidney m1ka Mus musculus cDNA clone IMAGE:2065215 5' similar to gb:X57958 60S RIBOSOMAL PROTEIN L7 (HUMAN); gb:M29015 Mouse ribosomal protein L7 (MOUSE); mRNA sequence.

ACCESSION A1747399
VERSION A1747399
KEYWORDS GI:5125663
SOURCE EST.
ORGANISM Mus musculus (house mouse)

REFERENCE
AUTHORS Mus musculus
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murine; Mus.
1 (bases 1 to 554)
Marrar,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Stepecoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Page,D., Harvey,N., Schurr,R., Ritzer,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,

TITLE Waterston,R. and Wilson,R.
JOURNAL The WashU-NCI Mouse EST Project 1999
COMMENT Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through BLNT; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: custom primer used
High quality sequence stop: 519.
Location/Qualifiers
1. 554
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:2065215"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="Sugano mouse kidney m1ka"
/note="Organ: kidney; Vector: pM185-F13; Site 1: DraIII (CACCTGTG); Site 2: DraIII (CACCTGTG); 1st strand cDNA was primed with an oligo(dt) primer
[ATGCGCCCTTTTCTTTTCTTTT]; double-stranded cDNA was ligated to a DraIII adaptor (TGTGCGCTCTGTG), digested and cloned into distinct DraIII sites of the pM185-F13 vector (5' site CACCTGTG, 3' site CACCTGTG). XhoI should be used to isolate the cDNA insert. Site selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTGCTGCTTAAAGTGTGCG and 3' end primer CAGCTCGAGCTCGACAC."

ORIGIN
Query Match 75.0%; Score 24; DB 1; Length 554;
Best Local Similarity 84.4%; Pred. No. 20;
Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TTAATAGGTCCTGCGCTGCCAGAAACC 32
Db 96 TTATTAAGGTCCTGCGCTGCCAGAAACC 127

RESULT 28
LOCUS AA686665 202 bp mRNA linear EST 13-JAN-1998
DEFINITION EST110976 Rat PC-12 cells, NGF-created (9 days) Rattus norvegicus cDNA 5' and similar to Ribosomal protein L7, mRNA sequence.

ACCESSION AA686665
VERSION AA686665
KEYWORDS GI:2673263
SOURCE EST.
ORGANISM Rattus norvegicus (Norway rat)

REFERENCE
AUTHORS Rattus norvegicus
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murine; Rattus.
1 (bases 1 to 202)
Lee,N.H., Weinsteck,K.G., Kirkness,E.F., Earle-Hughes,J.A., Fulcher,R.A., Marmaras,S., Glodok,A., Gocayne,J.D., Adams,M.D., Kerlavage,A.R., Fraser,C.M. and Venter,J.C.
Comparative expressed-sequence-tag analysis of differential gene expression profiles in PC-12 cells before and after nerve growth factor treatment
Proc. Natl. Acad. Sci. U.S.A. 92, 8303-8307 (1995)
7667285
Other ESTs: TC44726
Contact: Lee, NH

The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13 Reverse.

FEATURES

source

```
1. .202
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="ATCC (thost):2005132"
/db_xref="taxon:10116"
/clone_lib="Rat PC-12 cells, NGF-treated (9 days)"
/notes="Vector: Bluescript SK-; Site 1: EcoRI; Site 2:
XhoI; poly(A)+ RNA was purified from 9-day NGF treated
PC12 cells. cDNA was constructed using an oligo-dT primer
and directionally cloned using the lambda ZAP II Vector
Kit by Stratagene"
```

ORIGIN

Query Match 74.4%; Score 23.8; DB 1; Length 202;
Best Local Similarity 92.6%; Pred. No. 21;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AATPAGGTCCTCGGTCGCGCAAAACC 32
|||
53 AAAAAGTCTCTCGGTCGCGCAAAACC 79

RESULT 29 212 bp mRNA linear EST 03-APR-1998
LOCUS AA686627
DEFINITION BstII0842 Rat PC-12 cells, NGF-treated (9 days) Rattus norvegicus
cDNA clone RPBN47 5' end similar to Ribosomal protein L7, mRNA
sequence.

ACCESSION AA686627
VERSION AA686627.1 GI:2673225

KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus

ORGANISM Bkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE

AUTHORS

Lee, N.H., Weinstein, K.G., Kirkness, E.F., Earle-Hughes, J.A.,
Fulder, R.A., Marmaras, S., Glodok, A., Gocayne, J.D., Adams, M.D.,
Kerlavage, A.R., Fraser, C.M. and Venter, J.C.
Comparative expressed-sequence-tag analysis of differential gene
expression profiles in PC-12 cells before and after nerve growth
factor treatment
Proc. Natl. Acad. Sci. U.S.A. 92, 8303-8307 (1995)

COMMENT 7667285
Other ESTs: TC44726

FEATURES

PUBMED

The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13 Reverse.
Location/Qualifiers

FEATURES

source

```
1. .212
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="ATCC (thost):2005002"
/db_xref="taxon:10116"
/clone_lib="Rat PC-12 cells, NGF-treated (9 days)"
/notes="Vector: Bluescript SK-; Site 1: EcoRI; Site 2:
XhoI; poly(A)+ RNA was purified from 9-day NGF treated
PC12 cells. cDNA was constructed using an oligo-dT primer
and directionally cloned using the lambda ZAP II Vector
Kit by Stratagene"
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ORIGIN

Query Match 74.4%; Score 23.8; DB 1; Length 212;
Best Local Similarity 92.6%; Pred. No. 21;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AATPAGGTCCTCGGTCGCGCAAAACC 32
|||
36 AAAAAGTCTCTCGGTCGCGCAAAACC 62

RESULT 30 289 bp mRNA linear EST 06-JAN-2006
LOCUS DW320563
DEFINITION IRAGB045391 Liver regeneration after partial hepatectomy Rattus
norvegicus cDNA, mRNA sequence.

ACCESSION DW320563
VERSION DW320563.1 GI:84548946

KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus

ORGANISM Bkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 289)
XU, C.S.
Liver regeneration after PH
Unpublished (2003)
Contact: Cun-Shuan Xu
Henan Bioengineering Key Lab
Henan Normal University
No. 148 Jianshe Road, Xinxiang City, P.R.China
Tel: 00863733328084
Fax: 0086373326524
Email: xuc@x263.net.

FEATURES

source

```
1. .289
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/issue_type="liver"
/clone_lib="Liver regeneration after partial hepatectomy"
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ORIGIN

Query Match 74.4%; Score 23.8; DB 10; Length 289;
Best Local Similarity 92.6%; Pred. No. 22;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AATPAGGTCCTCGGTCGCGCAAAACC 32
|||
82 AAAAAGTCTCTCGGTCGCGCAAAACC 108

RESULT 31 299 bp mRNA linear EST 13-JAN-1998
LOCUS AA685796
DEFINITION BstII08189 Rat PC-12 cells, untreated Rattus norvegicus cDNA 5' end
similar to Ribosomal protein L7, mRNA sequence.

ACCESSION AA685796
VERSION AA685796.1 GI:2672394

FEATURES

source

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1. .289
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone_lib="Liver regeneration after partial hepatectomy"
/notes="Vector: Bluescript SK-; Site 1: EcoRI; Site 2:
XhoI; poly(A)+ RNA was purified from 9-day NGF treated
PC12 cells. cDNA was constructed using an oligo-dT primer
and directionally cloned using the lambda ZAP II Vector
Kit by Stratagene"
```

JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 92, 8303-8307 (1995)

COMMENT
7667285
Other ESTs: TC44726
Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13 Reverse.
Location/Qualifiers
1. .299
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="ATCC (inhost):2002867"
/db_xref="taxon:10116"
/clone_lib="Rat PC-12 cells, untreated"
/note="Vector: Bluescript SK-; Site 1: EcoRI; Site 2: XhoI; poly(A) + RNA was purified from untreated PC12 cells cultured for 9 days. cDNA was constructed using an oligo-dT primer and directionally cloned using the Lambda ZAP II Vector Kit by Stratagene"

ORIGIN
Query Match 74.4%; Score 23.8; DB 1; Length 299;
Best Local Similarity 92.6%; Pred. No. 22;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AATAAGTGCTGCGGTGCCAGAAACC 32
|||
42 AAAAAGTTCCTGCGGTGCCAGAAACC 68
|||

RESULT 32
DW300318 323 bp mRNA linear EST 06-JAN-2006
LOCUS IMAGE062146 Liver regeneration after partial hepatectomy Rattus
DEFINITION norvegicus cDNA, mRNA sequence.
ACCESSION DW300318.1 GI:84528697
VERSION DW300318
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE Xu, C.S.
TITLE Liver regeneration after PH
JOURNAL Unpublished (2003)
COMMENT Contact: Cun-Shuan Xu
Henan Bioengineering Key Lab
Henan Normal University
No. 148 Jianshe Road, Xinxiang City, P.R.China
Tel: 00863733328084
Fax: 00863733326524
Email: xucs@x263.net.

FEATURES
source
1. .323
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone_lib="Liver regeneration after partial hepatectomy"

ORIGIN
Query Match 74.4%; Score 23.8; DB 10; Length 323;
Best Local Similarity 92.6%; Pred. No. 22;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AATAAGTGCTGCGGTGCCAGAAACC 32
|||
199 AAAAAGTTCCTGCGGTGCCAGAAACC 173
|||

RESULT 33
AA685923 341 bp mRNA linear EST 03-APR-1998
LOCUS EST108644 Rat PC-12 cells, NGF-treated (9 days) Rattus norvegicus
DEFINITION cDNA clone RPNAD62 5' end similar to Ribosomal protein L7, mRNA sequence.
ACCESSION AA685923
VERSION AA685923.1 GI:2672521
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE Lee, N.H., Weinstein, K.G., Kirkness, E.F., Earle-Hughes, J.A., Pridmore, R.A., Marmar, S., Glodde, A., Gocayne, J.D., Adams, M.D., Karlayage, A.R., Fraser, C.M., and Venter, J.C.
TITLE Comparative expressed-sequence-tag analysis of differential gene expression profiles in PC-12 cells before and after nerve growth factor treatment
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 92, 8303-8307 (1995)
COMMENT Other ESTs: TC44726
7667285
Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13 Reverse.
Location/Qualifiers
1. .341
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="ATCC (inhost):2003267"
/db_xref="taxon:10116"
/clone_lib="RPNAD62"
/clone_lib="Rat PC-12 cells, NGF-treated (9 days)"
/note="Vector: Bluescript SK-; Site 1: EcoRI; Site 2: XhoI; poly(A) + RNA was purified from 9-day NGF treated PC12 cells. cDNA was constructed using an oligo-dT primer and directionally cloned using the Lambda ZAP II Vector Kit by Stratagene"

ORIGIN
Query Match 74.4%; Score 23.8; DB 1; Length 341;
Best Local Similarity 92.6%; Pred. No. 22;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AATAAGTGCTGCGGTGCCAGAAACC 32
|||
41 AAAAAGTTCCTGCGGTGCCAGAAACC 67
|||

RESULT 34
BE127031 344 bp mRNA linear EST 15-JUN-2000
LOCUS DBPA0780 Rat Lambda ZAP Express Library Rattus norvegicus cDNA 5',
DEFINITION mRNA sequence.
ACCESSION BE127031.1 GI:8549739
VERSION BE127031
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE Sleeman, M.A., Murlison, J.G., Strachan, L., Kumble, K.D., Glenn, M.P., McGrath, A., Grierson, A., Havukkala, I., Tan, P.L.J. and Watson, J.D.

TITLE Expressed sequence tags of cDNA clones from rat dermal papilla cells
JOURNAL Unpublished (2000)
COMMENT Contact: Sleeman MA
Biology
Genesis Research and Development Corporation Limited
P.O. Box 50, 1 Fox St, Parnell, Auckland, New Zealand
Tel: 0064 9 373 5600
Fax: 0064 9 373 2189
Email: m.sleeman@genesis.co.nz
Seq primer: T3 forward
High quality sequence stop: 344.
Location/Qualifiers
1. 346
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Dark-Agouti"
/db_xref="taxon:10116"
/issue_type="vibrissae"
/cell_type="dermal papilla"
/clone_lib="Rat Lambda ZAP Express Library"

ORIGIN
Query Match 74.4%; Score 23.8; DB 7; Length 344;
Best Local Similarity 92.6%; Pred. No. 22;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 AATAAGTGCTGCGGTGCCGAAACC 32
Db 40 AAAAGGTTCTGCGGTGCCGAAACC 66

RESULT 35
AI229881 346 bp mRNA linear EST 20-JAN-1999
LOCUS ST226576 Normalized rat embryo, Bento Soares Rattus sp. cDNA clone
DEFINITION RENC80 3' end, mRNA sequence.
ACCESSION AI229881
VERSION AI229881.1 GI:3813768
KEYWORDS EST.
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Rattus.
1 (bases 1 to 346)
Lee, N.H., Glodok, A., Chandra, I., Mason, T.M., Quackenbush, J., Kerlavage, A.R. and Adams, M.D.
Rat Genome Project: Generation of a Rat EST (RST) Catalog & Rat Gene Index
Unpublished (1998)
JOURNAL Contact: Lee, NH
COMMENT The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13-21.
Location/Qualifiers
1. 346
/organism="Rattus sp."
/mol_type="mRNA"
/db_xref="ATCC (inhost):2036659"
/db_xref="taxon:10118"
/clone_lib="RENC80"
/dev_stage="embryo 8, 12, 18 dpc"
/clone_lib="Normalized rat embryo, Bento Soares"
/note="Vector: pT73Pac; Site_1: EcoRI; Site_2: NotI"

ORIGIN
Query Match 74.4%; Score 23.8; DB 1; Length 346;
Best Local Similarity 92.6%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 AATAAGTGCTGCGGTGCCGAAACC 32
Db 73 AAAAGGTTCTGCGGTGCCGAAACC 99

RESULT 36
H35039 346 bp mRNA linear EST 02-APR-1998
LOCUS EST109541 Rat PC-12 cells, NGF-treated (9 days) Rattus norvegicus
DEFINITION cDNA clone RPNAS64 similar to Ribosomal protein L7, mRNA sequence.
ACCESSION H35039
VERSION H35039.1 GI:980456
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Rattus.
1 (bases 1 to 346)
Lee, N.H., Weinstein, K.G., Kirkness, E.F., Barle-Hughes, J.A., Pulder, R.A., Marmar, S., Glodok, A., Gocayne, J.D., Adams, M.D., Kerlavage, A.R., Fraser, C.M. and Venter, J.C.
Comparative expressed-sequence-tag analysis of differential gene expression profiles in PC-12 cells before and after nerve growth factor treatment
Proc. Natl. Acad. Sci. U.S.A. 92, 8303-8307 (1995)
7667285
Other ESTs: TC226
Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
For clone availability please contact the TIGR Database (tdbinfo@tigr.org) TC (tentative consensus) numbers represent assemblies of ESTs.
Location/Qualifiers
1. 346
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="ATCC (inhost):2003904"
/db_xref="taxon:10116"
/clone_lib="RPNAS64"
/clone_lib="Rat PC-12 cells, NGF-treated (9 days)"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; poly(A)+ RNA was purified from 9-day NGF treated PC12 cells. cDNA was constructed using an oligo-dT primer and directionally cloned using the lambda ZAP II Vector Kit by Stratagene"

ORIGIN
Query Match 74.4%; Score 23.8; DB 10; Length 346;
Best Local Similarity 92.6%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 AATAAGTGCTGCGGTGCCGAAACC 32
Db 69 AAAAGGTTCTGCGGTGCCGAAACC 95

RESULT 37
DM311724 347 bp mRNA linear EST 06-JAN-2006
LOCUS LRAGE072552 Liver regeneration after partial hepatectomy Rattus norvegicus cDNA, mRNA sequence.
DEFINITION DM311724
ACCESSION DM311724
VERSION DM311724.1 GI:84540107
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

REFERENCE      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
AUTHORS        Sciurognathi; Muridae; Muridae; Murinae; Rattus.
TITLE          1 (bases 1 to 347)
JOURNAL        Liver regeneration after PH
COMMENT        Unpublished (2003)
                Contact: Cun-Shuan Xu
                Henan Bioengineering Key Lab
                Henan Normal University
                No. 148 Jianshe Road, Xinxiang City, P.R.China
                Tel: 0086373328084
                Fax: 0086373326524
                Email: xucsx263.net.

FEATURES
  source        Location/Qualifiers
                1..347
                /organism="Rattus norvegicus"
                /mol_type="mRNA"
                /db_xref="taxon:10116"
                /rlnsue type="liver"
                /clone_lib="liver regeneration after partial hepatectomy"

ORIGIN
Query Match    74.4%; Score 23.8; DB 10; Length 347;
Best Local Similarity 92.6%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY
6 AATTAAGTGCCTCGGTCGCGCAGAAACC 32
|||
248 AAAAAGTTCCTCGGTCGCGCAGAAACC 222

RESULT 38
LOCUS          DM380853          350 bp      mRNA      linear      EST 14-JUN-2006
DEFINITION    IRAGS025508 Liver regeneration after partial hepatectomy Rattus
                norvegicus cDNA, mRNA sequence.
ACCESSION     DM380853
VERSION       DM380853.1 GI:84884975
KEYWORDS      EST.
SOURCE        Rattus norvegicus (Norway rat)
ORGANISM      Rattus norvegicus
REFERENCE     1
AUTHORS       Xu, C.S.
TITLE         Liver regeneration after PH
JOURNAL       Unpublished (2003)
COMMENT       Contact: Cun-Shuan Xu
                Henan Bioengineering Key Lab
                Henan Normal University
                No. 148 Jianshe Road, Xinxiang City, P.R.China
                Tel: 0086373328084
                Fax: 0086373326524
                Email: xucsx263.net.

FEATURES
  source        Location/Qualifiers
                1..350
                /organism="Rattus norvegicus"
                /mol_type="mRNA"
                /db_xref="taxon:10116"
                /rlnsue type="liver"
                /clone_lib="liver regeneration after partial hepatectomy"

ORIGIN
Query Match    74.4%; Score 23.8; DB 10; Length 350;
Best Local Similarity 92.6%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY
6 AATTAAGTGCCTCGGTCGCGCAGAAACC 32
|||
74 AAAAAGTTCCTCGGTCGCGCAGAAACC 100

```

```

RESULT 39
LOCUS          AJ647449          359 bp      mRNA      linear      EST 07-JUL-2004
DEFINITION    AJ647449 CSERAN19 Sus scrofa cDNA clone C0003105_L12, mRNA
                sequence.
ACCESSION     AJ647449
VERSION       AJ647449.1 GI:49324294
KEYWORDS      EST.
SOURCE        Sus scrofa (pig)
ORGANISM      Sus scrofa
REFERENCE     1
AUTHORS       Anderson, S.T., Finlayson, H.A. and Archibald, A.L.
TITLE         Development of cDNA and EST resources for studying reproduction and
                embryo development in pigs and cattle
JOURNAL       Unpublished (2004)
COMMENT       Contact: Anderson SI
                Genomics and Bioinformatics
                Roslin Institute
                Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
                Single pass sequencing. Bases called and trimmed with phred
                v0.020425.c. Vector identified by cross match with the -minscore 20
                and -mismatch 12 options. Vector: Bluescript1 (KS) R. Site1: EcoRI
                R. Site2: NotI 5' Seg Primer M13P Normalised library constructed
                from pooled ovaries. Clones available from UK Centre for Functional
                Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
                EH25 9PS, www.ark-genomics.org.

FEATURES
  source        Location/Qualifiers
                1..359
                /organism="Sus scrofa"
                /mol_type="mRNA"
                /db_xref="taxon:9823"
                /clone="C0003105_L12"
                /rlnsue type="ovary"
                /clone_lib="CSERAN19"
                /note="Vector: Bluescript1 (KS+); Site 1: EcoRI; Site 2:
                NotI; Single pass sequencing; Normalised library
                constructed from pooled ovaries"

ORIGIN
Query Match    74.4%; Score 23.8; DB 1; Length 359;
Best Local Similarity 92.6%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY
6 AATTAAGTGCCTCGGTCGCGCAGAAACC 32
|||
69 AAAAAGTTCCTCGGTCGCGCAGAAACC 95

RESULT 40
LOCUS          BE128703          367 bp      mRNA      linear      EST 15-JUN-2000
DEFINITION    DEPA2453 Rat Lambda ZAP Express library Rattus norvegicus cDNA 5',
                mRNA sequence.
ACCESSION     BE128703
VERSION       BE128703.1 GI:8551456
KEYWORDS      EST.
SOURCE        Rattus norvegicus (Norway rat)
ORGANISM      Rattus norvegicus
REFERENCE     1
AUTHORS       Steeman, M.A., Murison, J.G., Strachan, L., Kumble, K.D., Glenn, M.P.,
                McGrath, A., Grierison, A., Havukkala, I., Tan, P.L.U. and Watson, J.D.
TITLE         Expressed sequence tags of cDNA clones from rat dermal papilla
                cells
JOURNAL       Unpublished (2000)
COMMENT       Contact: Steeman MA
                Biology
                Genests Research and Development Corporation Limited

```

P.O. Box 50, 1 Fox St, Parnell, Auckland, New Zealand
Tel: 0064 9 373 5600
Fax: 0064 9 373 2189
Email: m.sleeman@genesis.co.nz

Seq primer: T3 forward
High quality sequence stop: 367.
Location/Qualifiers

1. 367

/organism="Rattus norvegicus"
/mol_type="mRNA"

/strain="Dark-Agouti"

/db_xref="taxon:10116"

/tissue_type="vibrissae"

/cell_type="dermal papilla"

/clone_lib="Rat Lambda Zap Express Library"

ORIGIN

Query Match 74.4%; Score 23.8; DB 7; Length 367;
Best Local Similarity 92.6%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AATAGGTGCTGCGGCGCAAAACC 32
DB 41 AAAAGGTTCTCGGTCGCAAAACC 67

RESULT 41

CV971013

LOCUS CV971013 386 bp mRNA linear EST 30-NOV-2004
DEFINITION LR9801012 Liver regeneration after partial hepatectomy Rattus
norvegicus cDNA, mRNA sequence.

ACCESSION

CV971013

VERSION CV971013.1

KEYWORDS EST.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

REFERENCE Xu, C.S.

AUTHORS Liver regeneration after PH

TITLE Unpublished (2003)

JOURNAL Contact: Cun-Shuan Xu

COMMENT Henan Bioengineering Key Lab

Henan Normal University

No. 148 Jianshe Road, Xinxiang City, P.R.China

Tel: 0086373328084

Fax: 0086373326524

Email: xucsx263.net.

Location/Qualifiers

1. 386

/organism="Rattus norvegicus"

/mol_type="mRNA"

/db_xref="taxon:10116"

/tissue_type="liver"

/clone_lib="Liver regeneration after partial hepatectomy"

ORIGIN

Query Match 74.4%; Score 23.8; DB 8; Length 386;
Best Local Similarity 92.6%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AATAGGTGCTGCGGCGCAAAACC 32
DB 110 AAAAGGTTCTCGGTCGCAAAACC 136

RESULT 42

DM383713

LOCUS DM383713 386 bp mRNA linear EST 14-JAN-2006
DEFINITION LR98028724 Liver regeneration after partial hepatectomy Rattus
norvegicus cDNA, mRNA sequence.

ACCESSION DM383713
VERSION DM383713.1

KEYWORDS GI:84887835

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

REFERENCE Xu, C.S.

AUTHORS Liver regeneration after PH

TITLE Unpublished (2003)

JOURNAL Contact: Cun-Shuan Xu

COMMENT Henan Bioengineering Key Lab

Henan Normal University

No. 148 Jianshe Road, Xinxiang City, P.R.China

Tel: 0086373328084

Fax: 0086373326524

Email: xucsx263.net.

Location/Qualifiers

1. 386

/organism="Rattus norvegicus"

/mol_type="mRNA"

/db_xref="taxon:10116"

/tissue_type="liver"

/clone_lib="Liver regeneration after partial hepatectomy"

ORIGIN

Query Match 74.4%; Score 23.8; DB 10; Length 386;
Best Local Similarity 92.6%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AATAGGTGCTGCGGCGCAAAACC 32
DB 110 AAAAGGTTCTCGGTCGCAAAACC 136

RESULT 43

DM383827

LOCUS DM383827 387 bp mRNA linear EST 14-JAN-2006
DEFINITION LR98028667 Liver regeneration after partial hepatectomy Rattus
norvegicus cDNA, mRNA sequence.

ACCESSION

DM383827

VERSION DM383827.1

KEYWORDS GI:84887949

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

REFERENCE Xu, C.S.

AUTHORS Liver regeneration after PH

TITLE Unpublished (2003)

JOURNAL Contact: Cun-Shuan Xu

COMMENT Henan Bioengineering Key Lab

Henan Normal University

No. 148 Jianshe Road, Xinxiang City, P.R.China

Tel: 0086373328084

Fax: 0086373326524

Email: xucsx263.net.

Location/Qualifiers

1. 387

/organism="Rattus norvegicus"

/mol_type="mRNA"

/db_xref="taxon:10116"

/tissue_type="liver"

/clone_lib="Liver regeneration after partial hepatectomy"

ORIGIN

Query Match 74.4%; Score 23.8; DB 10; Length 387;
Best Local Similarity 92.6%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AATAGGTGCTGCGGCGCAAAACC 32
DB 110 AAAAGGTTCTCGGTCGCAAAACC 136

Qy 6 AATAGGTGCTGGCGTCCAGAAACC 32
 |||||
 Db 115 AAAAAGTCTCTGGTCCAGAAACC 141

RESULT 44
 DW385499/c 398 bp mRNA linear EST 14-JAN-2006
 LOCUS LWAG029676 Liver regeneration after partial hepatectomy Rattus
 DEFINITION norvegicus cDNA, mRNA sequence.
 ACCESSION DW385499
 VERSION DW385499.1 GI:84889621
 KEYWORDS EST.
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
 1 (bases 1 to 398)
 Xu, C.S.
 Liver regeneration after PH
 TITLE Unpublished (2003)
 JOURNAL Contact: Cun-Shuan Xu
 COMMENT Henan Bioengineering Key Lab
 Henan Normal University
 No. 148 Jianshe Road, Xinxiang City, P.R.China
 Tel: 0086373328084
 Fax: 0086373326524
 Email: xucs@x263.net.

FEATURES
 source 1..398
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /db_xref="taxon:10116"
 /cissue_type="liver"
 /clone_idb="Liver regeneration after partial hepatectomy"

ORIGIN
 Query Match 74.4%; Score 23.8; DB 10; Length 398;
 Best Local Similarity 92.6%; Pred. No. 23;
 Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 AATAGGTGCTGGCGTCCAGAAACC 32
 |||||
 Db 235 AAAAAGTCTCTGGTCCAGAAACC 209

RESULT 45
 DW386589/c 401 bp mRNA linear EST 14-JAN-2006
 LOCUS LWAG029928 Liver regeneration after partial hepatectomy Rattus
 DEFINITION norvegicus cDNA, mRNA sequence.
 ACCESSION DW386589
 VERSION DW386589.1 GI:84890711
 KEYWORDS EST.
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
 1 (bases 1 to 401)
 Xu, C.S.
 Liver regeneration after PH
 TITLE Unpublished (2003)
 JOURNAL Contact: Cun-Shuan Xu
 COMMENT Henan Bioengineering Key Lab
 Henan Normal University
 No. 148 Jianshe Road, Xinxiang City, P.R.China
 Tel: 0086373328084
 Fax: 0086373326524
 Email: xucs@x263.net.

FEATURES
 Location/Qualifiers

source 1..401
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /db_xref="taxon:10116"
 /cissue_type="liver"
 /clone_idb="Liver regeneration after partial hepatectomy"

ORIGIN
 Query Match 74.4%; Score 23.8; DB 10; Length 401;
 Best Local Similarity 92.6%; Pred. No. 23;
 Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 AATAGGTGCTGGCGTCCAGAAACC 32
 |||||
 Db 238 AAAAAGTCTCTGGTCCAGAAACC 212

RESULT 46
 AA956776 415 bp mRNA linear EST 04-JUL-1999
 LOCUS UI-R-E1-fr-f-11-0-UI-g1 UI-R-E1 Rattus norvegicus cDNA clone
 DEFINITION UI-R-E1-fr-f-11-0-UI 3' similar to gi|206735|gb|M17422|BAYRBL7 Rat
 ribosomal protein L7 mRNA, 5' end, mRNA sequence.
 AA956776
 VERSION AA956776
 KEYWORDS AA956776.1 GI:4239250
 SOURCE EST.
 ORGANISM Rattus norvegicus (Norway rat)
 Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
 1 (bases 1 to 415)
 Bonaldo, M.F., Lennon, G. and Soares, M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 PUBMED 8889548
 COMMENT On May 7, 1998 this sequence version replaced gi:3120471.
 Contact: Soares, MB
 Coordinated Laboratory for Computational Genomics
 University of Iowa
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: bento-soares@uiowa.edu
 The sequence tag present in the cDNA between the NotI site and the
 oligo-dt track served to identify it as a clone from the normalized
 adult 18-Day-Embryo library. cDNA library preparation: M. Fatima
 Bonaldo, Ph.D. Clone distribution: clones will be available through
 Research Genetics This clone is also available through the
 I.M.A.G.E. Consortium at LNL (infoimage.lnl.gov). IMAGE
 ID=1779946
 Seq primer: M13 Forward
 POLYA=No.

FEATURES
 source 1..415
 Location/Qualifiers
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-E1-fr-f-11-0-UI"
 /dev_stage="adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_idb="UI-R-E1"
 /note="Vector: p773D-PacI, Site 1: Not I, Site 2: Eco RI;
 The UI-R-E1 library is a subtracted library derived from
 the UI-R-E0 library. The UI-R-E0 library consisted of a
 mixture of individually tagged normalized libraries
 constructed from 8, 12 and 18-day embryo. The tag is a
 string of 3-5 nucleotides present between the Not I site
 and the oligo-dt track which allows identification of the
 library of origin of a clone within the mixture. The
 subtracted library (UI-R-E1) was constructed as follows:

PCR amplified cDNA inserts from a pool of UI-R-E0 clones from which 3' ESTs had been derived was used as a driver in a hybridization with the UI-R-E0 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-E1 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996)".

ORIGIN

Query Match 74.4%; Score 23.8; DB 1; Length 415;
Best Local Similarity 92.6%; Pred. No. 23;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AATPAGTGCTGCGTGCCGAGAAC 32
|||
90 AAAAGGTTCTCGGTGCCAGAAC 116

RESULT 47 478 bp mRNA linear EST 31-MAY-2004
LOCUS CP273504
DEFINITION IGAM6 Rat Lambda Zap 4 h light-exposed retina cDNA library Rattus norvegicus CDNA 5', mRNA sequence.
ACCESSION CP273504
VERSION CP273504.1 GI:4782552
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 478)
Grewal, R., Stepczynski, J., Erickson, T., Kellin, R.M., Darrow, R., Barsalou, L., Patterson, M.L., Organisciak, D.T. and Wong, P.
Specific changes in ribosomal protein gene expression during light-induced retinal degeneration
Unpublished (2003)
CONTACT: Wong P
UNIVERSITY OF ALBERTA
5502 Biological Sciences Centre, Edmonton, Alberta T6G 2E9 Canada
Tel: 780 492 3590
Fax: 780 492 9234
Email: p.wong@ualberta.ca
PCR PRIMERS
FORWARD: T3
BACKWARD: T7
Seq primer: SK.

FEATURES

source

1..478
Location/Qualifiers
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/sex="male"
/tissue_type="retina"
/dev_stage="adult"
/clone_lib="Rat Lambda Zap 4 h light-exposed retina cDNA library"
/note="Vector: Uni-ZAP XR; The Rat Lambda Zap 4 h light-exposed retina cDNA library was constructed from retinal RNA isolated from weanling male albino Sprague-Dawley rats, which were maintained in darkness for 40 days. At 61 days of age rats were exposed to intense visible light (490-580 nm; 1200 to 1400 lux) for 4 hours."

ORIGIN

Query Match 74.4%; Score 23.8; DB 5; Length 478;
Best Local Similarity 92.6%; Pred. No. 24;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AATPAGTGCTGCGTGCCGAGAAC 32
|||
Db 111 AAAAGGTTCTCGGTGCCAGAAC 137

RESULT 48 490 bp mRNA linear EST 16-JUN-1998
LOCUS AA944687
DEFINITION EST200186 Normalized rat embryo, Bento Soares Rattus sp. cDNA clone
REMARK 79 3' end, mRNA sequence.

ACCESSION AA944687
VERSION AA944687.1 GI:3104603
KEYWORDS EST.
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 490)
Lee, N.H., Glodok, A., Chandra, I., Mason, T.M., Quackenbush, J., Kerlavage, A.R. and Adams, M.D.
Rat Genome Project: Generation of a Rat EST (RESE) Catalog & Rat Gene Index
Unpublished (1998)
CONTACT: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13-21.

JOURNAL
COMMENT

FEATURES
source

1..490
Location/Qualifiers
/organism="Rattus sp."
/mol_type="mRNA"
/db_xref="ATCC (inhost):201451"
/db_xref="taxon:10118"
/clone="REMAN79"
/dev_stage="embryo 8, 12, 18 dpc"
/clone_lib="Normalized rat embryo, Bento Soares"
/note="Vector: pT73pac; Site_1: EcoRI; Site_2: NotI"

ORIGIN

Query Match 74.4%; Score 23.8; DB 1; Length 490;
Best Local Similarity 92.6%; Pred. No. 24;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AATPAGTGCTGCGTGCCGAGAAC 32
|||
Db 73 AAAAGGTTCTCGGTGCCAGAAC 99

RESULT 49 498 bp mRNA linear EST 07-JUN-2004
LOCUS AJ647149
DEFINITION AJ647149 CSERAN19 Sus scrofa cDNA clone C0003104_N19, mRNA
sequence.

ACCESSION AJ647149
VERSION AJ647149.1 GI:49323994
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae; Sus.

REFERENCE 1 (bases 1 to 498)
Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
Unpublished (2004)
CONTACT: Anderson SI
Genomics and Bioinformatics

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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2006, 05:34:58 ; Search time 225.028 Seconds
(without alignments)
650.664 Million cell updates/sec

Title: US-10-601-913-85

Perfect score: 21

Sequence: 1 CAGGACACAGTGGCTTTGAC 21

Scoring table: IDENTITY_NUC

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Database :

1: N_Geneseq.8:*
2: geneseqn1980s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
C 1	100.0	21	2	AAT72382 Human Pap
C 2	100.0	21	2	AAT72381 Human Pap
C 3	100.0	21	2	AAT72384 Human Pap
C 4	100.0	21	2	AAT72383 Human Pap
C 5	100.0	21	2	AAN93015 Probe for
C 6	100.0	24	1	AAN91584 Probe 6 f
C 7	100.0	100	2	AAV39991 B6 oncoge
C 8	100.0	138	6	ABQ73533 HPV-PTM r
C 9	100.0	133	6	ABQ73531 HPV-PTM r
C 10	100.0	452	14	ADX26909 Human pap
C 11	100.0	456	2	ABQ76223 Human pap
C 12	100.0	459	1	ADG37149 459bp HPV
C 13	100.0	464	5	ADT17963 Human ova
C 14	100.0	464	5	ADL37114 Human ova
C 15	100.0	477	10	ADP09607 Human pap
C 16	100.0	477	10	AAU54430 B6 siRNA
C 17	100.0	477	10	AAU54445 HPV16 B6
C 18	100.0	477	14	ADX26908 Human pap

C 19	21	100.0	477	14	AEA5113 Human pap
C 20	21	100.0	519	2	AAT31834 Human pap
C 21	21	100.0	543	10	ADF31984 Human pap
C 22	21	100.0	570	2	AAQ75470 HPV16 B6/
C 23	21	100.0	598	5	ADL43498 Human ova
C 24	21	100.0	712	1	AAN91600 Partial n
C 25	21	100.0	743	5	ADL63123 Human ova
C 26	21	100.0	745	4	AAH72718 Human cer
C 27	21	100.0	747	12	ADQ44067 Nucleotid
C 28	21	100.0	747	12	ADQ44065 Nucleotid
C 29	21	100.0	747	12	ADQ44061 Nucleotid
C 30	21	100.0	747	12	ADQ44063 Nucleotid
C 31	21	100.0	747	12	ADQ44069 Nucleotid
C 32	21	100.0	747	12	ADQ44071 Nucleotid
C 33	21	100.0	768	13	ADR47004 Human pap
C 34	21	100.0	768	15	AEF40156 Human pap
C 35	21	100.0	776	2	AAT14663 HPV B6/7
C 36	21	100.0	779	2	AAK89756 Probe seq
C 37	21	100.0	790	2	AAQ29389 DNA encod
C 38	21	100.0	801	2	AAT18133 Human pap
C 39	21	100.0	822	2	AAK78792 HPV fusio
C 40	21	100.0	822	2	AAK29781 Prot.D1/3
C 41	21	100.0	822	14	AED52633 Fusion pr
C 42	21	100.0	879	2	AAK78795 HPV fusio
C 43	21	100.0	879	2	AAK29784 CLYTA-B6-
C 44	21	100.0	879	14	AED52641 Fusion pr
C 45	21	100.0	921	3	AAQ09477 Human pap
C 46	21	100.0	939	6	AAQ5101 Human pap
C 47	21	100.0	1000	2	AAQ08627 HPV-16 fr
C 48	21	100.0	1005	1	AAN91784 DNA probe
C 49	21	100.0	1116	2	AAK78793 HPV fusio
C 50	21	100.0	1116	2	AAK29782 Prot.D1/3
C 51	21	100.0	1116	14	AED52637 Fusion pr
C 52	21	100.0	1173	2	AAK78797 CLYTA-B6
C 53	21	100.0	1173	2	AAK29786 CLYTA-B6
C 54	21	100.0	1173	5	AED52645 Fusion pr
C 55	21	100.0	7840	14	AAFS5127 Nucleotid
C 56	21	100.0	7902	2	AAQ09847 Human pap
C 57	21	100.0	7904	2	AAT94724 Human pap
C 58	21	100.0	7904	2	AAT94723 Human pap
C 59	21	100.0	7904	2	AAK33881 HPV-16 ge
C 60	21	100.0	7904	2	AAV99946 Nucleotid
C 61	21	100.0	7904	2	AAV99952 Nucleotid
C 62	21	100.0	7904	8	ADAQ3127 HPV B6 se
C 63	21	100.0	7904	11	ADQ58335 Human pap
C 64	21	100.0	7904	14	ADZ45647 Human pap
C 65	21	95.2	20	2	AAQ10240 D99 prime
C 66	20	95.2	20	3	AAA56745 Human pap
C 67	20	95.2	20	6	ABK10263 Human pap
C 68	20	95.2	20	8	ABZ77461 PCR prime
C 69	20	95.2	20	10	ADP56472 Human pap
C 70	20	95.2	20	10	ACA62207 Human pap
C 71	20	95.2	20	12	ADQ42880 Primer of
C 72	20	95.2	20	15	AER63214 Human pap
C 73	20	95.2	21	10	ADQ36618 Human pap
C 74	20	95.2	21	10	ADQ36632 Human pap
C 75	19	90.5	19	6	AAU48278 Ribozyme
C 76	19	90.5	20	2	AAQ48549 Human pap
C 77	19	90.5	20	6	ABSS5744 HPV B6/7
C 78	19	90.5	20	9	ACF35816 HPV16 B6
C 79	19	90.5	20	14	ADX26911 RT-PCR pr
C 80	19	90.5	29	2	AAQ76065 HPV prime
C 81	18.4	87.6	20	2	AAQ10241 Anti-D99
C 82	18.4	87.6	115	6	ABQ73534 HPV-PTM r
C 83	18.4	87.6	2321	5	AAAS84294 DNA encod
C 84	18.4	87.6	2545	12	ADP26917 Human cad
C 85	18.4	87.6	2550	2	AAT85402 Human cad
C 86	18.4	87.6	2550	2	AAT85403 Human cad
C 87	18.4	87.6	2742	14	AEC83055 Breast ca
C 88	18.4	87.6	2929	10	ADG42064 Human CDH
C 89	18.4	87.6	3136	2	AAT85406 Rat full
C 90	18.4	87.6	3136	2	AAT61917 Full leng
C 91	18.4	87.6	192427	10	ADL13825 Osteoarth

92	18	85.7	51	2	AAQ75487	AAQ75487 HPV prlme	165	16.8	80.0	3569	4	AAK90472	AAK90472 Human dig
93	18	85.7	193	6	AAQ73532	AAQ73532 HPV-PTM r	166	16.8	80.0	4012	4	ABA07314	ABA07314 Human pan
94	17.8	84.8	766	4	AAH70910	AAH70910 Human cer	167	16.8	80.0	4012	4	ABA07315	ABA07315 Human pan
95	17.8	84.8	2617	12	ADG31274	ADG31274 Novel mou	168	16.8	80.0	4012	4	AAK90474	AAK90474 Human dig
96	17.8	84.8	127917	13	ADRS2731	ADRS2731 Drug ether	169	16.8	80.0	4012	4	AAK90473	AAK90473 Human dig
97	17.4	82.9	371	5	ABV61675	ABV61675 Human pro	170	16.8	80.0	5206	5	ABA21476	ABA21476 Human ner
98	17.4	82.9	83300	15	AERF07227	AERF07227 HMTLL3.1	171	16.8	80.0	6426	4	AAK90475	AAK90475 Human dig
99	17.4	81.0	157	2	AAV39992	AAV39992 B6 oncogene	172	16.8	80.0	6426	4	AAK90476	AAK90476 Human dig
100	17	81.0	4646	9	ADA36974	ADA36974 Prostegla	173	16.8	80.0	6427	8	AAK90477	AAK90477 Human dig
101	16.8	80.0	105	4	AAI15705	AAI15705 Human bre	174	16.8	80.0	6427	8	AAK90478	AAK90478 Human dig
102	16.8	80.0	300	12	ACH82514	ACH82514 Human gen	175	16.8	80.0	18653	4	AAK75859	AAK75859 Human tim
103	16.8	80.0	301	8	ABZ19422	ABZ19422 Group III	176	16.8	80.0	28564	10	ADDS5336	ADDS5336 Human gen
104	16.8	80.0	389	8	ABZ20067	ABZ20067 Group III	177	16.8	80.0	28564	10	ADA46681	ADA46681 Human gen
105	16.8	80.0	389	8	ABZ19388	ABZ19388 Group III	178	16.8	80.0	30781	6	AAQ67712	AAQ67712 Human DBH
106	16.8	80.0	392	6	ABV95494	ABV95494 Human pan	179	16.8	80.0	38653	12	ADH26544	ADH26544 Human hea
107	16.8	80.0	408	4	AAE31074	AAE31074 Human dia	180	16.4	78.1	247	4	AAQ08132	AAQ08132 Mammalian
108	16.8	80.0	415	3	AAK10714	AAK10714 Human bec	181	16.4	78.1	364	5	ABV08305	ABV08305 Human pro
109	16.8	80.0	432	8	ABZ19346	ABZ19346 Group III	182	16.4	78.1	379	10	ABT22525	ABT22525 Breast ca
110	16.8	80.0	458	11	ADL22559	ADL22559 Human dia	183	16.4	78.1	387	5	ADL72839	ADL72839 Human ova
111	16.8	80.0	499	6	AAQ02060	AAQ02060 DNA encod	184	16.4	78.1	387	5	ADL72839	ADL72839 Human ova
112	16.8	80.0	499	6	ABQ72465	ABQ72465 Human MDD	185	16.4	78.1	421	10	ABT22568	ABT22568 Breast ca
113	16.8	80.0	511	12	ACH77850	ACH77850 Human gen	186	16.4	78.1	431	3	AAQ0813	AAQ0813 Human sec
114	16.8	80.0	512	12	ACH68814	ACH68814 Human gen	187	16.4	78.1	435	5	ABV38213	ABV38213 Human pro
115	16.8	80.0	513	10	ADP58150	ADP58150 Human pol	188	16.4	78.1	462	5	ADL44362	ADL44362 Human ova
116	16.8	80.0	516	12	ACH72790	ACH72790 Human gen	189	16.4	78.1	472	5	ABV25330	ABV25330 Human pro
117	16.8	80.0	518	6	ABK62830	ABK62830 Human fce	190	16.4	78.1	472	5	ADL63473	ADL63473 Human ova
118	16.8	80.0	518	6	ABK11031	ABK11031 Human gen	191	16.4	78.1	481	13	ADV39831	ADV39831 Rat cardit
119	16.8	80.0	548	5	AAK45111	AAK45111 cDNA enco	192	16.4	78.1	587	12	AAK91932	AAK91932 Human CDN
120	16.8	80.0	570	4	AAK31073	AAK31073 Human dia	193	16.4	78.1	587	12	ADL28359	ADL28359 5' end of
121	16.8	80.0	579	4	ABK37238	ABK37238 Human liv	194	16.4	78.1	798	6	ABK35912	ABK35912 cDNA sequ
122	16.8	80.0	607	5	AAK88222	AAK88222 DNA encod	195	16.4	78.1	842	5	AAK93459	AAK93459 Human CDN
123	16.8	80.0	608	5	AAK85728	AAK85728 DNA encod	196	16.4	78.1	842	12	ADL29886	ADL29886 5' end of
124	16.8	80.0	609	11	ADL22558	ADL22558 Human dia	197	16.4	78.1	964	6	ABK71554	ABK71554 Human dit
125	16.8	80.0	657	4	AAH4439	AAH4439 Human alk	198	16.4	78.1	964	6	ABK6129	ABK6129 Human dit
126	16.8	80.0	676	4	AAK72650	AAK72650 DNA encod	199	16.4	78.1	990	6	ABZ11198	ABZ11198 Human pol
127	16.8	80.0	678	4	ABA08751	ABA08751 Human sec	200	16.4	78.1	990	12	ADM43716	ADM43716 Novel hum
128	16.8	80.0	678	10	ADDS9949	ADDS9949 Human con	201	16.4	78.1	1048	12	ADJ74318	ADJ74318 Rat CDN
129	16.8	80.0	694	4	AAK26254	AAK26254 Human CDN	202	16.4	78.1	1048	12	ADJ74318	ADJ74318 Rat CDN
130	16.8	80.0	694	8	AAK73595	AAK73595 Human nov	203	16.4	78.1	1076	6	ABK62587	ABK62587 Rat sequ
131	16.8	80.0	720	4	AAH05506	AAH05506 Human CDN	204	16.4	78.1	1076	10	ADBS6208	ADBS6208 Toxicity-
132	16.8	80.0	755	4	AAH05501	AAH05501 Human CDN	205	16.4	78.1	1076	10	ADBS6208	ADBS6208 Toxicity-
133	16.8	80.0	767	4	AAH08267	AAH08267 Human CDN	206	16.4	78.1	1076	10	ABT40843	ABT40843 Toxicity
134	16.8	80.0	798	5	AAK42498	AAK42498 Human CDN	207	16.4	78.1	1076	11	ADM21717	ADM21717 Rat hepat
135	16.8	80.0	798	5	AAK42498	AAK42498 Human CDN	208	16.4	78.1	1076	11	ADM21717	ADM21717 Rat hepat
136	16.8	80.0	985	11	ACN85682	ACN85682 Breast ca	209	16.4	78.1	1076	14	ADP71898	ADP71898 Renal tox
137	16.8	80.0	1030	11	ACN91368	ACN91368 Breast ca	210	16.4	78.1	1076	13	ADP61478	ADP61478 Rat Decr2
138	16.8	80.0	1075	6	ABQ72666	ABQ72666 Human MDD	211	16.4	78.1	1821	8	ACA28878	ACA28878 Prokaryot
139	16.8	80.0	1144	8	ABK71156	ABK71156 Novel hum	212	16.4	78.1	1863	10	ADBO7058	ADBO7058 Novel cod
140	16.8	80.0	1319	14	AAK19744	AAK19744 Novel hum	213	16.4	78.1	2476	4	AAK94905	AAK94905 Human ful
141	16.8	80.0	1486	10	ADD35904	ADD35904 Human hep	214	16.4	78.1	2476	12	ADJ32092	ADJ32092 Full leng
142	16.8	80.0	1526	13	ADK59703	ADK59703 Plant ful	215	16.4	78.1	2483	8	AAU51556	AAU51556 Human nuc
143	16.8	80.0	1536	12	ADQ83558	ADQ83558 Human tum	216	16.4	78.1	3513	12	ADJ33240	ADJ33240 Rabbit ca
144	16.8	80.0	1548	13	ADK63601	ADK63601 Plant ful	217	16.4	78.1	3555	12	ADJ33240	ADJ33240 Rabbit ca
145	16.8	80.0	1715	5	AAK92934	AAK92934 DNA encod	218	16.4	78.1	177587	11	ACN44806	ACN44806 Human gen
146	16.8	80.0	1905	4	AAH15913	AAH15913 Human CDN	219	16.4	78.1	177587	11	ACN44806	ACN44806 Human gen
147	16.8	80.0	2015	6	ABQ93385	ABQ93385 Human CDN	220	16.2	77.1	23	12	ADL13195	ADL13195 Human gen
148	16.8	80.0	2070	11	ADM02964	ADM02964 Human CDN	221	16.2	77.1	31	2	AAK33870	AAK33870 HPV-16 in
149	16.8	80.0	2070	14	AEC85894	AEC85894 Human CDN	222	16.2	77.1	31	2	AAK33870	AAK33870 HPV-16 in
150	16.8	80.0	2092	4	AAH15908	AAH15908 Human pat	223	16.2	77.1	352	13	ADK30001	ADK30001 Mouse gen
151	16.8	80.0	2097	5	AAH15908	AAH15908 Human CDN	224	16.2	77.1	354	3	AAK75748	AAK75748 Human ORF
152	16.8	80.0	2228	4	AAK81594	AAK81594 DNA encod	225	16.2	77.1	401	5	ABV56411	ABV56411 Human pro
153	16.8	80.0	2233	5	AAK51909	AAK51909 Human pol	226	16.2	77.1	447	12	ADQ44108	ADQ44108 Nucleotid
154	16.8	80.0	2313	5	AAK92935	AAK92935 DNA encod	227	16.2	77.1	450	10	ADQ44108	ADQ44108 Nucleotid
155	16.8	80.0	2313	5	AAK92935	AAK92935 DNA encod	228	16.2	77.1	451	10	ADQ44108	ADQ44108 Nucleotid
156	16.8	80.0	2454	13	AAK74278	AAK74278 DNA encod	229	16.2	77.1	536	14	ABK33430	ABK33430 Human DNA
157	16.8	80.0	2468	10	ADK63358	ADK63358 Human tum	230	16.2	77.1	546	14	ABK33430	ABK33430 Human DNA
158	16.8	80.0	2478	8	ABK34518	ABK34518 Human CDN	231	16.2	77.1	546	14	ABK33430	ABK33430 Human DNA
159	16.8	80.0	2484	5	AAK85729	AAK85729 Human mdd	232	16.2	77.1	601	14	ADV74085	ADV74085 Human DNA
160	16.8	80.0	2688	13	ADK97904	ADK97904 Protein f	233	16.2	77.1	667	4	AAK93177	AAK93177 Human sec
161	16.8	80.0	3113	13	ADK06779	ADK06779 Full leng	234	16.2	77.1	795	4	AAK93177	AAK93177 Human sec
162	16.8	80.0	3233	4	AAH18195	AAH18195 Human CDN	235	16.2	77.1	795	4	AAK93177	AAK93177 Human sec
163	16.8	80.0	3569	4	ABA07313	ABA07313 Human pan	236	16.2	77.1	795	12	ADL28144	ADL28144 5' end of
164	16.8	80.0	3569	4	ABA07313	ABA07313 Human pan	237	16.2	77.1	795	12	ADL30157	ADL30157 3' end of

238	16.2	77.1	930	2	AAK27361	Aax27361 Human sec	c 311	16.2	76.2	154799	13	AD836467	Ad836467 Human aut
239	16.2	77.1	930	2	AAK27446	Aax27446 Human sec	c 312	15.8	75.2	20	12	AD008483	Ad008483 Human pap
240	16.2	77.1	930	9	ADA07325	Ada07325 Human cDN	c 313	15.8	75.2	142	12	AA537808	Aa537808 Novel hum
241	16.2	77.1	930	9	ADA07240	Ada07240 Human cDN	c 314	15.8	75.2	355	5	ABV53573	ABV53573 Human pro
242	16.2	77.1	930	12	ADN41022	Adn41022 Novel hum	c 315	15.8	75.2	403	8	ABX62635	ABX62635 Arabidops
243	16.2	77.1	930	12	ADN40971	Adn40971 Novel hum	c 316	15.8	75.2	413	8	ABX639174	ABX639174 Bovine ES
244	16.2	77.1	1023	12	AAQ48575	Aaq48575 Hpv Be/77	c 317	15.8	75.2	439	4	AA115635	AA115635 Probe #55
245	16.2	77.1	1316	11	ACT29486	Act29486 Rice ablo	c 318	15.8	75.2	439	4	ABA57656	ABA57656 Human foe
246	16.2	77.1	1568	14	AEBD9640	Aebd9640 Human bre	c 319	15.8	75.2	439	4	AA137224	AA137224 Probe #59
247	16.2	77.1	1790	3	AA468172	Aa468172 Pinus rad	c 320	15.8	75.2	439	4	ABA27073	ABA27073 Probe #55
248	16.2	77.1	1790	3	ADDA1922	Addda1922 4-coumata	c 321	15.8	75.2	439	4	AAK31330	AAK31330 Human bon
249	16.2	77.1	1837	13	AD54854	Ad54854 Plant ful	c 322	15.8	75.2	439	4	AAK05712	AAK05712 Human bra
250	16.2	77.1	1839	4	AAAD05301	Adad05301 Human sec	c 323	15.8	75.2	439	4	AAK31010	AAK31010 Human liv
251	16.2	77.1	2149	13	ADT18449	Adt18449 Plant cDN	c 324	15.8	75.2	439	6	AB506082	AB506082 Human gen
252	16.2	77.1	2150	10	ADG84150	Adg84150 Human TMD	c 325	15.8	75.2	543	4	AA124860	AA124860 Probe #14
253	16.2	77.1	2447	10	ADA52985	Ada52985 Human cod	c 326	15.8	75.2	543	4	ABA70278	ABA70278 Human foe
254	16.2	77.1	2538	11	ADM02363	Adm02363 Human cDN	c 327	15.8	75.2	543	4	AA150413	AA150413 Probe #19
255	16.2	77.1	2538	11	AEC85313	Aec85313 Human cDN	c 328	15.8	75.2	543	4	ABA36990	ABA36990 Probe #15
256	16.2	77.1	2811	12	AD126182	Ad126182 Human cDN	c 329	15.8	75.2	543	4	AAK44419	AAK44419 Human bon
257	16.2	77.1	3043	10	AD858882	Ad858882 Toxicity-	c 330	15.8	75.2	543	4	AAK18506	AAK18506 Human bra
258	16.2	77.1	3043	13	ADR15097	Adr15097 Rat elec	c 331	15.8	75.2	543	4	AB544075	AB544075 Human liv
259	16.2	77.1	3043	14	AEC12533	Aec12533 Rat surto	c 332	15.8	75.2	543	6	AB518654	AB518654 Human gen
260	16.2	77.1	3034	14	AEC11889	Aec11889 Rat surto	c 333	15.8	75.2	664	10	ACD93097	ACD93097 Human col
261	16.2	77.1	3058	13	ADR08114	Adr08114 Full leng	c 334	15.8	75.2	688	2	AAV34216	AAV34216 Human sec
262	16.2	77.1	3174	11	ADM03469	Adm03469 Human cDN	c 335	15.8	75.2	688	8	ACD08087	ACD08087 cDNA enco
263	16.2	77.1	3174	14	AEC86399	Aec86399 Human cDN	c 336	15.8	75.2	688	14	AD212273	Ad212273 Human sec
264	16.2	77.1	3191	2	AAQ04092	Aaq04092 3.2 Kb Kp	c 337	15.8	75.2	737	8	AAV34270	AAV34270 Human sec
265	16.2	77.1	3633	12	ADM91299	Adm91299 DNA homol	c 338	15.8	75.2	737	8	ACD08141	ACD08141 cDNA enco
266	16.2	77.1	3693	12	ADM14003	Adm14003 Mouse cDN	c 339	15.8	75.2	737	16	AD212337	Ad212337 Human sec
267	16.2	77.1	4442	8	ADA41592	Ada41592 Human sec	c 340	15.8	75.2	747	6	AB214829	AB214829 Arabidops
268	16.2	77.1	4442	10	ADA574679	Ada574679 Human sec	c 341	15.8	75.2	747	8	ADA66608	ADA66608 Arabidops
269	16.2	77.1	4442	10	ADA57733	Ada57733 BAC fragm	c 342	15.8	75.2	747	10	AD015077	AD015077 Thale cre
270	16.2	77.1	4443	8	ADA41590	Ada41590 Human sec	c 343	15.8	75.2	747	14	ABE92380	ABE92380 Phenyl pr
271	16.2	77.1	4443	10	ADC74677	Adc74677 Human sec	c 344	15.8	75.2	747	15	AEF35110	AEF35110 A. thalia
272	16.2	77.1	4443	10	ADA57731	Ada57731 BAC fragm	c 345	15.8	75.2	747	10	AD016937	AD016937 DNA (Seqi
273	16.2	77.1	8605	4	AAK77438	Aak77438 Human imm	c 346	15.8	75.2	925	6	ABK65341	ABK65341 Arabidops
274	16.2	77.1	10445	4	AAK03692	Aa03692 Human rep	c 347	15.8	75.2	925	12	AD143630	Ad143630 Plant tra
275	16.2	77.1	11355	4	AAK77435	Aak77435 Human imm	c 348	15.8	75.2	925	12	AD003438	AD003438 Thalecres
276	16.2	77.1	20754	14	AEB04890	Aeb04890 Cancer-as	c 349	15.8	75.2	930	10	AAH31624	AAH31624 Human oif
277	16.2	77.1	25738	12	ADJ47541	Adj47541 Human H19	c 350	15.8	75.2	931	4	ADK59521	ADK59521 Plant DNA
278	16.2	77.1	31949	4	ABL05410	Ab05410 Human rep	c 351	15.8	75.2	933	5	AAF85190	AAF85190 Nucleotid
279	16.2	77.1	31949	4	ABL98269	Ab198269 Human tes	c 352	15.8	75.2	933	5	AAAD5128	AAAD5128 Human REM
280	16.2	77.1	32186	4	ABL05411	Ab105411 Human rep	c 353	15.8	75.2	942	4	AAH32136	Aah32136 Human oif
281	16.2	77.1	32186	4	ABL98270	Ab198270 Human tes	c 354	15.8	75.2	945	5	AA542394	AA542394 Human cDN
282	16.2	77.1	34917	4	AAK70686	Aak70686 Human imm	c 355	15.8	75.2	945	6	ABQ88414	ABQ88414 Human G P
283	16.2	77.1	38678	14	AEB32373	Aeb32373 Human gen	c 356	15.8	75.2	945	6	ABQ88387	ABQ88387 Human G P
284	16.2	77.1	38684	14	AEB32391	Aeb32391 Human gen	c 357	15.8	75.2	945	6	ABK68542	ABK68542 Human DNA
285	16.2	77.1	39353	14	AEB32370	Aeb32370 Human gen	c 358	15.8	75.2	945	6	ABK37680	ABK37680 DNA encod
286	16.2	77.1	40558	12	AD147542	Ad147542 Human H19	c 359	15.8	75.2	945	10	AD104310	AD104310 Human G-P
287	16.2	77.1	49375	12	AD112449	Ad112449 DNA fragm	c 360	15.8	75.2	945	10	AD104364	AD104364 Human G-P
288	16.2	77.1	58845	11	ACN43874	Actn43874 Human gen	c 361	15.8	75.2	952	6	ABK40103	ABK40103 cDNA enco
289	16.2	77.1	73930	11	ACN43877	Actn43877 Human can	c 362	15.8	75.2	956	6	ABK14221	ABK14221 A. thalia
290	16.2	77.1	74424	14	ADQ10962	Adq10962 Human STR	c 363	15.8	75.2	973	10	ABX17889	ABX17889 cDNA enco
291	16.2	77.1	88892	12	ADQ97695	Adq97695 Human can	c 364	15.8	75.2	987	4	AAH31710	Aah31710 Human oif
292	16.2	77.1	101685	12	ADQ17329	Adq17329 Human can	c 365	15.8	75.2	1008	6	ABZ43182	Abz43182 Human GPC
293	16.2	77.1	103375	11	ABD32761	Abd32761 Human can	c 366	15.8	75.2	1074	3	AAAC98014	AAAC98014 Human col
294	16.2	77.1	110000	11	ACN45090_1	Adcn45090 (2 of	c 367	15.8	75.2	1104	4	AAAC91343	AAAC91343 Human pol
295	16.2	77.1	114793	4	AAAD08215	Adad08215 Human gen	c 368	15.8	75.2	1172	10	ADC86270	ADC86270 Human GPC
296	16.2	77.1	114912	10	ADG65530	Adg65530 Human GPC	c 369	15.8	75.2	1331	14	AEC04453	Aec04453 Human bre
297	16.2	77.1	149111	14	AEBD9423	Aebd9423 Human bre	c 370	15.8	75.2	1331	15	AEE80007	Aee80007 Human ova
298	16.2	77.1	153752	12	ADQ97531	Adq97531 Human can	c 371	15.8	75.2	1333	10	AEC85948	Aec85948 Human GPC
299	16.2	77.1	153752	12	ADQ97531	Adq97531 Human can	c 372	15.8	75.2	1461	10	ADP25150	ADP25150 Fertility
300	16.2	77.1	157230	14	AED98424	Aed98424 Human bre	c 373	15.8	75.2	1461	12	ADN61185	ADN61185 Radish nu
301	16.2	77.1	160198	10	ADL13962	Adl13962 Osteoarth	c 374	15.8	75.2	1463	5	AAFP93752	AAFP93752 Human cDN
302	16.2	77.1	170508	14	AEDB9422	Aedb9422 Human bre	c 375	15.8	75.2	1483	14	ADY63014	ADY63014 Human clo
303	16.2	77.1	173115	14	AEDB9425	Aedb9425 Human bre	c 376	15.8	75.2	1498	3	AACT76022	AACT76022 Human ORF
304	16.2	77.1	215974	12	ADQ97523	Adq97523 Human can	c 377	15.8	75.2	1653	5	AAAS83168	AAAS83168 DNA encod
305	16.2	77.1	247461	13	ABD33153	Abd33153 Murine ca	c 378	15.8	75.2	1705	5	AAAS42292	AAAS42292 Bacterial
306	16.2	76.2	4133	5	ABAI5343	Abai5343 Human ner	c 379	15.8	75.2	1863	13	AD548498	AD548498 cDNA enco
307	16.2	76.2	10899	5	ABAI5344	Abai5344 Human ner	c 380	15.8	75.2	3377	5	AAAS45292	AAAS45292 cDNA enco
308	16.2	76.2	12758	5	ABAI5345	Abai5345 Human ner	c 381	15.8	75.2	3529	14	AEC04423	Aec04423 Human bre
309	16.2	76.2	13456	15	AEP92609	Aep92609 Human Cyt	c 382	15.8	75.2	3529	15	AER79977	Aer79977 Human ova
310	16.2	76.2	28420	4	AAK78286	Aak78286 Human imm	c 383	15.8	75.2	6883	4	AA136998	AA136998 Human mus

C 384	15.8	75.2	6883	8	ABX59986	Abx59986 cDNA enco	C 457	15.4	73.3	4217	6	ABT10142	Abt10142 Human bre
C 385	15.8	75.2	6883	12	ADJ30736	Adj30736 Human mmu	C 458	15.4	73.3	4217	10	ADD67641	Add67641 Human ly6
C 386	15.8	75.2	7918	12	ADM92537	Adm92537 Thalecres	C 459	15.4	73.3	4217	12	ADQ21677	Adq21677 Human scf
C 387	15.8	75.2	7918	15	AER35047	Aer35047 A. thaila	C 460	15.4	73.3	4217	13	ADR52732	Adr52732 Drug chr
C 388	15.8	75.2	7918	15	AER35011	Aer35011 A. thaila	C 461	15.4	73.3	4217	13	ADP90187	Adp90187 Human gen
C 389	15.8	75.2	8026	14	ABN01650	Abn01650 Rheusu mo	C 462	15.4	73.3	4217	13	ADT90082	Adt90082 Human gen
C 390	15.8	75.2	23654	14	ABL17664	Ab117664 Drosophi1	C 463	15.4	73.3	4217	13	ADT90220	Adt90220 Human gen
C 391	15.8	75.2	100998	14	ABD18472	Abd18472 Fibrinolyt	C 464	15.4	73.3	4484	5	AAI60755	Aai60755 Human gen
C 392	15.8	75.2	110000	6	ABA30521_08	Contribution (3 of	C 465	15.4	73.3	4492	3	AAI58969	Aai58969 Human ORF
C 393	15.8	75.2	110000	14	AER60206_04	Continuation (9 of	C 466	15.4	73.3	4492	3	AAI58969	Aai58969 Human ORF
C 394	15.8	75.2	110000	15	AER60206_04	Continuation (5 of	C 467	15.4	73.3	4494	5	ADQ09191	Adq09191 DNA enco
C 395	15.8	75.2	118067	12	ADP13110	Adp13110 Hypermeth	C 468	15.4	73.3	4494	5	ADB48951	Adb48951 Novel hum
C 396	15.8	75.2	118067	12	ADT37256	Adt37256 Hypermeth	C 469	15.4	73.3	4716	10	ACC72797	Acc72797 Human can
C 397	15.8	75.2	185371	6	ABT10718	Abt10718 Human bre	C 470	15.4	73.3	4716	12	ADQ28654	Adq28654 Human ten
C 398	15.8	75.2	189158	11	ACN44124	Acn44124 Mouse gen	C 471	15.4	73.3	4716	14	AEC83057	Aec83057 Breast ca
C 399	15.8	75.2	191284	12	ADQ97957	Adq97957 Mouse can	C 472	15.4	73.3	4724	2	AAT35514	Aat35514 Human res
C 400	15.8	75.2	347001	12	ADP43517	Adp43517 Human MAD	C 473	15.4	73.3	4724	2	AAT94725	Aat94725 Human res
C 401	15.4	73.3	21	13	AAP6636	Aap6636 Human gen	C 474	15.4	73.3	4724	2	AAT70489	Aat70489 Human res
C 402	15.4	73.3	25	13	ADR54240	Adr54240 Drug chr	C 475	15.4	73.3	5213	4	AAK52661	Aak52661 Human pol
C 403	15.4	73.3	65	6	ABN52695	Abn52695 Mouse spl	C 476	15.4	73.3	5213	4	AAK51677	Aak51677 Human pol
C 404	15.4	73.3	140	10	ADJ24647	Adj24647 Intestina	C 477	15.4	73.3	5385	12	ADQ25484	Adq25484 Human scf
C 405	15.4	73.3	294	10	AAI23701	Aai23701 Human bre	C 478	15.4	73.3	5646	4	ABL26452	Ab126452 Drosophi1
C 406	15.4	73.3	343	11	AAAC05123	Aaac05123 Human sec	C 479	15.4	73.3	5769	14	ABN01933	Abn01933 Human lun
C 407	15.4	73.3	352	11	ACN91927	Acn91927 Breast ca	C 480	15.4	73.3	6074	6	ABN95880	Abn95880 Gene #237
C 408	15.4	73.3	415	5	AAF64290	Aaf64290 Novel hum	C 481	15.4	73.3	6450	12	ADJ27244	Adj27244 Human TR1
C 409	15.4	73.3	425	5	AAF64289	Aaf64289 Novel hum	C 482	15.4	73.3	6450	12	ABN67779	Abn67779 Human rec
C 410	15.4	73.3	426	4	AAI14839	Aai14839 Human bre	C 483	15.4	73.3	6625	6	AAAD05595	Aad05595 Human sec
C 411	15.4	73.3	441	9	ACH14611	Ach14611 Human adu	C 484	15.4	73.3	6729	9	ADB91309	Adb91309 Human sec
C 412	15.4	73.3	486	4	ABA53519	Abas53519 Human foe	C 485	15.4	73.3	6729	10	ADA56398	Ada56398 Gene enco
C 413	15.4	73.3	486	4	ABA43104	Abas43104 Human bre	C 486	15.4	73.3	9589	6	ABA99282	Abas99282 Human ALD
C 414	15.4	73.3	486	4	AAK7247	Aak7247 Human bon	C 487	15.4	73.3	9589	6	ABA99369	Abas99369 Human ALD
C 415	15.4	73.3	486	4	AAK01790	Aak01790 Human bira	C 488	15.4	73.3	32191	4	AAK26704	Aak26704 Human gen
C 416	15.4	73.3	486	5	AAI01760	Aai01760 Probe #17	C 489	15.4	73.3	32191	8	ABX74053	Abx74053 Human nov
C 417	15.4	73.3	573	4	ABA60025	Abas60025 Human foe	C 490	15.4	73.3	43632	14	AER35213	Aer35213 Human Gef
C 418	15.4	73.3	573	4	AAI39899	Aai39899 Probe #85	C 491	15.4	73.3	49561	4	AAK82012	Aak82012 Human tim
C 419	15.4	73.3	573	4	ABA28423	Abas28423 Probe #68	C 492	15.4	73.3	50013	11	ACN44708	Acn44708 Mouse gen
C 420	15.4	73.3	573	4	AAK34177	Aak34177 Human bon	C 493	15.4	73.3	57759	14	ABC32873	Aec32873 Breast ca
C 421	15.4	73.3	573	4	AAK08299	Aak08299 Human bira	C 494	15.4	73.3	57759	14	AEC82540	Aec82540 Breast ca
C 422	15.4	73.3	573	4	ABX83972	Abas83972 Human liv	C 495	15.4	73.3	80423	13	ABD32546	Abd32546 Mouse can
C 423	15.4	73.3	573	6	ABX08934	Abso8934 Human gen	C 496	15.4	73.3	10856	2	ABD32933	Abd32933 Mouse can
C 424	15.4	73.3	573	13	ADU13377	Adu13377 Solid tum	C 497	15.4	73.3	110000	12	AAV21209_02	Contribution (3 of
C 425	15.4	73.3	589	14	ABCI2551	Aeci2551 Rat burro	C 498	15.4	73.3	110000	15	AER10213_0	Aer10213 Human pro
C 426	15.4	73.3	589	14	ABCI1961	Aeci1961 Rat burro	C 499	15.4	73.3	130480	10	AAF58833	Aaf58833 R. marinu
C 427	15.4	73.3	632	13	ADQ50862	Adq50862 Novel can	C 500	15.4	73.3	168276	11	ACN43942	Acn43942 Human gen
C 428	15.4	73.3	701	15	AER10170	Aer10170 Protein k	C 501	15.4	73.3	240102	13	ABD32546	Abd32546 Mouse can
C 429	15.4	73.3	812	8	ABX25084	Abx25084 Aepersgill	C 502	15.4	73.3	260160	12	ADQ20017	Adq20017 Human scf
C 430	15.4	73.3	868	6	ABK74047	Abk74047 Bacillus	C 503	15.4	73.3	330354	14	AER50508	Aer50508 Cancer-as
C 431	15.4	73.3	889	11	ACN84864	Acn84864 Breast ca	C 504	15.2	72.4	20	12	ADK95663	Adk95663 Primer of
C 432	15.4	73.3	952	6	AB199313	Ab199313 Mouse lsc	C 505	15.2	72.4	41	5	AAI65227	Aai65227 Human FDI
C 433	15.4	73.3	1084	6	ABK97640	Abk97640 Human pro	C 506	15.2	72.4	75	2	AAQ30886	Aaq30886 Prtmer 31
C 434	15.4	73.3	1221	3	AAAC40469	Aaac40469 Atrbidops	C 507	15.2	72.4	77	2	AAT88485	Aat88485 Secretory
C 435	15.4	73.3	1277	8	ACC62492	Acc62492 Human sec	C 508	15.2	72.4	156	6	ABN78655	Abn78655 Human str
C 436	15.4	73.3	1554	8	AAZ10643	Aaz10643 cDNA enco	C 509	15.2	72.4	275	4	AAAC91335	Aac91335 Human pol
C 437	15.4	73.3	1554	8	ADA39692	Ada39692 Human sec	C 510	15.2	72.4	277	2	AAV20339	Aav20339 Probe (24
C 438	15.4	73.3	1554	10	ADC73425	Adc73425 Human sec	C 511	15.2	72.4	292	6	AB184772	Ab184772 Human ova
C 439	15.4	73.3	1554	10	ADJ37550	Adj37550 Human sec	C 512	15.2	72.4	295	4	AAI13113	Aai13113 Human CDN
C 440	15.4	73.3	1554	10	ADA55883	Ada55883 Gene enco	C 513	15.2	72.4	318	5	AAH66073	Aah66073 C. glutam1
C 441	15.4	73.3	1645	6	AA62534	Aae62534 cDNA sequ	C 514	15.2	72.4	318	8	ACA00337	Aca00337 C. glutam1
C 442	15.4	73.3	1645	6	AA62534	Aae62534 cDNA sequ	C 515	15.2	72.4	358	2	AAV09788	Aav09788 DNA enco
C 443	15.4	73.3	1692	14	ABN01934	Abn01934 Human lun	C 516	15.2	72.4	358	2	AAQ30889	Aaq30889 Tisectr pm
C 444	15.4	73.3	1752	13	ADK14448	Adk14448 Plant ful	C 517	15.2	72.4	381	4	AAI12838	Aai12838 Probe #27
C 445	15.4	73.3	2315	6	AAAD32330	Aaad32330 Human lun	C 518	15.2	72.4	381	4	ABIA4541	Abia4541 Human foe
C 446	15.4	73.3	2896	6	AAAF3882	Aaf3882 Human CDN	C 519	15.2	72.4	381	4	AAI34194	Aai34194 Probe #28
C 447	15.4	73.3	2896	14	ADY63272	Ady63272 Human cto	C 520	15.2	72.4	381	4	ABIA4085	Abia4085 Human bre
C 448	15.4	73.3	2924	6	AB190347	Ab190347 Human sec	C 521	15.2	72.4	381	4	ABIA4323	Abia4323 Probe #27
C 449	15.4	73.3	2924	6	AB190347	Ab190347 Human pol	C 522	15.2	72.4	381	4	AAK28273	Aak28273 Human bon
C 450	15.4	73.3	2924	6	AB190347	Ab190347 Human sec	C 523	15.2	72.4	381	4	AAK02831	Aak02831 Human bira
C 451	15.4	73.3	2924	10	ADA56705	Ada56705 Gene enco	C 524	15.2	72.4	381	4	ABX27877	Abx27877 Human liv
C 452	15.4	73.3	3196	4	ABL26453	Ab126453 Drosophi1	C 525	15.2	72.4	381	5	AAI02756	Aai02756 Probe #27
C 453	15.4	73.3	3811	10	ABD59159	Abd59159 Toxicity-	C 526	15.2	72.4	381	6	ABX02787	Abx02787 Human gen
C 454	15.4	73.3	3811	13	ADVA1774	Adv1774 Rat cardit	C 527	15.2	72.4	401	10	ADK26743	Adk26743 Human l1d
C 455	15.4	73.3	3986	5	ABV28780	Abv28780 Human pro	C 528	15.2	72.4	401	6	ABN19379	Abn19379 Human ORF
C 456	15.4	73.3	3986	5	ABV22948	Abv22948 Human pro	C 529	15.2	72.4	421	4	ABK41640	Abk41640 cDNA enco

530	15.2	72.4	421	9	ADB59307	AdB59307	Connectiv	603	15.2	72.4	1813	13	ADX62476	Adx62476	Plant ful
531	15.2	72.4	461	2	AAO30905	AAQ30905	PMR1001	604	15.2	72.4	1892	13	ADX46997	Adx46997	Plant ful
532	15.2	72.4	468	9	ACH36668	ACH36668	Human end	605	15.2	72.4	1894	5	ABA82999	ABa82999	Human tra
533	15.2	72.4	478	13	ADR29677	Adr29677	Mouse gen	606	15.2	72.4	1924	12	ADJ41493	AdJ41493	Plant cdn
534	15.2	72.4	496	10	ADDI9536	AdDI9536	Oreochrom	607	15.2	72.4	1926	10	ABG80345	ABg80345	A. fumiga
535	15.2	72.4	504	10	ADBI1324	AdBI1324	Human dla	608	15.2	72.4	1975	5	AA887646	AAe87646	DNA encod
536	15.2	72.4	514	15	AE884233	Aee84233	Human EST	609	15.2	72.4	2000	12	ADJ40930	AdJ40930	Plant cdn
537	15.2	72.4	518	12	ACH78733	Ach78733	Human gen	610	15.2	72.4	2022	12	ADDO0488	AdDO0488	Novel hum
538	15.2	72.4	548	13	AAH51788	Aah51788	Chromosome	611	15.2	72.4	2032	12	ADN98919	Adn98919	Novel hum
539	15.2	72.4	548	14	AEE23112	Aee23112	Chromosome	612	15.2	72.4	2031	12	ADDO0464	AdDO0464	Novel hum
540	15.2	72.4	561	6	ABQ59250	Abq59250	Human col	613	15.2	72.4	2091	12	ADN98895	Adn98895	Novel hum
541	15.2	72.4	563	13	ACF84276	Acf84276	Human SIR	614	15.2	72.4	2092	10	ADBO7040	AdBO7040	Novel cod
542	15.2	72.4	577	4	AAI20339	AAi20339	Probe #10	615	15.2	72.4	2161	10	ADAS2739	AdAS2739	Human cod
543	15.2	72.4	577	4	ABA65377	ABa65377	Human foe	616	15.2	72.4	2186	12	ADOG3105	ADoG3105	Novel hum
544	15.2	72.4	577	4	AAI45544	AAI45544	Probe #14	617	15.2	72.4	2236	6	AAK52776	AAK52776	Human pol
545	15.2	72.4	577	4	ABA47487	ABa47487	Human bre	618	15.2	72.4	2232	6	AAD23604	AAAD23604	Human pro
546	15.2	72.4	577	4	ABA32475	ABa32475	Probe #10	619	15.2	72.4	2264	11	ADA16066	ADA16066	Secreted
547	15.2	72.4	577	4	AAK39529	AAK39529	Human bon	620	15.2	72.4	2277	10	ADA53743	ADA53743	Human cod
548	15.2	72.4	577	4	AAK13785	AAK13785	Human bra	621	15.2	72.4	2280	11	ADM03740	AdM03740	Human cdn
549	15.2	72.4	577	4	ABS39119	ABs39119	Human liv	622	15.2	72.4	2280	14	AEC86670	AeC86670	Human cdn
550	15.2	72.4	577	5	AAI06041	AAI06041	Probe #60	623	15.2	72.4	2316	4	AAH16219	AaH16219	Human cdn
551	15.2	72.4	577	6	ABS13619	ABs13619	Human gen	624	15.2	72.4	2317	13	ADQ83565	ADq83565	Human tum
552	15.2	72.4	584	10	ACA56220	ACa56220	Human s1g	625	15.2	72.4	2342	4	AAI60594	AAI60594	Human pol
553	15.2	72.4	584	12	ADIS6016	AdI66016	Human pol	626	15.2	72.4	2354	10	ACC62121	ACC62121	Human ali
554	15.2	72.4	587	12	ACH71121	Ach71121	Human gen	627	15.2	72.4	2354	12	ADH18021	ADh18021	Murine ap
555	15.2	72.4	605	4	AAH07232	AaH07232	Human cdn	628	15.2	72.4	2354	12	ADQ32562	ADQ32562	Human apo
556	15.2	72.4	616	2	AAH85742	AAH85742	Novel cdn	629	15.2	72.4	2354	15	AEP04511	AeP04511	Mouse apo
557	15.2	72.4	628	13	ADQ51949	AdQ51949	Novel can	630	15.2	72.4	2354	15	ABR12729	ABr12729	Mouse apo
558	15.2	72.4	671	8	ABZ36273	ABz36273	Human sec	631	15.2	72.4	2359	4	AAI58808	AAI58808	Human pol
559	15.2	72.4	687	5	AAA42780	AAa42780	Human sec	632	15.2	72.4	2359	5	ADQ99029	ADq99029	DNA encod
560	15.2	72.4	702	5	AA581106	AA581106	Human sec	633	15.2	72.4	2359	5	ADB48789	ADb48789	Novel hum
561	15.2	72.4	713	5	AA567277	AA567277	DNA encod	634	15.2	72.4	2376	13	ADH51635	ADH51635	Plant ful
562	15.2	72.4	721	4	AAI95208	AAI95208	Human neu	635	15.2	72.4	2416	4	AAI60592	AAI60592	Human pol
563	15.2	72.4	760	2	AAV84625	AAv84625	Human sec	636	15.2	72.4	2426	4	AAI58806	AAI58806	Human pol
564	15.2	72.4	760	2	ABA83286	ABa83286	Human sec	637	15.2	72.4	2426	5	ADQ99027	ADQ99027	DNA encod
565	15.2	72.4	760	9	ACH04916	ACH04916	Novel hum	638	15.2	72.4	2426	9	ADB48787	ADb48787	Novel hum
566	15.2	72.4	760	9	ACD44726	ACd44726	Human cdn	639	15.2	72.4	2433	10	ADB69898	ADb69898	C. neofor
567	15.2	72.4	792	4	AAH06456	AaH06456	Human cdn	640	15.2	72.4	2493	5	AAH66933	AAH66933	C. glutami
568	15.2	72.4	798	13	ADBS7143	ADBS7143	Bacterial	641	15.2	72.4	2508	11	ADM02890	AdM02890	Human cdn
569	15.2	72.4	874	4	AAH06905	AaH06905	Human cdn	642	15.2	72.4	2508	11	AEC85820	AeC85820	Human cdn
570	15.2	72.4	901	11	ADL22557	ADl22557	Human dla	643	15.2	72.4	2532	5	AA574327	AA574327	DNA encod
571	15.2	72.4	908	6	ABL99906	ABl99906	Human sec	644	15.2	72.4	2532	13	ADR07040	ADr07040	Full leng
572	15.2	72.4	923	6	ABL99793	ABl99793	Human sec	645	15.2	72.4	2537	4	AE895466	AE895466	Mouse NTK
573	15.2	72.4	963	6	ABN74248	ABn74248	Bovine em	646	15.2	72.4	2560	2	AAO30910	AAO30910	PMR1002
574	15.2	72.4	963	14	AE801515	AeE01515	Corynefor	647	15.2	72.4	2566	10	ADA53384	ADA53384	Human cod
575	15.2	72.4	977	10	ADBS9177	AdBS9177	Toxicity	648	15.2	72.4	2598	13	ADY41027	ADy41027	Rat cardl
576	15.2	72.4	977	10	ADBS3878	ADbs3878	Primary r	649	15.2	72.4	2616	14	AED71219	AED71219	Corynebac
577	15.2	72.4	981	6	ABN68346	ABn68346	Streptoco	650	15.2	72.4	2623	8	ACC74489	ACC74489	CaIdicell
578	15.2	72.4	984	13	ADV84695	ADv84695	Streptoco	651	15.2	72.4	2710	5	AA579139	AA579139	DNA encod
579	15.2	72.4	1011	3	ACA33028	ACa33028	Prokaryot	652	15.2	72.4	2714	8	ABX70934	ABx70934	Novel hum
580	15.2	72.4	1103	3	ACA36944	ACa36944	Arbidops	653	15.2	72.4	2718	12	ADDO0362	ADDO0362	Novel hum
581	15.2	72.4	1320	5	AA581556	AA581556	DNA encod	654	15.2	72.4	2718	12	ADN98793	ADn98793	Novel hum
582	15.2	72.4	1320	12	ADN98893	ADn98893	Novel hum	655	15.2	72.4	2718	12	ADN99082	ADn99082	Novel hum
583	15.2	72.4	1320	12	ADDO0463	ADDO0463	Novel hum	656	15.2	72.4	2718	12	ADDO0651	ADDO0651	Novel hum
584	15.2	72.4	1320	12	ADDO0462	ADDO0462	Novel hum	657	15.2	72.4	2732	4	AAH17926	AAH17926	Human cdn
585	15.2	72.4	1320	12	ADN98994	ADn98994	Novel hum	658	15.2	72.4	2770	8	ACC46353	ACC46353	Human dit
586	15.2	72.4	1377	9	ADA23670	AdA23670	DNA encod	659	15.2	72.4	2847	10	ADAS3169	ADAS3169	Human cod
587	15.2	72.4	1380	13	ADV87665	ADv87665	Streptoco	660	15.2	72.4	2869	13	ADR07356	ADr07356	Full leng
588	15.2	72.4	1380	13	ADV78918	ADv78918	Streptoco	661	15.2	72.4	2880	10	ACA56527	ACa56527	Human s1g
589	15.2	72.4	1386	5	AAI65222	AAI65222	Human FDI	662	15.2	72.4	2880	12	ADIS6323	ADIS6323	Human pol
590	15.2	72.4	1489	2	AAV19970	AAV19970	CNP trans	663	15.2	72.4	2997	9	ACC00144	ACC00144	Zinc flng
591	15.2	72.4	1512	6	AAAD3678	AAAD3678	Protein k	664	15.2	72.4	3006	6	AB573864	AB573864	Human cdn
592	15.2	72.4	1614	13	ADX54675	ADx54675	Plant ful	665	15.2	72.4	3011	5	ADL62267	ADL62267	Human ova
593	15.2	72.4	1615	5	ABV24966	ABv24966	Human pro	666	15.2	72.4	3059	12	ADL61123	ADL61123	Human tyr
594	15.2	72.4	1626	4	AAH18158	AAH18158	Human CDN	667	15.2	72.4	3059	12	ADNO5159	ADNO5159	AntipBori
595	15.2	72.4	1632	6	ABN81207	ABn81207	Human CYP	668	15.2	72.4	3059	14	ADY18214	ADY18214	DNA encod
596	15.2	72.4	1632	14	ADVA2935	ADvA2935	Human gen	669	15.2	72.4	3067	10	ADL02661	ADL02661	Human cod
597	15.2	72.4	1647	4	ABL12759	ABl12759	Drosophila	670	15.2	72.4	3088	6	ABV77934	ABv77934	Human CDN
598	15.2	72.4	1662	14	ABED71217	ABeD71217	Corynebaci	671	15.2	72.4	3250	6	ADH14797	ADh14797	Human brc
599	15.2	72.4	1675	6	ABA05891	ABa05891	Human per	672	15.2	72.4	3250	10	ADNO4316	ADNO4316	AntipBori
600	15.2	72.4	1712	11	ADY27183	ADy27183	Mouse inw	673	15.2	72.4	3250	13	ADP24081	ADp24081	PPO polyP
601	15.2	72.4	1770	9	AA58457	AA58457	Mouse per	674	15.2	72.4	3250	13	ADP24081	ADp24081	PPO polyP
602	15.2	72.4	1794	8	ADA72403	ADa72403	Rice gene	675	15.2	72.4	3250	14	AEC90337	AEC90337	Human cdn

676	15.2	72.4	3313	6	ABL60545	Ab160545 Human Kln	749	15.2	72.4	42979	4	ABL20870	Ab120870 Drosophila
677	15.2	72.4	3342	5	AAS92930	Aas92930 DNA encod	750	15.2	72.4	47115	9	ADA02627	Ada02627 Mouse Flt
678	15.2	72.4	3543	11	AAS72713	Aas72713 Novel hum	751	15.2	72.4	47115	10	ADB72365	Adb72365 Mouse Flt
679	15.2	72.4	3564	12	ADN05553	Adn05553 Antiprot	752	15.2	72.4	47115	10	ADB95875	Adb95875 Mouse Flt
680	15.2	72.4	3785	3	AAF18025	Aaf18025 Lung Canc	753	15.2	72.4	47493	9	ADA02549	Ada02549 Mouse Wnt
681	15.2	72.4	3807	4	AAH18340	Aah18340 Human CDN	754	15.2	72.4	47493	10	ADB72287	Adb72287 Mouse Wnt
682	15.2	72.4	3807	13	ADR6735	Adr6735 Human pro	755	15.2	72.4	47493	11	ADB95797	Adb95797 Mouse Wnt
683	15.2	72.4	3825	13	ADQ83562	Adq83562 Human tum	756	15.2	72.4	49152	11	ACN44278	Acn44278 Human gen
684	15.2	72.4	3946	12	ABL12758	Ab112758 Drosophi	757	15.2	72.4	55770	13	ADV16129	Adv16129 Xenothom
685	15.2	72.4	3946	14	AD044180	Ad044180 DNA encod	758	15.2	72.4	56192	14	AER04832	Aer04832 Cancer-as
686	15.2	72.4	4323	10	AD099821	Ad099821 Novel DNA	759	15.2	72.4	60430	11	ACN45002	Acn45002 Human gen
687	15.2	72.4	4355	11	ADR06957	Adr06957 Full leng	760	15.2	72.4	63079	14	ADB12509	Adb12509 Murine ca
688	15.2	72.4	4380	11	ACN92855	Acn92855 Breast ca	761	15.2	72.4	67093	13	ADB32671	Adb32671 Mouse can
689	15.2	72.4	4420	4	AAK52954	Aak52954 Human pol	762	15.2	72.4	70000	6	AA042934	Aa042934 Human pho
690	15.2	72.4	4482	6	ABL20566	Ab120566 Drosophi	763	15.2	72.4	73038	12	AD059401	Ad059401 Human can
691	15.2	72.4	5102	6	ABO79929	Abq79929 Human CYP	764	15.2	72.4	73038	14	ADP13670	Adp13670 Murine ca
692	15.2	72.4	5102	6	ABK35468	Abk35468 Human end	765	15.2	72.4	73100	12	ADP44145	Adp44145 Human TEK
693	15.2	72.4	5102	6	ABL62883	Ab162883 Breast ca	766	15.2	72.4	73725	9	ADA02650	Ada02650 Human FLI
694	15.2	72.4	5102	6	ABK64720	Abk64720 Human ben	767	15.2	72.4	73725	10	ADB72428	Adb72428 Human FLI
695	15.2	72.4	5102	6	AA139861	Aa139861 Human all	768	15.2	72.4	73725	10	ADB72428	Adb72428 Human FLI
696	15.2	72.4	5102	10	ADD14611	Add14611 Human arc	769	15.2	72.4	77777	12	ADQ94674	Adq94674 Human chr
697	15.2	72.4	5102	10	ACC46768	Acc46768 Human CDP	770	15.2	72.4	77777	12	ADQ94674	Adq94674 Human chr
698	15.2	72.4	5102	11	AD132100	Ad132100 Human CDN	771	15.2	72.4	83688	6	ABN85767	Abn85767 Arabidops
699	15.2	72.4	5102	13	AD52879	Ad52879 Drug Ther	772	15.2	72.4	90650	13	ADV35004	Adv35004 Murine CD
700	15.2	72.4	5102	13	AD884167	Ad884167 Human lym	773	15.2	72.4	92099	14	AD212547	Ad212547 Murine ca
701	15.2	72.4	5127	13	ADP25395	Adp25395 PRO polyP	774	15.2	72.4	93483	9	ADA03083	Ada03083 Mouse mCG
702	15.2	72.4	5128	6	ABV78036	Abv78036 Hypoxia-r	775	15.2	72.4	93483	9	ADA66367	Ada66367 Mouse mCG
703	15.2	72.4	5128	8	ABV77942	Abv77942 Hypoxia-r	776	15.2	72.4	93483	11	ADB72821	Adb72821 Mouse gen
704	15.2	72.4	5128	8	ACF34492	Acf34492 Gene enco	777	15.2	72.4	93483	10	ADB72761	Adb72761 Mouse gen
705	15.2	72.4	5128	8	ACC50124	Acc50124 Breast ca	778	15.2	72.4	100301	6	AB088176	Ab088176 Human ost
706	15.2	72.4	5128	12	ADN03862	Adn03862 Antiprot	779	15.2	72.4	100301	13	ADQ20754	Adq20754 Human col
707	15.2	72.4	5128	13	ADR24572	Adr24572 Breast ca	780	15.2	72.4	106544	13	ABQ32659	Abq32659 Human can
708	15.2	72.4	5128	13	ADP54343	Adp54343 Human PRO	781	15.2	72.4	110000	4	AAK95240_07	AAK95240_07
709	15.2	72.4	5128	14	ADY14786	Ady14786 DNA encod	782	15.2	72.4	110000	6	ABN71527_17	Abn71527_17
710	15.2	72.4	5128	14	ADY14788	Ady14788 DNA encod	783	15.2	72.4	110000	6	ABN71527_17	Abn71527_17
711	15.2	72.4	5128	15	AES84829	Aee84829 IMPDH mar	784	15.2	72.4	110000	6	ABT0010_07	Abt0010_07
712	15.2	72.4	5131	10	AD857797	Ad857797 Human gen	785	15.2	72.4	110000	6	ABT01503_07	Abt01503_07
713	15.2	72.4	5134	6	ABK88882	Abk88882 Human CYP	786	15.2	72.4	110000	11	ACN44582_2	Acn44582_2
714	15.2	72.4	5329	6	AAS94902	Aas94902 Human CYP	787	15.2	72.4	110000	11	ADW70291_07	Adw70291_07
715	15.2	72.4	5421	4	AAS30523	Aas30523 DNA encod	788	15.2	72.4	110000	12	ADH77486_07	Adh77486_07
716	15.2	72.4	5421	4	AAU06301	Aau06301 Human rep	789	15.2	72.4	110000	13	ADQ97138_3	Adq97138_3
717	15.2	72.4	5522	4	AAH73300	Aah73300 Human cer	790	15.2	72.4	110000	13	ABD32535_2	Abd32535_2
718	15.2	72.4	5801	10	ADC30426	Adc30426 Human nov	791	15.2	72.4	110000	14	ADV81204_19	Adv81204_19
719	15.2	72.4	5879	4	AAS41722	Aas41722 Genomic s	792	15.2	72.4	110000	14	AD213035_2	Ad213035_2
720	15.2	72.4	6236	4	AAS41724	Aas41724 Genomic s	793	15.2	72.4	110000	14	AED76257_7	Aed76257_7
721	15.2	72.4	6238	4	AAS41723	Aas41723 Genomic s	794	15.2	72.4	110000	14	AER04876_5	Aer04876_5
722	15.2	72.4	6336	4	AA161104	Aa161104 Human pol	795	15.2	72.4	110000	15	ABT10213_1	Abt10213_1
723	15.2	72.4	6336	12	ADM87468	Adm87468 Human EST	796	15.2	72.4	110218	11	ACN44744	Acn44744
724	15.2	72.4	6473	10	ADF74236	Adf74236 Human nov	797	15.2	72.4	110838	14	ADY97721	Ady97721
725	15.2	72.4	6491	13	ADQ84361	Adq84361 Human tum	798	15.2	72.4	120644	14	AD213239	Ad213239
726	15.2	72.4	6514	14	ADZ6768	Adz6768 Human sch	799	15.2	72.4	12656	13	ABD33616	Abd33616
727	15.2	72.4	6609	13	AD884509	Ad884509 Asepgy11	800	15.2	72.4	135800	11	ACN44446	Acn44446
728	15.2	72.4	7062	10	ADG17588	Adg17588 Human OTB	801	15.2	72.4	137000	12	ADH77370	Adh77370
729	15.2	72.4	7095	14	ABE17094	Abe17094 Alzhelmer	802	15.2	72.4	137000	15	AES96219	Aes96219 Human PTP
730	15.2	72.4	7260	14	ADY19187	Ady19187 DNA encod	803	15.2	72.4	143239	14	ADQ17729	Adq17729 Human gen
731	15.2	72.4	7291	14	ADZ36770	Adz36770 Human sch	804	15.2	72.4	145244	14	AEA62867	Aea62867 Rat glyco
732	15.2	72.4	7784	10	AD871190	Ad871190 Novel hum	805	15.2	72.4	151212	10	ADL13728	Adl13728 Osteoarth
733	15.2	72.4	7784	10	ADF74241	Adf74241 Human nov	806	15.2	72.4	152759	13	ABD33075	Abd33075 Human can
734	15.2	72.4	8115	5	ABA16258	Ab16258 Human ner	807	15.2	72.4	192639	10	ADL13676	Adl13676 Osteoarth
735	15.2	72.4	10254	6	ABN81206	Abn81206 Human CYP	808	15.2	72.4	201239	8	ACA64924	Ac64924 Human PLZ
736	15.2	72.4	12177	14	ADY14790	Ady14790 DNA encod	809	15.2	72.4	256493	11	ACN44514	Acn44514 Human gen
737	15.2	72.4	12988	8	AAK80680	Aak80680 Human imm	810	15.2	72.4	262090	12	ADQ59207	Adq59207 MSI-H car
738	15.2	72.4	12988	8	ABZ74054	Abz74054 Secreted	811	15.2	72.4	349980	5	AAH68530	Aah68530 C glutam1
739	15.2	72.4	13988	10	ADC20775	Adc20775 Novel hum	812	15.2	72.4	349980	5	AAH68530	Aah68530 C glutam1
740	15.2	72.4	13941	12	ADN00359	Adn00359 Novel hum	813	15.2	72.4	349980	5	AAH68530	Aah68530 C glutam1
741	15.2	72.4	15129	4	AAU03207	Aau03207 Human rep	814	15.2	72.4	349980	5	AAH68530	Aah68530 C glutam1
742	15.2	72.4	16132	9	AAV58467	Aav58467 Mouse per	815	15.2	72.4	349980	5	AAH68530	Aah68530 C glutam1
743	15.2	72.4	17112	8	ABV74561	Abv74561 Human per	816	15.2	72.4	349980	5	AAH68530	Aah68530 C glutam1
744	15.2	72.4	23064	9	ADA01479	Ada01479 Human per	817	15.2	72.4	349980	5	AAH68530	Aah68530 C glutam1
745	15.2	72.4	24174	14	AER04893	Aer04893 Cancer-as	818	15.2	72.4	349980	5	AAH68530	Aah68530 C glutam1
746	15.2	72.4	36383	11	ACN45196	Acn45196 Mouse gen	819	15.2	72.4	349980	5	AAH68530	Aah68530 C glutam1
747	15.2	72.4	40506	11	ACN44658	Acn44658 Human gen	820	15.2	72.4	349980	5	AAH68530	Aah68530 C glutam1
748	15.2	72.4	42881	5	AAF97868	Aaf97868 Human neu	821	15.2	72.4	349980	5	AAH68530	Aah68530 C glutam1

C 822	15	71.4	478	6	ABN73437	Adn73437 Bovine em	895	14.8	70.5	395	5	ABA12808	AbA12808 Human ner
C 823	15	71.4	510	6	ABN63326	AbN63326 Human can	896	14.8	70.5	403	6	ABL63187	AbL63187 Human pol
C 824	15	71.4	520	10	ADP57243	AdP57243 Toxicity-	897	14.8	70.5	403	6	ABL66135	AbL66135 Lung can
C 825	15	71.4	520	12	ADP72269	AdP72269 Renal tox	898	14.8	70.5	403	6	ABL64802	AbL64802 Lung can
C 826	15	71.4	563	6	ABK09688	AbK09688 Human ova	899	14.8	70.5	403	6	ABL65575	AbL65575 Lung can
C 827	15	71.4	581	4	AAI00907	AAI00907 Human rep	900	14.8	70.5	403	6	ACH18414	ACH18414 Human adu
C 828	15	71.4	791	3	AAC34648	AAC34648 Arabidops	901	14.8	70.5	411	13	ADO35686	ADG35686 Novel can
C 829	15	71.4	791	15	AEF29884	AEF29884 Lead Cere	902	14.8	70.5	419	4	AAK63296	AAK63296 Human imm
C 830	15	71.4	1217	15	ADX38731	AdX38731 Human can	903	14.8	70.5	425	3	AAC27730	AAC27730 Human sec
C 831	15	71.4	1495	14	AA889498	AA889498 DNA encod	904	14.8	70.5	441	8	ADA23046	ADA23046 Zee mayB
C 832	15	71.4	1496	3	AAC77297	AAC77297 Human ORF	905	14.8	70.5	444	6	AAD35160	AAD35160 Human Kid
C 833	15	71.4	1583	14	ADX38729	AdX38729 Human can	906	14.8	70.5	457	5	AA542486	AA542486 Human end
C 834	15	71.4	1941	4	AAI61209	AAI61209 Human pol	907	14.8	70.5	463	9	ACH34974	ACH34974 Human cdn
C 835	15	71.4	2130	5	AA572743	AA572743 DNA encod	908	14.8	70.5	473	4	AAH99869	AAH99869 Human pro
C 836	15	71.4	2218	5	AA584316	AA584316 DNA encod	909	14.8	70.5	473	12	ADM87613	ADM87613 Human EST
C 837	15	71.4	2795	10	ADB69537	ADB69537 C. neofor	910	14.8	70.5	478	3	AAC00809	AAC00809 Human sec
C 838	15	71.4	2955	14	ADX38715	AdX38715 Human can	911	14.8	70.5	482	14	ADM05992	ADM05992 Human gen
C 839	15	71.4	3006	6	AB573885	AB573885 Human can	912	14.8	70.5	486	6	ABK71633	ABK71633 Human dit
C 840	15	71.4	3231	6	ABK09769	ABK09769 Human ova	913	14.8	70.5	487	12	ADO17982	ADO17982 Human sof
C 841	15	71.4	3255	12	AD086192	AdG6192 Human tun	914	14.8	70.5	495	14	ACT61542	ACT61542 Human col
C 842	15	71.4	3255	13	AD087344	AdG67344 Human tun	915	14.8	70.5	521	4	AA531024	AA531024 Human dia
C 843	15	71.4	3255	13	ACN38853	ACN38853 Tumour-ab	916	14.8	70.5	521	6	ABQ72457	ABQ72457 Human MDD
C 844	15	71.4	3268	14	ADZ49475	ADZ49475 Insulin s	917	14.8	70.5	530	10	ADC32587	ADC32587 Human nov
C 845	15	71.4	3277	4	AAI60316	AAI60316 Human pol	918	14.8	70.5	546	3	AAA16461	AAA16461 Human col
C 846	15	71.4	3297	4	AAI58530	AAI58530 Human pol	919	14.8	70.5	557	3	AAA44330	AAA44330 Human sec
C 847	15	71.4	3297	5	ADQ98747	AdG98747 DNA encod	920	14.8	70.5	560	6	ABK35222	ABK35222 Human cdn
C 848	15	71.4	3297	9	ADB48507	AdB48507 Novel hum	921	14.8	70.5	583	4	AAK45599	AAK45599 Human imm
C 849	15	71.4	4795	10	ADB69176	AdB69176 C. neofor	922	14.8	70.5	589	4	ABA61039	ABA61039 Human foe
C 850	15	71.4	5055	4	AAK51999	AAK51999 Human pol	923	14.8	70.5	589	4	AAI40937	AAI40937 Probe #96
C 851	15	71.4	5181	4	AAI66941	AAI66941 SSD-conta	924	14.8	70.5	589	4	AAK35221	AAK35221 Human bon
C 852	15	71.4	5396	14	ADX25899	ADX25899 Novel cel	925	14.8	70.5	589	4	AAK09332	AAK09332 Human bra
C 853	15	71.4	6759	4	AB199920	AB199920 Rat mucoc	926	14.8	70.5	589	4	AB534967	AB534967 Human liv
C 854	15	71.4	6759	4	AAK6181	AAK6181 Human imm	927	14.8	70.5	589	6	AB509645	AB509645 Human gen
C 855	15	71.4	9060	10	AA050411	AA050411 Human Wil	928	14.8	70.5	591	11	ADY96259	ADY96259 Colon can
C 856	15	71.4	9183	4	AAI04447	AAI04447 Human rep	929	14.8	70.5	591	11	ADX42741	ADX42741 Human cdn
C 857	15	71.4	14346	4	AA532551	AA532551 Human gen	930	14.8	70.5	602	4	AAK57308	AAK57308 Human imm
C 858	15	71.4	16354	12	AD097798	AdG97798 Human can	931	14.8	70.5	626	8	AB218524	AB218524 Group III
C 859	15	71.4	26865	12	ADM67421	AdM67421 Prostate	932	14.8	70.5	629	12	ADK19690	ADK19690 Mouse cdn
C 860	15	71.4	73465	6	ABQ88161	AbQ88161 Human orb	933	14.8	70.5	629	12	AD035352	AD035352 Novel mou
C 861	15	71.4	86453	14	ADY25730	AdY25730 SULF rela	934	14.8	70.5	659	6	ABQ72466	ABQ72466 Human MDD
C 862	15	71.4	110000	14	AE842401_02	AE842401_02 Contamination (3 of	935	14.8	70.5	695	2	AAV88509	AAV88509 EST clone
C 863	15	71.4	110000	14	AED76254_00	AED76254 Mouse CA	936	14.8	70.5	717	10	ACC61063	ACC61063 Gene sequ
C 864	15	71.4	176594	13	ABD33387	ABD33387 Murine ca	937	14.8	70.5	717	10	ADK62837	ADK62837 Disease t
C 865	15	71.4	185555	11	ACMA5180	ACMA5180 Mouse gen	938	14.8	70.5	717	13	ADR47272	ADR47272 Bacterial
C 866	15	71.4	264965	12	ADN16203	AdN16203 Human sul	939	14.8	70.5	729	5	ABA11739	ABA11739 Human ner
C 867	15	71.4	268685	6	AB556563	AB556563 Human SUL	940	14.8	70.5	747	4	AAK70017	AAK70017 Human imm
C 868	14.8	70.5	60	6	ABN40915	ABN40915 Human spl	941	14.8	70.5	747	4	AAK70016	AAK70016 Human imm
C 869	14.8	70.5	80	10	ADD18158	Add18158 Human G-P	942	14.8	70.5	747	4	AAK70018	AAK70018 Human imm
C 870	14.8	70.5	100	8	ACD72996	AdC72996 E. coli K	943	14.8	70.5	750	8	ACA33940	ACA33940 Prokaryot
C 871	14.8	70.5	153	12	ADP93780	AdP93780 Cotton ex	944	14.8	70.5	750	12	AD583866	AD583866 Chemokine
C 872	14.8	70.5	167	5	AD169658	AdI69658 Human ova	945	14.8	70.5	788	4	AA550729	AA550729 Staphyloc
C 873	14.8	70.5	167	5	AD175995	AdI75995 Human ova	946	14.8	70.5	788	8	ACA18039	ACA18039 Prokaryot
C 874	14.8	70.5	213	4	AA548985	AA548985 Staphyloc	947	14.8	70.5	828	4	AAH06689	AAH06689 Human cdn
C 875	14.8	70.5	213	4	AA548889	AA548889 Staphyloc	948	14.8	70.5	854	4	AAAD13387	AAAD13387 Human sec
C 876	14.8	70.5	213	8	ACA16239	ACA16239 Prokaryot	949	14.8	70.5	877	4	AAH03789	AAH03789 Human cdn
C 877	14.8	70.5	213	8	ACA16146	ACA16146 Prokaryot	950	14.8	70.5	888	4	AAH72572	AAH72572 Human cer
C 878	14.8	70.5	252	14	ACS58164	ACS58164 Human col	951	14.8	70.5	924	8	ACA26792	ACA26792 Prokaryot
C 879	14.8	70.5	256	6	AA531061	AA531061 Human dia	952	14.8	70.5	925	5	ABA18327	ABA18327 Human ner
C 880	14.8	70.5	256	6	ABK71617	ABK71617 Human ova	953	14.8	70.5	926	12	ADN13728	ADN13728 Human pro
C 881	14.8	70.5	301	5	ADL41231	ADL41231 Human ova	954	14.8	70.5	927	7	AAH32077	AAH32077 Human oif
C 882	14.8	70.5	308	8	ACC46339	ACC46339 Human dit	955	14.8	70.5	930	6	AB243012	AB243012 Human GPC
C 883	14.8	70.5	333	8	AA549281	AA549281 Staphyloc	956	14.8	70.5	930	6	ABK68458	ABK68458 Human DNA
C 884	14.8	70.5	333	8	ACA16506	ACA16506 Prokaryot	957	14.8	70.5	935	6	ABL55954	ABL55954 Human G-P
C 885	14.8	70.5	334	6	ABN18866	ABN18866 Human ORF	958	14.8	70.5	945	10	ADD18115	ADD18115 Human G-P
C 886	14.8	70.5	338	4	CAAC00814	CAAC00814 Human sec	959	14.8	70.5	947	16	AD104360	AD104360 Human G-P
C 887	14.8	70.5	345	4	AAI01813	AAI01813 Human rep	960	14.8	70.5	950	6	AB558764	AB558764 Human G-P
C 888	14.8	70.5	345	4	ABL97126	ABL97126 Human tes	961	14.8	70.5	960	6	AAH32023	AAH32023 Human oif
C 889	14.8	70.5	351	9	ADH12007	ADH12007 Altiococ	962	14.8	70.5	960	3	AB212543	AB212543 Arabidops
C 890	14.8	70.5	352	4	AAK60950	AAK60950 Human imm	963	14.8	70.5	960	3	ABA43321	ABA43321 Arabidops
C 891	14.8	70.5	370	3	AAAC00812	AAAC00812 Human sec	964	14.8	70.5	990	6	ADA68004	ADA68004 Arabidops
C 892	14.8	70.5	377	5	AAAF65535	AAAF65535 Novel hum	965	14.8	70.5	1006	6	AB558800	AB558800 Human G-P
C 893	14.8	70.5	382	3	AAAC57081	AAAC57081 Pinus rad	966	14.8	70.5	1017	5	AA542311	AA542311 Human cdn
C 894	14.8	70.5	386	4	AAI92225	AAI92225 Human pol	967	14.8	70.5	1017	5	AA542311	AA542311 Human cdn

C 968	14.8	70.5	101.7	6	ABK37597	Abk37597 DNA encod
C 969	14.8	70.5	101.7	14	ADY72224	Ady72224 Human BMY
C 970	14.8	70.5	101.7	14	ADY72223	Ady72223 Human BMY
C 971	14.8	70.5	1021	10	ADC86548	Adc86548 Human GPC
C 972	14.8	70.5	1039	13	ACN39428	Acn39428 Tumour-48
C 973	14.8	70.5	1120	10	ADG08782	Adg08782 Novel DNA
C 974	14.8	70.5	1131	5	ADP03820	Adp03820 Bacterial
C 975	14.8	70.5	1149	5	AA885492	Aa885492 DNA encod
C 976	14.8	70.5	1188	2	AAZ52916	Aaz52916 Human pro
C 977	14.8	70.5	1210	5	ADL62148	Adl62148 Human ova
C 978	14.8	70.5	1246	6	ABR89741	Abi89741 Human pol
C 979	14.8	70.5	1247	6	ABK71649	Abk71649 Human dlc
C 980	14.8	70.5	1261	6	ABBS1788	Abbs1788 Human mtd
C 981	14.8	70.5	1266	10	ADC90749	Adc90749 E. faeciu
C 982	14.8	70.5	1271	3	AAc45355	Aac45355 Arabidops
C 983	14.8	70.5	1330	10	ADC85574	Adc85574 Human GPC
C 984	14.8	70.5	1338	3	AAC34830	Aac34830 Arabidops
C 985	14.8	70.5	1360	12	AD116270	Ad116270 Human nuc
C 986	14.8	70.5	1374	13	ADX30111	Adx30111 Plant ful
C 987	14.8	70.5	1379	13	ADX30109	Adx30109 Plant ful
C 988	14.8	70.5	1458	12	ADP10589	Adp10589 Reference
C 989	14.8	70.5	1461	10	ADBS96111	Adbs96111 Human uri
C 990	14.8	70.5	1461	10	ADK15020	Adk15020 Urinary s
C 991	14.8	70.5	1500	13	ADU05459	Adu05459 DNA encod
C 992	14.8	70.5	1512	12	ADM87151	Adm87151 Human pro
C 993	14.8	70.5	1520	6	ABK36130	Abk36130 CDNA sequ
C 994	14.8	70.5	1545	13	ADK45523	Adk45523 Human exc
C 995	14.8	70.5	1559	4	AAI99074	Aai99074 Human exc
C 996	14.8	70.5	1559	5	AAI63424	Aai63424 Human kid
C 997	14.8	70.5	1611	6	ABQ54790	Abq54790 Human ova
C 998	14.8	70.5	1626	8	ADA06097	Ada06097 Human fat
C 999	14.8	70.5	1632	4	AAH15344	Aah15344 Human CDN
C 1000	14.8	70.5	1664	13	ADR26077	Adr26077 Breast ca

ALIGNMENTS

```

RESULT 1
ID AAT72382/c
AC AAT72382;
AT 09-FEB-1998 (first entry)
DE Human Papillomavirus Type 16 target region.
XX
XX Human Papillomavirus; probe; target region; genital cancer; HPV;
XX cervical smear; ss.
XX
XX Human papillomavirus.
XX
XX BP774518-A2.
XX
XX 21-MAY-1997.
XX
XX 15-NOV-1996; 96EP-00308264.
XX
XX 15-NOV-1995; 95US-0006854P.
XX
XX (GENP-) GEN-PROBE INC.
XX
XX Gordon P, Brentano ST, Carter NM, Hammond PW;
XX
XX WPI; 1997-274349/25.
XX
XX Probes for detection of Human Papillomavirus Type 16 and Type 18 - can
XX distinguish between Type 16 and 18, associated with genital cancers.
XX
XX Claim 8; Page 52; 70pp; English.
XX
XX Novel hybridisation assay probes have been developed comprising an

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CC oligonucleotide which will hybridise under selected conditions to Human
CC Papillomavirus (HPV) Type 16 and/or 18 (but not Types 6, 11, 31, 33, 35,
CC 39, 45, 51, 52, or 58) target nucleic acids to form detectable target;
CC probe duplex. The present sequence represents a specifically claimed
CC target region. Oligonucleotides are useful to detect HPV Type 16 and/or
CC 18 in samples e.g. cervical smears, body fluid, and distinguish these
CC from other HPV variants. Papillomaviruses are small DNA viruses and HPV
CC Types 16 and 18 are associated with genital cancers. HPV PCR primers can
CC amplify HPV Type 16 and/or 18 nucleic acid in a sample. HPV Type 16
CC and/or 18 can be detected by adding a probe and detecting probe:target
CC duplex formation; target nucleic acid is optionally amplified. Type 16 or
CC 18 can be specifically detected by amplifying nucleic acids with at least
CC one specifically claimed PCR primer. For Type 18 detection, a helper
CC probe may be used. Oligonucleotides can distinguish target sequences from
CC phylogenetically close HPV Types 16 and 18 whilst available detection
CC sera react with antigens of all papillomaviruses
CC
SQ Sequence 21 BP; 5 A; 6 C; 5 G; 5 T; 0 U; 0 Other;
Query Match 100.0%; Score 21; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CAGGACACAGTGGCTTTGAC 21
Db 21 CAGGACACAGTGGCTTTGAC 1
RESULT 2
AAT72381
ID AAT72381 standard; DNA; 21 BP.
AC AAT72381;
AT 09-FEB-1998 (first entry)
DE Human Papillomavirus Type 16 target region.
XX
XX Human Papillomavirus; probe; target region; genital cancer; HPV;
XX cervical smear; ss.
XX
XX Human papillomavirus.
XX
XX BP774518-A2.
XX
XX 21-MAY-1997.
XX
XX 15-NOV-1996; 96EP-00308264.
XX
XX 15-NOV-1995; 95US-0006854P.
XX
XX (GENP-) GEN-PROBE INC.
XX
XX Gordon P, Brentano ST, Carter NM, Hammond PW;
XX
XX WPI; 1997-274349/25.
XX
XX Probes for detection of Human Papillomavirus Type 16 and Type 18 - can
XX distinguish between Type 16 and 18, associated with genital cancers.
XX
XX Claim 8; Page 52; 70pp; English.
XX
XX Novel hybridisation assay probes have been developed comprising an
CC oligonucleotide which will hybridise under selected conditions to Human
CC Papillomavirus (HPV) Type 16 and/or 18 (but not Types 6, 11, 31, 33, 35,
CC 39, 45, 51, 52, or 58) target nucleic acids to form detectable target;
CC probe duplex. The present sequence represents a specifically claimed
CC target region. Oligonucleotides are useful to detect HPV Type 16 and/or
CC 18 in samples e.g. cervical smears, body fluid, and distinguish these
CC from other HPV variants. Papillomaviruses are small DNA viruses and HPV
CC Types 16 and 18 are associated with genital cancers. HPV PCR primers can
CC amplify HPV Type 16 and/or 18 nucleic acid in a sample. HPV Type 16
CC and/or 18 can be detected by adding a probe and detecting probe:target

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CC duplex formation; target nucleic acid is optionally amplified. Type 16 or
 CC 18 can be specifically detected by amplifying nucleic acids with at least
 CC one specifically claimed PCR primer. For Type 18 detection, a helper
 CC probe may be used. Oligonucleotides can distinguish target sequences from
 CC phylogenetically close HPV Types 16 and 18 whilst available detection
 CC sera react with antigens of all papillomaviruses

XX Sequence 21 BP; 5 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGGACACAGTGGCTTTGAC 21
 1 CAGGACACAGTGGCTTTGAC 21
 Db 1 CAGGACACAGTGGCTTTGAC 21

RESULT 3

AAT72384/C
 ID AAT72384 standard; RNA; 21 BP.

XX AAT72384;

AC 09-FEB-1998 (first entry)

XX Human Papillomavirus Type 16 target region.

XX Human Papillomavirus; probe; target region; genital cancer; HPV;

KW cervical smear; ss.

XX Human papillomavirus.

OS EP774518-A2.

XX 21-MAY-1997.

XX 15-NOV-1996; 96BP-00308264.

XX 15-NOV-1995; 95US-0006854P.

XX (GENP-) GEN-PROBE INC.

PI Gordon P, Brentano ST, Carter NM, Hammond PW;

XX WPI; 1997-274349/25.

XX Probes for detection of Human Papillomavirus Type 16 and Type 18 - can
 PT distinguish between Type 16 and 18, associated with genital cancers.

XX Claim 8; Page 53; 70pp; English.

XX Novel hybridisation assay probes have been developed comprising an
 CC oligonucleotide which will hybridise under selected conditions to Human
 CC Papillomavirus (HPV) Type 16 and/or 18 (but not Types 6, 11, 31, 33, 35,
 CC 39, 45, 51, 52, or 58) target nucleic acids to form detectable target:
 CC probe duplex. The present sequence represents a specifically claimed
 CC target region. Oligonucleotides are useful to detect HPV Type 16 and/or
 CC 18 in samples e.g. cervical smears, body fluid, and distinguish these
 CC from other HPV variants. Papillomaviruses are small DNA viruses and HPV
 CC Types 16 and 18 are associated with genital cancers. HPV PCR primers can
 CC amplify HPV Type 16 and/or 18 nucleic acid in a sample. HPV Type 16
 CC and/or 18 can be detected by adding a probe and detecting probe:target
 CC duplex formation; target nucleic acid is optionally amplified. Type 16 or
 CC 18 can be specifically detected by amplifying nucleic acids with at least
 CC one specifically claimed PCR primer. For Type 18 detection, a helper
 CC probe may be used. Oligonucleotides can distinguish target sequences from
 CC phylogenetically close HPV Types 16 and 18 whilst available detection
 CC sera react with antigens of all papillomaviruses

XX Sequence 21 BP; 5 A; 6 C; 5 G; 0 T; 5 U; 0 Other;

Query Match 100.0%; Score 21; DB 2; Length 21;

Best Local Similarity 100.0%; Pred. No. 1;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGGACACAGTGGCTTTGAC 21
 1 CAGGACACAGTGGCTTTGAC 21
 Db 21 CAGGACACAGTGGCTTTGAC 1

RESULT 4

AAT72383
 ID AAT72383 standard; RNA; 21 BP.

XX AAT72383;

AC 09-FEB-1998 (first entry)

XX Human Papillomavirus Type 16 target region.

XX Human Papillomavirus; probe; target region; genital cancer; HPV;

KW cervical smear; ss.

XX Human papillomavirus.

OS EP774518-A2.

XX 21-MAY-1997.

XX 15-NOV-1996; 96BP-00308264.

XX 15-NOV-1995; 95US-0006854P.

XX (GENP-) GEN-PROBE INC.

PI Gordon P, Brentano ST, Carter NM, Hammond PW;

XX WPI; 1997-274349/25.

XX Probes for detection of Human Papillomavirus Type 16 and Type 18 - can
 PT distinguish between Type 16 and 18, associated with genital cancers.

XX Claim 8; Page 53; 70pp; English.

XX Novel hybridisation assay probes have been developed comprising an
 CC oligonucleotide which will hybridise under selected conditions to Human
 CC Papillomavirus (HPV) Type 16 and/or 18 (but not Types 6, 11, 31, 33, 35,
 CC 39, 45, 51, 52, or 58) target nucleic acids to form detectable target:
 CC probe duplex. The present sequence represents a specifically claimed
 CC target region. Oligonucleotides are useful to detect HPV Type 16 and/or
 CC 18 in samples e.g. cervical smears, body fluid, and distinguish these
 CC from other HPV variants. Papillomaviruses are small DNA viruses and HPV
 CC Types 16 and 18 are associated with genital cancers. HPV PCR primers can
 CC amplify HPV Type 16 and/or 18 nucleic acid in a sample. HPV Type 16
 CC and/or 18 can be detected by adding a probe and detecting probe:target
 CC duplex formation; target nucleic acid is optionally amplified. Type 16 or
 CC 18 can be specifically detected by amplifying nucleic acids with at least
 CC one specifically claimed PCR primer. For Type 18 detection, a helper
 CC probe may be used. Oligonucleotides can distinguish target sequences from
 CC phylogenetically close HPV Types 16 and 18 whilst available detection
 CC sera react with antigens of all papillomaviruses

XX Sequence 21 BP; 5 A; 5 C; 6 G; 0 T; 5 U; 0 Other;

Query Match 100.0%; Score 21; DB 2; Length 21;
 Best Local Similarity 76.2%; Pred. No. 1;
 Matches 16; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGGACACAGTGGCTTTGAC 21
 1 CAGGACACAGTGGCTTTGAC 21
 Db 1 CAGGACACAGTGGCTTTGAC 21

RESULT 5

AAN93015

ID AAN93015 standard; DNA; 24 BP.
 AC AAN93015;
 XX
 XX
 DT 31-OCT-2002 (revised)
 DT 13-FEB-1990 (first entry)
 XX
 XX Probe for detecting human papillomavirus.
 KM Human papillomavirus; polynucleotide probe.
 XX
 OS Human papillomavirus.
 XX
 XX WO8905357-A.
 PN
 XX 15-JUN-1989.
 PD
 XX
 XX 06-DEC-1988; 88WO-US004355.
 PF
 XX
 XX 09-DEC-1987; 87US-00130709.
 PR
 XX (MICR-) MICROPROBE CORP.
 PA
 XX Schwartz DE;
 PI
 XX WPI; 1989-192703/26.
 DR
 XX
 XX Vol. exclusion agents for enhancing in situ hybridisation - used for in
 PT situ determ. of poly-nucleotide targets in cells by fixing cells to
 PT inert transparent solid support and hybridising, etc.
 XX
 PS Disclosure; Page 22; 28pp; English.
 XX
 XX The probe is complementary to Human Papillomavirus (HPV) mRNA. It detects
 CC bases 420-444 in gene E6 of HPV type 16. See also AAN93011-N93031.
 CC (Updated on 31-OCT-2002 to add missing OS field.)
 CC
 XX
 SQ Sequence 24 BP; 5 A; 6 C; 6 G; 7 T; 0 U; 0 Other;
 XX
 Query Match 100.0%; Score 21; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAGGACACAGTGGCTTTGAC 21
 Db 4 CAGGACACAGTGGCTTTGAC 24
 DB
 RESULT 6
 AAN91584
 ID AAN91584 standard; DNA; 24 BP.
 XX
 XX AAN91584;
 AC
 XX 27-AUG-2003 (revised)
 DT 17-JUL-1990 (first entry)
 XX
 XX Probe 6 for the detection of human papilloma virus (HPV) type 16 in in
 DE situ hybridisation assay.
 XX
 KM Human papilloma virus; type 16; in situ hybridisation assay;
 KM cellular smear; probe 6; benign wart; cervical cancer.
 XX
 OS Human papillomavirus.
 XX
 XX WO8902934-A.
 PN
 XX 06-APR-1989.
 PD
 XX 30-SEP-1988; 88WO-US003367.
 PF
 XX 02-OCT-1987; 87US-00103979.
 PR
 XX

PA (MICR-) MICROPROBE CORP.
 XX
 XX Schwartz DE; Adams TH;
 PI
 XX WPI; 1989-114406/15.
 DR
 XX
 XX Hybridisation test for human papilloma virus in cell smears - by reaction
 PT with long labelled probe specific for particular virus types, esp. for
 PT examining cervical smears.
 XX
 XX Disclosure; Page 19; 39pp; English.
 PS
 XX The patent is for a rapid in situ hybridisation assay for detecting and
 CC typing human papilloma virus (HPV) in non-frozen cellular smears fixed to
 CC a support in absence of aldehyde-based crosslinking reagents. The assay
 CC comprises: (1) combining nucleic acid in the sample with at least one
 CC detectable probe able to hybridise with 1 or more HPV types; and (2)
 CC detecting presence or absence of hybrid complexes. Opt. several probes
 CC are used, eg one for HPV types 6 and 11, associated with benign warts,
 CC and one for types 16, 18, 31, 33 and 35, associated with cervical cancer.
 CC The assay can differentiate between HPV types. It is esp. used as a
 CC secondary test. The probes can be synthesised or cloned. (Updated on 27-
 CC AUG-2003 to correct OS field.)
 CC
 SQ Sequence 24 BP; 5 A; 6 C; 6 G; 7 T; 0 U; 0 Other;
 XX
 Query Match 100.0%; Score 21; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAGGACACAGTGGCTTTGAC 21
 Db 4 CAGGACACAGTGGCTTTGAC 24
 DB
 RESULT 7
 AAV3991
 ID AAV3991 standard; DNA; 100 BP.
 XX
 XX AAV3991;
 AC
 XX 08-OCT-1998 (first entry)
 DT
 XX E6 oncogene from HPV 16 target sequence.
 DE
 XX Human papillomavirus; target; probe; detection; hybridisation;
 KM looped nucleic acid; diagnosis; pathogen; ss.
 KM
 OS Human papillomavirus.
 OS Synthetic.
 OS
 PN WO827225-A1.
 PD
 XX 25-JUN-1998.
 PF
 XX 16-DEC-1997; 97WO-GB003449.
 PR
 XX 16-DEC-1996; 96GB-00026074.
 PA (CYTO-) CYTOCELL LTD.
 XX
 XX Cardy DUN;
 PI
 XX WPI; 1998-362792/31.
 DR
 XX Detecting target nucleic acid by hybridisation with probe that generates
 PT looped-out region - then using second probe, hybridised to this region,
 PT to initiate nucleic acid synthesis, for disease diagnosis, detecting
 PT pathogens etc.
 XX
 XX Example 4; Page 19; 48pp; English.
 PS
 CC A method has been developed for detecting a target nucleic acid in a

CC sample by: (a) hybridising the target with a first probe (P1) having 3' and 5' portions complementary to adjacent regions of the target, with an intervening, non-complementary portion so that the resulting CC hybridisation complex includes a looped-out region in which non-contiguous regions of P1 are brought close together; (b) hybridising CC second probe (P2) to these non-contiguous regions; (c) initiating nucleic acid synthesis, dependent on hybridisation of P2 to P1, and (d) detecting CC newly formed nucleic acid. In a modification, the looped-out region is formed from the target rather than P1, and then P2 hybridises to non-contiguous regions of the target. The present sequence represents a target sequence used in an example from the present invention. The method is used for diagnosis of infectious disease or chromosomal abnormalities; for detecting *Salmonella* in foods or *Escherichia coli* in water. The CC method does not require making copies of the target or long traces of CC sequence; is applicable to DNA or RNA (including those without discrete ends); involves at least 2 hybridisation events to generate a signal (for improved specificity) and the hybridised probe may be detected without additional processing

SQ Sequence 100 BP; 20 A; 25 C; 18 G; 37 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CAGGACACAGTGGCTTTGAC 21
71 CAGGACACAGTGGCTTTGAC 91

Db

RESULT 8
ABQ73533
ID ABQ73533 standard; DNA; 138 BP.

XX
AC ABQ73533;
DT 02-OCT-2002 (first entry)
XX
XX HPV-PTM related oligonucleotide #5.

DE
XX Pre-trans-acting molecule; PTM; spliceosome; cytosolic; gene therapy;
KW immunosuppressive; antimicrobial; gene regulation; gene repair; cancer;
KW targeted cell death; genetic disorder; infectious disorder;
KW autoimmune disease; proliferative disorder; PCR primer; ss.
XX
OS Human papillomavirus.
OS Synthetic.
XX
PN WO200253581-A2.
XX
PD 11-JUL-2002.
XX
PF 08-JAN-2002; 2002WO-US000416.
XX
PR 08-JAN-2001; 2001US-00756095.
PR 08-JAN-2001; 2001US-00756096.
PR 08-JAN-2001; 2001US-00756097.
PR 20-APR-2001; 2001US-00838858.
PR 29-AUG-2001; 2001US-00941492.
XX
XX (INTR-) INTRON INC.
PA Mitchell LG, Garcia-Blanco MA, Baker CC, Puttaraju M,
PI Mansfield GS, Chao H;
XX
XX WPI; 2002-566693/60.
XX
XX Novel cell having pre-trans-acting molecules with target binding
PT domains that target binding of PTM to pre-mRNA, 3' or 5' splice region,
PT spacer region, nucleotide sequence to be trans-spliced to target-pre-mRNA.
PT
XX
XX Example; Fig 54; 229pp; English.
PS

XX The present invention describes a cell (I) comprising pre-trans-splicing CC molecules (PTMs) (II) which have one or more target binding domains (Iia) CC that target binding of PTM to pre-mRNA, 3' splice region (Iib) that CC includes branch point pyrimidine tract and 3' splice acceptor site, or 5' CC splice site (Iic), spacer region (Iid) that separates RNA splice site CC from target binding domain, and nucleotide sequence to (Iie) be trans-spliced to target-pre-mRNA. Optionally, the cell comprises (II) either CC comprising: (A) (Iib) and (Iie); or (B) (Iic), (Iid) and (Iie). The cell CC may comprise a recombinant vector expressing (II). (I) has cytosolic, CC immunosuppressive and antimicrobial activities, and can be used in gene CC therapy. (II) comprising one or more (preferably two or more) (Iia) and CC (Iib) (or (Iic)), (Iid) and (Iie), or (II) comprising either (A) or (B) CC (excluding (Iid)), is useful for producing a chimeric RNA molecule in a CC cell which involves contacting a target pre-mRNA expressed in the cell CC with (II) that is recognised by nuclear splicing components. The chimeric CC RNA produced comprises sequences encoding a toxin or translatable CC protein. The nucleotide sequence to be trans-spliced to target pre-mRNA CC preferably comprises nucleotide sequences comprising exons 1-10 of cystic CC fibrosis trans-membrane conductance regulator (CFTR). The chimeric RNA CC molecule produced using (II) which either comprises (A) or (B) further CC comprises a nucleotide sequence tag. (I) can be used for gene regulation, CC gene repair and targeted cell death. (I) can be used for the treatment of CC various diseases including genetic, infectious or autoimmune diseases and CC proliferative disorders such as cancer and to regulate gene expression in CC plants. ABQ73414 to ABQ73536 represent sequences used in the CC exemplification of the present invention

SQ Sequence 138 BP; 45 A; 32 C; 22 G; 39 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 6; Length 138;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CAGGACACAGTGGCTTTGAC 21
39 CAGGACACAGTGGCTTTGAC 59

Db

RESULT 9
ABQ73531
ID ABQ73531 standard; DNA; 193 BP.

XX
AC ABQ73531;
DT 02-OCT-2002 (first entry)
XX
XX HPV-PTM related oligonucleotide #3.

DE
XX Pre-trans-acting molecule; PTM; spliceosome; cytosolic; gene therapy;
KW immunosuppressive; antimicrobial; gene regulation; gene repair; cancer;
KW targeted cell death; genetic disorder; infectious disorder;
KW autoimmune disease; proliferative disorder; PCR primer; ss.
XX
OS Human papillomavirus.
OS Synthetic.
XX
PN WO200253581-A2.
XX
PD 11-JUL-2002.
XX
PF 08-JAN-2002; 2002WO-US000416.
XX
PR 08-JAN-2001; 2001US-00756095.
PR 08-JAN-2001; 2001US-00756096.
PR 08-JAN-2001; 2001US-00756097.
PR 20-APR-2001; 2001US-00838858.
PR 29-AUG-2001; 2001US-00941492.
XX
XX (INTR-) INTRON INC.
PA Mitchell LG, Garcia-Blanco MA, Baker CC, Puttaraju M,
PI Mansfield GS, Chao H;
XX
XX Example; Fig 54; 229pp; English.
PS

XX WPI; 2002-566693/60.
XX
XX Novel cell having pre-trans-splicing molecules with target binding
PT domains that target binding of PTM to pre-mRNA, 3' or 5' splice region,
PT spacer region, nucleotide sequence to be trans-spliced to target-pre-
PT mRNA.
XX
XX Example; Fig 53; 229pp; English.
XX
XX The present invention describes a cell (I) comprising pre-trans-splicing
CC molecules (PTM) (II) which have one or more target binding domains (IIB)
CC that target binding of PTM to pre-mRNA, 3' splice region (IIB) that
CC includes branch point pyrimidine tract and 3' splice acceptor site, or 5'
CC splice site (IIC), spacer region (IID) that separates RNA splice site
CC from target binding domain, and nucleotide sequence to (IIE) be trans-
CC spliced to target-pre-mRNA. Optionally, the cell comprises (II) either
CC comprising: (A) (IIB) and (IIE); or (B) (IIC), (IID) and (IIE). The cell
CC may comprise a recombinant vector expressing (II). (I) has cytosstatic,
CC immunosuppressive and antimicrobial activities, and can be used in gene
CC therapy. (II) comprising one or more (preferably two or more) (IIA) or (B)
CC (IIB) (or (IIC)) and (IIE), or (II) comprising either (A) or (B)
CC (excluding (IIB)), is useful for producing a chimeric RNA molecule in a
CC cell which involves contacting a target pre-mRNA expressed in the cell
CC with (II) that is recognized by nuclear splicing components. The chimeric
CC RNA produced comprises sequences encoding a toxin or translatable
CC protein. The nucleotide sequence to be trans-spliced to target pre-mRNA
CC preferably comprises nucleotide sequences comprising exons 1-10 of cystic
CC fibrosis trans-membrane conductance regulator (CFTR). The chimeric RNA
CC molecule produced using (II) which either comprises (A) or (B) further
CC comprises a nucleotide sequence tag. (I) can be used for gene regulation,
CC gene repair and targeted cell death. (I) can be used for the treatment of
CC various diseases including genetic, infectious or autoimmune diseases and
CC proliferative disorders such as cancer and to regulate gene expression in
CC plants. ABQ73414 to ABQ7536 represent sequences used in the
CC exemplification of the present invention
XX
XX Sequence 193 BP; 46 A; 32 C; 22 G; 40 T; 0 U; 53 Other;
SQ
XX
XX Query Match 100.0%; Score 21; DB 6; Length 193;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAGGACACAGTGGCTTTGAC 21
DB 92 CAGGACACAGTGGCTTTGAC 112
XX
XX RESULT 10
ADX26909/c
ID ADX26909 standard; DNA; 452 BP.
XX
XX ADX26909;
AC
XX 05-MAY-2005 (first entry)
XX
XX Human papillomavirus type 16 E6 delta151 mutant DNA.
DB
XX cell culture; immortalization; Gynecology and obstetrics; Andrology;
KM cancer; neoplasm; mutant; ds.
XX
XX Human papillomavirus type 16.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH misc_difference 3..4
FT /tag= a
FT /note= "Wild-type bases 4-25 have been removed"
FT misc_difference 449..450
FT /tag= b
FT /note= "Wild-type bases 472-474 have been removed"
XX
XX JP2005046117-A.

XX 24-FEB-2005.
PD
XX
XX 31-JUL-2003; 2003JP-00283911.
PF
XX
XX 31-JUL-2003; 2003JP-00283911.
PR
XX
XX (UYKA-) UNITV KANAZAWA TLO YG.
PA (KOKU-) KOKURITSU GAN CENT SOCHO.
XX
XX WPI; 2005-175815/19.
DR
XX
XX Immortalized endometrial glandular epithelial cell strain containing
PT exogenous immortalizing gene and maintains properties of non-cancer cell
PT and typical glandular epithelial cells, useful in field of research of
PT reproduction.
XX
XX Claim 5; SEQ ID NO 4; 22pp; Japanese.
PS
XX
XX The invention relates to a novel immortalized endometrial glandular
CC epithelial cell strain in which an exogenous immortalizing gene is
CC introduced and the properties of the cell line as non-cancer typical
CC glandular epithelial cells, are maintained. The cell line of the
CC invention may be useful for research of reproduction, particularly for
CC analyzing the adhesion of the fertilized egg during implantation,
CC analyzing the effect of steroid hormones, analyzing the mechanism of
CC multistep canceration of the inner glandular epithelial membrane by
CC genetic engineering of the cell line which is otherwise non-cancerous,
CC and analyzing the effect of carcinogenic substances on the cell line. The
CC cell line maintains the properties of normal somatic cells and the
CC properties of endometrial glandular epithelial cells. The current
CC sequence is that of the Human papillomavirus type 16 E6 delta151 mutant
CC DNA of the invention.
XX
XX Sequence 452 BP; 156 A; 70 C; 98 G; 128 T; 0 U; 0 Other;
SQ
XX
XX Query Match 100.0%; Score 21; DB 14; Length 452;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAGGACACAGTGGCTTTGAC 21
DB 336 CAGGACACAGTGGCTTTGAC 316
XX
XX RESULT 11
ABQ76223/c
ID ABQ76223 standard; DNA; 456 BP.
XX
XX ABQ76223;
AC
XX 21-OCT-2002 (first entry)
XX
XX Human papillomavirus E6 tumour antigen derived DNA.
DE
XX Tumour antigen; human; vaccine; cellular immune response; immunogen; E6;
KM cancer; tumour; ds.
XX
XX Human papillomavirus.
OS
XX US6287569-B1.
PN
XX 11-SEP-2001.
XX
XX 06-APR-1998; 98US-00056105.
PF
XX 10-APR-1997; 97US-0043467P.
PR
XX (REGC) UNITV CALIFORNIA.
XX
XX k1pys TJ, Wu Y;
PI
XX
XX WPI; 1998-583198/49.
DR

XX	Generating cellular immune response in patient to target protein
PT	comprises introducing vector with nucleotide sequence encoding immunogen
PT	comprising protein processing signal into cell of patient.
XX	
PS	Disclosure; Col 91-92; 61pp; English.
XX	
CC	This invention describes a novel method for generating a cellular immune
CC	response in a patient to a target protein or its fragment. The method
CC	involves introducing a vector containing a nucleotide sequence encoding a
CC	chimeric immunogen comprising a protein processing signal and the target
CC	protein or its fragment. The immunogen is produced by the cells and
CC	processed so that the target protein or its fragment is presented to the
CC	patients immune system and a cellular immune response is initiated. The
CC	method and vectors can be used as a form of vaccination and could be used
CC	to generate a cellular immune response in patients to, e.g. cancerous
CC	tumours. The cellular immune response is the predominant immune response
CC	in the patient. This sequence represents a DNA fragment which encodes a
CC	tumour antigen from human papillomavirus E6 described in the method of
CC	the invention. Note: The information in this spec has been previously
CC	disclosed in WO199845444 however this spec contained no sequence
CC	information
XX	
SO	Sequence 456 BP; 156 A; 70 C; 101 G; 129 T; 0 U; 0 Other;
	Query Match 100.0%; Score 21; DB 2; Length 456;
	Best Local Similarity 100.0%; Pred. No. 1.7;
	Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CAGGACACAGCGCTTTGAC 21
DB	337 CAGGACACAGCGCTTTGAC 317
RESULT 12	
ADC37149/C	
ID	ADC37149 standard; DNA; 459 BP.
XX	
AC	ADC37149;
XX	
DT	18-DEC-2003 (first entry)
XX	
DE	459bp HPV16 subgenomic fragment DNA sequence.
XX	
KW	Immortalised non-tumorigenic; human Schwann; schwannoma cell line;
KW	screening cancer chemotherapeutic; antineoplastic activity;
KW	carcinogenicity; neuroprotective; neurodegeneration; SV40;
KW	Shulan Virus 40; adenovirus; human papilloma virus; E6; E7; cytostatic;
KW	gene therapy; cancer; HPV16; da.
XX	
OS	Human papillomavirus type 16.
XX	
PN	WO2003073996-A2.
XX	
PD	12-SEP-2003.
XX	
PF	03-MAR-2003; 2003WO-US006314.
XX	
PR	01-MAR-2002; 2002US-0361528P.
XX	
PA	(HOU5-) HOUSE EAR INST.
XX	
PI	Hung G, LI X;
XX	
DR	WPI; 2003-722006/68.
XX	
PT	Producing an immortalized non-tumorigenic human Schwann or schwannoma
PT	cell line for treating cancer or neurodegenerative disorder comprises
PT	selecting for immortalized cells that express the exogenous immortalizing
PT	gene.
XX	
PS	Disclosure; SEQ ID NO 1; 29pp; English.
XX	

CC	The invention relates to a the production of an immortalised non-
CC	tumorigenic human Schwann or schwannoma cell line comprising: providing
CC	a cell culture of human Schwann or schwannoma cells; introducing a
CC	polynucleotide comprising an exogenous immortalising gene into the cells,
CC	and selecting for immortalised cells that express the exogenous
CC	immortalising gene and retain phenotypic properties of Schwann or
CC	schwannoma cells. The invention further comprises: determining the effect
CC	of a pharmacological agent on human Schwann or schwannoma cells;
CC	screening cancer chemotherapeutic and antineoplastic activity of an agent
CC	; testing carcinogenicity of an agent; screening the neuroprotective
CC	activity of an agent; treating neurodegeneration in a patient; and a kit
CC	for screening a pharmacological agent on schwannomas cells. In the method
CC	of producing an immortalised non-tumorigenic human Schwann or schwannoma
CC	cell line, the polynucleotide is a subgenomic fragment of a virus
CC	consisting of SV40 (Simian Virus 40), adenovirus and human papilloma
CC	virus, comprising the E6 and E7 genes of the human papilloma virus
CC	consisting of types 18, 31, 33 or 35, but preferably 16. The immortalised
CC	non-tumorigenic human Schwann or schwannoma cell line has cytosstatic and
CC	neuroprotective activity and be useful in treating disorders by gene
CC	therapy. The method is useful for producing an immortalised non-
CC	tumorigenic human Schwann or schwannoma cell line useful for screening
CC	cancer chemotherapeutic and antineoplastic activity of an agent, testing
CC	carcinogenicity of an agent and screening a neuroprotective activity of
CC	an agent and for preparing a composition for diagnosing or treating
CC	neurodegenerative disorders and cancer. This polynucleotide represents
CC	the DNA of a 459bp HPV16 sequence, a subgenomic fragment used in the
CC	production of the immortalised non-tumourigenic human Schwann or
CC	schwannoma cell line of the invention.
XX	
SQ	Sequence 459 BP; 157 A; 71 C; 100 G; 131 T; 0 U; 0 Other;
	Query Match 100.0%; Score 21; DB 10; Length 459;
	Best Local Similarity 100.0%; Pred. No. 1.7;
	Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Gy	1 CAGACGACAGTGGCTTTGAC 21
D6	338 CAGACGACAGTGGCTTTGAC 318
RESULT 13	
AD171963/c	
ID	AD171963 standard; DNA; 464 BP.
XX	
AC	AD171963;
XX	
DT	20-MAY-2004 (first entry)
XX	
DE	Human ovarian cancer DNA marker #4705.
XX	
KW	Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
OS	Homo sapiens.
XX	
PN	WO200170979-A2.
XX	
PD	27-SEP-2001.
XX	
PE	21-MAR-2001, 2001MO-US009126.
XX	
PR	21-MAR-2000, 2000US-0191031P.
PR	25-MAY-2000, 2000US-0207124P.
PR	15-JUN-2000, 2000US-0211940P.
PR	07-JUL-2000, 2000US-0216820P.
PR	25-JUL-2000, 2000US-0220661P.
PR	21-DEC-2000, 2000US-0257672P.
XX	
PA	(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX	
PI	Lee J, Lallie J;
XX	
DR	WPI; 2001-611502/70.
XX	

PT Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
PT cancer cells as compared to their normal non-cancerous ovarian cells are
XX used to characterize stage, grade, histological type of ovarian cancer.
XX
XX Disclosure; SEQ ID NO 4705; 106pp; English.
XX
XX The invention relates to nucleic acid markers which are overexpressed in
CC ovarian cancer cells as compared to their expression in normal (i.e. non-
CC cancerous) ovarian cells. The invention also relates to polypeptides
CC encoded by the markers, antibodies that selectively bind to the
CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
CC of developing ovarian cancer involving inhibiting expression of a gene
CC corresponding to a marker of the invention and a method of treating a
CC patient afflicted with ovarian cancer comprising providing to cells of
CC the patient an antisense oligonucleotide complementary to a marker of the
CC invention. The markers are useful for assessing if a patient is afflicted
CC with ovarian cancer, which involves comparing the level of expression of
CC a marker in a patient sample and a normal level of expression of the
CC marker in a control non-ovarian cancer sample. A difference between the
CC expression levels indicates ovarian cancer. The level of expression of a
CC marker corresponds to a secreted protein or to a transcribed
CC polynucleotide or its portion. The level of expression of the marker is
CC assessed by detecting the presence in the sample, a protein or protein
CC fragment corresponding to the marker. The presence of protein or protein
CC fragment is detected using an antibody that specifically binds with the
CC protein or protein fragment. Alternatively, the level of expression of
CC the marker is assessed by detecting the presence of a transcribed
CC polynucleotide which anneals with the marker or anneals with a portion of
CC the polynucleotide comprising the marker, under stringent conditions. The
CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 464 BP; 139 A; 106 C; 117 G; 100 T; 0 U; 2 Other;
SQ
XX
XX Query Match 100.0%; Score 21; DB 5; Length 464;
XX Best Local Similarity 100.0%; Pred. No. 1.7;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAGGACACAGTGGCTTTGAC 21
Db 88 CAGGACACAGTGGCTTTGAC 68

RESULT 14
ADL37114/C
ID ADL37114 standard; DNA; 464 BP.
XX
XX ADL37114;
XX
XX 20-MAY-2004 (first entry)
XX
XX Human ovarian cancer DNA marker #11004.
XX
XX Human; ovarian cancer; de; tumour; cytostatic; DNA marker.
XX
XX Homo sapiens.
XX
XX MO200170979-A2.
XX
XX 27-SEP-2001.
XX
XX 21-MAR-2001; 2001MO-US009126.
XX
XX 21-MAR-2000; 2000US-0191031P.
XX
XX 25-MAY-2000; 2000US-0207124P.

PR 15-JUN-2000; 2000US-0211940P.
PR 07-JUL-2000; 2000US-0216820P.
PR 25-JUL-2000; 2000US-0220661P.
PR 21-DEC-2000; 2000US-0257672P.
XX
XX (MILLI-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Lee J, Little J;
XX
XX WPI; 2001-611502/70.
XX
XX
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
PT cancer cells as compared to their normal non-cancerous ovarian cells are
XX used to characterize stage, grade, histological type of ovarian cancer.
XX
XX Disclosure; SEQ ID NO 11004; 106pp; English.
XX
XX The invention relates to nucleic acid markers which are overexpressed in
CC ovarian cancer cells as compared to their expression in normal (i.e. non-
CC cancerous) ovarian cells. The invention also relates to polypeptides
CC encoded by the markers, antibodies that selectively bind to the
CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
CC of developing ovarian cancer involving inhibiting expression of a gene
CC corresponding to a marker of the invention and a method of treating a
CC patient afflicted with ovarian cancer comprising providing to cells of
CC the patient an antisense oligonucleotide complementary to a marker of the
CC invention. The markers are useful for assessing if a patient is afflicted
CC with ovarian cancer, which involves comparing the level of expression of
CC a marker in a patient sample and a normal level of expression of the
CC marker in a control non-ovarian cancer sample. A difference between the
CC expression levels indicates ovarian cancer. The level of expression of a
CC marker corresponds to a secreted protein or to a transcribed
CC polynucleotide or its portion. The level of expression of the marker is
CC assessed by detecting the presence in the sample, a protein or protein
CC fragment corresponding to the marker. The presence of protein or protein
CC fragment is detected using an antibody that specifically binds with the
CC protein or protein fragment. Alternatively, the level of expression of
CC the marker is assessed by detecting the presence of a transcribed
CC polynucleotide which anneals with the marker or anneals with a portion of
CC the polynucleotide comprising the marker, under stringent conditions. The
CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention.
XX
XX Sequence 464 BP; 139 A; 106 C; 117 G; 100 T; 0 U; 2 Other;
SQ
XX
XX Query Match 100.0%; Score 21; DB 5; Length 464;
XX Best Local Similarity 100.0%; Pred. No. 1.7;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAGGACACAGTGGCTTTGAC 21
Db 88 CAGGACACAGTGGCTTTGAC 68

RESULT 15
ADF09607/C
ID ADF09607 standard; cDNA; 477 BP.
XX
XX ADF09607;
XX
XX 12-FEB-2004 (first entry)
XX
XX Human papillomavirus 16 B6 cDNA SEQ ID NO:108.
XX
XX human; protein-protein interaction; virucide; cytostatic; vaccine;
XX human papilloma virus; HPV; cancer; ss; gene.
XX

PI Milner AJ;
 XX WPI; 2003-221850/21.
 DR
 XX
 PT Selective post-transcriptional silencing of an exogenous viral gene (e.g.
 PT human papilloma virus (HPV) B6), for treating e.g. cancer, comprises
 PT using a small interfering RNA (siRNA) construct homologous to an mRNA of
 PT the gene.
 XX
 PS Claim 11; Fig 11; 44pp; English.
 CC The invention relates to a novel method for selective post-translational
 CC silencing in a mammalian cell of the expression of an exogenous gene of
 CC viral origin. The method comprises introducing into the cell a small
 CC interfering RNA (siRNA) construct that is homologous to a part of the
 CC mRNA sequence of the gene. The method is useful for the selective post-
 CC transcriptional silencing of an exogenous gene of viral origin (e.g. an
 CC oncogene or human papilloma virus (HPV) gene) in a mammalian cell. The
 CC method or the siRNA is particularly useful for treating cancer, human
 CC cervical cancer, human immunodeficiency virus (HIV), smallpox, flu,
 CC common cold, or a disease caused by a HPV (e.g. genital warts, cervical
 CC cancer, penile cancer, malignant squamous cell carcinomas or verruca
 CC vulgaris). An siRNA construct or vector is useful for use as a medicament
 CC for the diseases mentioned. The polynucleotide sequence of the invention
 CC can be used to treat disorders by gene therapy. This polynucleotide
 CC sequence represents the DNA of a HPV siRNA sequence of the invention
 CC
 SO Sequence 477 BP; 167 A; 75 C; 104 G; 131 T; 0 U; 0 Other;
 Query Match 100.0%; Score 21; DB 10; Length 477;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAGGACACAGTGGCTTTGAC 21
 DB 358 CAGGACACAGTGGCTTTGAC 338
 RESULT 18
 ADX26908/c
 ID ADX26908 standard; DNA; 477 BP.
 AC ADX26908;
 XX
 XX 05-MAY-2005 (first entry)
 DT
 XX
 DE Human papillomavirus type 16 E6 wild-type gene.
 XX
 XX cell culture; immortalization; Gynecology and obstetrics; Andrology;
 XX cancer; neoplasm; ds.
 XX
 OS Human papillomavirus type 16.
 XX
 XX JP2005046117-A.
 PN
 XX
 XX 24-FEB-2005.
 PD
 XX
 PF 31-JUL-2003; 2003JP-00283911.
 XX
 PR 31-JUL-2003; 2003JP-00283911.
 XX
 XX (UYKA-) UNIV KANAZAWA TLO YG.
 PA (KOKU-) KOKURITSU GAN CENT SOCHO.
 XX
 XX WPI; 2005-175815/19.
 DR
 XX
 XX Immortalized endometrial glandular epithelial cell strain containing
 PT exogenous immortalizing gene and maintains properties of non-cancer cell
 PT and typical glandular epithelial cells, useful in field of research of
 PT reproduction.
 XX
 PS Claim 4; SEQ ID NO 3; 22pp; Japanese.
 XX

CC The invention relates to a novel immortalized endometrial glandular
 CC epithelial cell strain in which an exogenous immortalizing gene is
 CC introduced and the properties of the cell line as non-cancer typical
 CC glandular epithelial cells, are maintained. The cell line of the
 CC invention may be useful for research of reproduction, particularly for
 CC analyzing the adhesion of the fertilized egg during implantation,
 CC analyzing the effect of steroid hormones, analyzing the mechanism of
 CC multistep canceration of the inner glandular epithelial membrane by
 CC genetic engineering of the cell line which is otherwise non-cancerous,
 CC and analyzing the effect of carcinogenic substances on the cell line. The
 CC cell line maintains the properties of normal somatic cells and the
 CC properties of endometrial glandular epithelial cells. The current
 CC sequence is that of the Human papillomavirus type 16 B6 wild-type gene of
 CC the invention.
 CC
 SO Sequence 477 BP; 167 A; 76 C; 103 G; 131 T; 0 U; 0 Other;
 Query Match 100.0%; Score 21; DB 14; Length 477;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAGGACACAGTGGCTTTGAC 21
 DB 358 CAGGACACAGTGGCTTTGAC 338
 RESULT 19
 AEA5113/c
 ID AEA5113 standard; DNA; 477 BP.
 AC AEA5113;
 XX
 XX 11-AUG-2005 (first entry)
 DT
 XX
 DE Human papillomavirus type 16 E6/E7 gene fragment. SEQ ID NO: 17.
 XX
 XX Delivery mechanism; gene therapy; cytostatic; vulnerary; virucide;
 XX injury; infection; cancer; gastrointestinal disease;
 XX gynecology and obstetrics; tumor; colorectal tumor;
 XX uterine cervix tumor; squamous cell carcinoma; neoplasm; E7 gene; ds;
 XX B6 gene.
 XX
 OS Human papillomavirus.
 XX
 XX WO2005051431-A1.
 PN
 XX
 PD 09-JUN-2005.
 XX
 XX 25-NOV-2004; 2004WO-GB004979.
 PF
 XX 25-NOV-2003; 2003GB-00027409.
 PR
 XX 05-MAR-2004; 2004US-0549919P.
 XX
 XX (MILN/) MILNER A J.
 PA
 XX
 XX Milner AJ;
 PI
 XX
 DR WPI; 2005-405310/41.
 XX
 XX Composition useful for delivering an agent into a cell comprises the
 PT agent, a transfer agent and a solid or colloidal carrier medium.
 PT
 PS Disclosure; SEQ ID NO 17; 56pp; English.
 CC
 CC The present invention relates to a method and composition comprising a
 CC transfer agent and a solid or colloidal carrier medium for delivering a
 CC biological agent into cells. The invention is useful for the treatment
 CC of cancer, tumor, carcinoma of cutaneous, squamous or cervical epithelia
 CC and colorectal carcinoma, wounds, burns and scars. The invention is also
 CC useful in gene therapy. The present sequence is the human papillomavirus
 CC type 16 B6/E7 gene fragment. This sequence is useful in a method for
 CC treating carcinomas.
 CC

```

SQ Sequence 477 BP; 167 A; 75 C; 104 G; 131 T; 0 U; 0 Other;
Query Match      100.0%; Score 21; DB 14; Length 477;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 CAGGACACAGTGGCTTTTGAC 21
      |||||
Db      358 CAGGACACAGTGGCTTTTGAC 338

RESULT 20
AAT31834/c
ID AAT31834 standard; DNA; 519 BP.
XX
AC AAT31834;
XX
DT 27-AUG-2003 (revised)
DT 11-JAN-1997 (first entry)
XX
DE Human papilloma virus E6/E7 protein variant.
XX
KM Human papilloma virus; E6; E7; deletion mutant; HPV; immune response;
XX humoral immune response; cellular immune response; vaccine; ss.
XX
OS Human papillomavirus.
XX
FH Key Location/Qualifiers
FT CDS 1..519
FT /*tag= a
FT /product= "E6/E7 fusion protein (deletion mutant)."

```

```

FT misc_feature 154..156
FT /*tag= p
FT /transl_except= CAA encodes Ile
FT 157..159
FT /*tag= q
FT /transl_except= AAG encodes Arg
FT misc_feature 160..162
FT /*tag= r
FT /transl_except= CCA encodes Cys
XX
XX WO9619496-A1.
XX
XX 27-JUN-1996.
XX
XX 20-DEC-1995; 95WO-AU000868.
XX
XX 20-DEC-1994; 94AU-00000157.
XX
XX (CSLC-) CSL LTD.
XX (UYQU) UNIV QUEBENSAND.
XX
XX Edwards SJ, Cox J, Webb EA, Frazer I;
XX
XX WPI; 1996-309518/31.
XX
XX P-SDB; AAR97562.
XX
XX Vaccine variants of human papilloma virus antigens - contain variants of
XX E6 and/or E7 protein, pref. deletion mutants, and are used to treat or
XX prevent HPV infection.
XX
XX Example 3; Page 17; 37pp; English.
XX
XX A variant of the human papilloma virus (HPV) E6 or E7 protein which
XX elicits a humoral and/or cellular immune response against HPV can be used
XX in vaccines against HPV or to treat HPV infection. The variant is
XX preferably a deletion mutant comprising at least half, and preferably two
XX thirds of full length E6 or E7 protein starting from the N- or C-
XX terminal, or is a full length E6 moiety fused to a full length E7 moiety.
XX The variant optionally has a linkage moiety and a foreign protein or
XX peptide which facilitates the purification of, and enhances the
XX immunogenicity of, the fusion protein. This sequence encodes a fusion
XX between the C-terminal end of E6 and the N-terminal end of E7. The
XX protein is also a deletion mutant generated from the sequence described
XX in AAT31833. (Updated on 27-AUG-2003 to correct OS field.)
XX
XX SQ Sequence 519 BP; 175 A; 92 C; 113 G; 139 T; 0 U; 0 Other;
Query Match      100.0%; Score 21; DB 2; Length 519;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 CAGGACACAGTGGCTTTTGAC 21
      |||||
Db      172 CAGGACACAGTGGCTTTTGAC 152

RESULT 21
ADF31984/c
ID ADF31984 standard; DNA; 543 BP.
XX
AC ADF31984;
XX
DT 12-FEB-2004 (first entry)
DT
XX
DE Human papillomavirus fusion gene encoding sequence.
XX
KM human papillomavirus; cervix cancer; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..543
FT /*tag= a

```

XX CN1381583-A.
 XX 27-NOV-2002.
 XX 24-APR-2002; 2002CN-00117143.
 XX 24-APR-2002; 2002CN-00117143.
 XX (ONCO-) INST ONCOLOGY TUMOR HOSPITAL CHINESE ACA.
 XX Zhao Q;
 XX WPI; 2003-258260/26.
 XX P-PSDB; ADF31985.
 XX Human papillomavirus B6/E7 fusion gene and its efficient expression
 XX carrier and fusion protein vaccine.
 XX Claim 3; SEQ ID NO 1; 16pp; Chinese.
 XX The present invention relates to human papillomavirus B6/E7 fusion gene,
 XX its preparing process, the process for configuring the efficient
 XX expression carrier containing the gene and resultant expression carrier,
 XX the fusion protein prepared from the gene, and the application of the
 XX fusion gene and expression protein to medical science and medicine to
 XX treat cervix cancer are disclosed. The present sequence represents the
 XX human papillomavirus fusion gene encoding sequence.
 XX Sequence 543 BP; 185 A; 89 C; 118 G; 151 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 10; Length 543;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGACACAGTGGCTTTGAC 21
 |||||
 DB 358 CAGGACACAGTGGCTTTGAC 338

RESULT 22
 AAQ75470/c
 ID AAQ75470 standard; DNA; 570 BP.
 XX AAQ75470;
 AC 16-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 28-JUN-1995 (first entry)
 XX HPV16 B6/E7 encoding region.
 DE HPV16 B6/E7 encoding region.
 XX HPV16, HPV16, E6 protein, E7 protein, diagnosis; cervical dysplasia;
 KM cervix cancer; ds.
 XX Human papillomavirus; strain 16.
 OS
 XX
 FH Key Location/Qualifiers
 FT CDS 2..478
 FT /*tag= a
 FT /label= B6_encoding_region
 FT CDS 481..570
 FT /*tag= b
 FT /label= E7_encoding_region
 XX MO9426934-A2.
 XX 24-NOV-1994.
 XX 06-MAY-1994; 94MO-US005085.
 XX 06-MAY-1993; 93US-00058920.
 XX

PA (BAXT) BAXTER DIAGNOSTICS INC.
 XX Brown UT;
 XX WPI; 1995-006821/01.
 XX P-PSDB; AAR63865.
 XX Human papilloma virus detection assay - by amplification using self
 XX sustained sequence replication and hybridisation with a detector probe.
 XX Disclosure; Page 24-26; 79pp; English.
 XX The sequences of the E6 and E7 polypeptide-encoding regions of human
 XX papillomavirus (HPV) 16 and 18 are given in AAQ75470-71 and the encoded
 XX proteins in AAR63865-66, respectively. Probes and primers based on these
 XX sequences were used for HPV infection diagnosis; expression of E6 and E7
 XX is diagnostic for cervical cancer or pre-malignant states. (Updated on
 XX 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-2003 to standardise
 XX OS field)
 XX Sequence 570 BP; 199 A; 93 C; 119 G; 159 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 2; Length 570;
 Best Local Similarity 100.0%; Pred. No. 1.8;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGACACAGTGGCTTTGAC 21
 |||||
 DB 359 CAGGACACAGTGGCTTTGAC 339

RESULT 23
 ADL43498/c
 ID ADL43498 standard; DNA; 598 BP.
 XX ADL43498;
 AC 20-MAY-2004 (first entry)
 DT Human ovarian cancer DNA marker #17388.
 DE Human ovarian cancer; ds; tumour; cytostatic; DNA marker.
 XX Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
 XX Homo sapiens.
 XX WO200170979-A2.
 XX 27-SEP-2001.
 XX 21-MAR-2001; 2001MO-US009126.
 XX 21-MAR-2000; 2000US-0191031P.
 XX 25-MAY-2000; 2000US-0207124P.
 XX 15-JUN-2000; 2000US-0211940P.
 XX 07-JUL-2000; 2000US-0216820P.
 XX 25-JUL-2000; 2000US-0220661P.
 XX 21-DEC-2000; 2000US-0257672P.
 XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX Lee J, Lillie J;
 XX WPI; 2001-611502/70.
 XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
 XX cancer cells as compared to their normal non-cancerous ovarian cells are
 XX used to characterize stage, grade, histological type of ovarian cancer.
 XX Disclosure; SEQ ID NO 17388; 106pp; English.
 XX The invention relates to nucleic acid markers which are overexpressed in
 XX ovarian cancer cells as compared to their expression in normal (i.e. non-
 XX cancerous) ovarian cells. The invention also relates to polypeptides

CC patient afflicted with ovarian cancer comprising providing to cells of
 CC the patient an antisense oligonucleotide complementary to a marker of the
 CC invention. The markers are useful for assessing if a patient is afflicted
 CC with ovarian cancer, which involves comparing the level of expression of
 CC a marker in a patient sample and a normal level of expression of the
 CC marker in a control non-ovarian cancer sample. A difference between the
 CC expression levels indicates ovarian cancer. The level of expression of a
 CC marker corresponds to a secreted protein or to a transcribed
 CC polynucleotide or its portion. The level of expression of the marker is
 CC assessed by detecting the presence in the sample, a protein or protein
 CC fragment corresponding to the marker. The presence of protein or protein
 CC fragment is detected using an antibody that specifically binds with the
 CC protein or protein fragment. Alternatively, the level of expression of
 CC the marker is assessed by detecting the presence of a transcribed
 CC polynucleotide which anneals with the marker or anneals with a portion of
 CC the polynucleotide comprising the marker, under stringent conditions. The
 CC marker is also used for monitoring the progression of ovarian cancer in a
 CC patient which involves detecting expression of the marker in a patient
 CC sample at a first point in time, repeating the method at a subsequent
 CC time and comparing the level of expression. The method is carried out
 CC using an ovarian tissue sample. A composition comprising a marker,
 CC polypeptide or antibody of the invention is used to treat ovarian cancer.
 CC This sequence represents a human ovarian cancer DNA marker of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 743 BP; 192 A; 177 C; 159 G; 204 T; 0 U; 11 Other;

Query Match 100.0%; Score 21; DB 5; Length 743;
 Best Local Similarity 100.0%; Pred. No. 1.8;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGACACAGTGGCTTTGAC 21
 |||||
 DB 576 CAGGACACAGTGGCTTTGAC 596

RESULT 26

AAH72718
 AAH72718 standard; cDNA; 745 BP.

AAH72718;

19-SEP-2001 (first entry)

Human cervical cancer marker nucleic acid 3992.

Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.

Homo sapiens.

MO200142467-A2.

14-UTN-2001.

08-DEC-2000; 2000MO-US033312.

08-DEC-1999; 99US-0169681P.

21-DEC-1999; 99US-0171350P.

14-MAR-2000; 2000US-0189315P.

12-MAY-2000; 2000US-0203791P.

09-JUN-2000; 2000US-0210600P.

21-JUL-2000; 2000US-0220114P.

(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Schlegel R, Deeds J, Berger A, Zhao X;

WPI; 2001-375006/39.

New isolated nucleic acid for diagnosing and treating cervical cancer and
 PT for assessing and detecting compounds for treating the cancer.

XX Claim 1; Page 812; 1051bp; English.

XX The invention relates to novel genes (AAH68727-AAH73383) associated with
 CC cervical cancer with cytostatic activity. The nucleic acids and encoded
 CC polypeptides are useful: to assess if a patient is afflicted with
 CC cervical cancer or has a pre-malignant condition; to monitor the
 CC progression of cervical cancer or a premalignant condition in a patient;
 CC and to select and/or assess the efficacy of a compound or therapy for
 CC inhibiting cervical cancer in a patient. The nucleic acids may also be
 CC useful for gene therapy

Sequence 745 BP; 190 A; 185 C; 158 G; 208 T; 0 U; 4 Other;

Query Match 100.0%; Score 21; DB 4; Length 745;
 Best Local Similarity 100.0%; Pred. No. 1.8;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGACACAGTGGCTTTGAC 21
 |||||
 DB 573 CAGGACACAGTGGCTTTGAC 593

RESULT 27

ADO44067/c
 ADO44067 standard; DNA; 747 BP.

ADO44067;

15-JUL-2004 (first entry)

Nucleotide sequence of an E7B6 fusion protein.

B6 protein; E7 protein; fusion protein; HPV6; HPV-associated cancer;

cervical cancer; immune response; lower gastrointestinal tract cancer;

anal cancer; reproductive system cancer; penile cancer; vulvar cancer;

gene; ss.

Human papillomavirus type 16.

Synthetic.

Key Location/Qualifiers

CDS 1..747

/product= "E7B6 fusion protein"

MO2004030636-A2.

15-APR-2004.

02-OCT-2003; 2003MO-US031726.

03-OCT-2002; 2002US-0415929P.

(AMHP) WYETH HOLDINGS CORP.

Smith L, Casaccia MC;

WPI; 2004-316328/29.

P-PSDB; ADO44066.

New polypeptide comprising human papillomavirus B6 and E7 polypeptides,

PT useful for treating or preventing human papillomavirus (HPV)-associated

cancers, e.g. cervical cancer.

Example 1; Page 73; 101bp; English.

The present sequence encodes an E7B6 fusion protein, comprising wild type
 CC E7 and B6 polypeptides from human papillomavirus type 16 (HPV16). The
 CC specification describes human papillomavirus B6 and E7 polypeptides,
 CC where the E7 polypeptide has mutations at any one or more of the amino
 CC acids corresponding to amino acids 24, 26 or 91 of the sequence given in
 CC ADO44073 and the B6 polypeptide has no mutations or has mutations at any

CC one or more of the amino acids corresponding to amino acids 63 or 106 of
CC the sequence given in ADO44072. The polypeptides of the invention are
CC useful for treating or preventing human papillomavirus (HPV)-associated
CC cancers, such as cervical cancer. The fusion proteins and nucleic acids
CC encoding the fusion proteins are useful for generating immune responses
CC against HPV. They are also useful for treating lower gastrointestinal
CC tract cancers, e.g. anal cancer, and other cancers of the reproductive
CC system, including penile and vulvar cancer.

XX
SQ Sequence 747 BP; 247 A; 132 C; 166 G; 202 T; 0 U; 0 Other;
Query Match 100.0%; Score 21; DB 12; Length 747;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGACACAGTGGCTTTTGAC 21
DB 628 CAGGACACAGTGGCTTTTGAC 608

RESULT 28
ADO44065/C
ID ADO44065 standard; DNA; 747 BP.
XX
AC ADO44065;
XX
DT 15-JUL-2004 (first entry)
XX
DE Nucleotide sequence of a fusion protein designated E6E7PentM.
XX
KW B6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer;
KW cervical cancer; immune response; lower gastrointestinal tract cancer;
KW anal cancer; reproductive system cancer; penile cancer; vulvar cancer;
KW gene; ss.
XX
OS Human papillomavirus type 16.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1..747
FT /tag= a
FT /product= "E6E7PentM fusion protein"
XX
PN MO2004030635-A2.
XX
PD 15-APR-2004.
XX
PF 02-OCT-2003; 2003MO-US031726.
XX
PR 03-OCT-2002; 2002US-0415929P.
XX
PA (AMHP) WYETH HOLDINGS CORP.
XX
PI Smith L, Cassetti MC;
XX
DR WPI: 2004-316328/29.
DR P-PSDB; ADO44064.
XX
PT New polypeptide comprising human papillomavirus E6 and E7 polypeptides,
PT useful for treating or preventing human papillomavirus (HPV)-associated
PT cancers, e.g. cervical cancer.
XX
PS Claim 24, Page 71, 101pp; English.
XX
XX The present sequence encodes a fusion protein, comprising E6 and E7
CC polypeptides from human papillomavirus type 16 (HPV16). The fusion
CC protein is designated E6E7PentM, and comprises an E6 amino terminus
CC (where residues 63 and 106 have been replaced with glycine) and an E7
CC carboxy terminus (where residues 24, 26 and 91 have been replaced with
CC glycine). E6E7PentM is representative of fusion proteins of the
CC invention. The specification describes human papillomavirus E6 and E7
CC polypeptides, where the E7 polypeptide has mutations at any one or more
CC of the amino acids corresponding to amino acids 24, 26 or 91 of the

CC sequence given in ADO44073 and the E6 polypeptide has no mutations or has
CC mutations at any one or more of the amino acids corresponding to amino
CC acids 63 or 106 of the sequence given in ADO44072. The polypeptides of
CC the invention are useful for treating or preventing human papillomavirus
CC (HPV)-associated cancers, such as cervical cancer. The fusion proteins
CC and nucleic acids encoding the fusion proteins are useful for generating
CC immune responses against HPV. They are also useful for treating lower
CC gastrointestinal tract cancers, e.g. anal cancer, and other cancers of
CC the reproductive system, including penile and vulvar cancer.

XX
SQ Sequence 747 BP; 246 A; 132 C; 171 G; 198 T; 0 U; 0 Other;
Query Match 100.0%; Score 21; DB 12; Length 747;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGACACAGTGGCTTTTGAC 21
DB 337 CAGGACACAGTGGCTTTTGAC 317

RESULT 29
ADO44061/C
ID ADO44061 standard; DNA; 747 BP.
XX
AC ADO44061;
XX
DT 15-JUL-2004 (first entry)
XX
DE Nucleotide sequence of an E6E7 fusion protein.
XX
KW B6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer;
KW cervical cancer; immune response; lower gastrointestinal tract cancer;
KW anal cancer; reproductive system cancer; penile cancer; vulvar cancer;
KW gene; ss.
XX
OS Human papillomavirus type 16.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1..747
FT /tag= a
FT /product= "E6E7 fusion protein"
XX
PN MO2004030635-A2.
XX
PD 15-APR-2004.
XX
PF 02-OCT-2003; 2003MO-US031726.
XX
PR 03-OCT-2002; 2002US-0415929P.
XX
PA (AMHP) WYETH HOLDINGS CORP.
XX
PI Smith L, Cassetti MC;
XX
DR WPI: 2004-316328/29.
DR P-PSDB; ADO44060.
XX
PT New polypeptide comprising human papillomavirus E6 and E7 polypeptides,
PT useful for treating or preventing human papillomavirus (HPV)-associated
PT cancers, e.g. cervical cancer.
XX
PS Example 1; Page 68, 101pp; English.
XX
XX The present sequence encodes an E6E7 fusion protein, comprising wild type
CC E6 and E7 polypeptides from human papillomavirus type 16 (HPV16). The
CC specification describes human papillomavirus E6 and E7 polypeptides,
CC where the E7 polypeptide has mutations at any one or more of the amino
CC acids corresponding to amino acids 24, 26 or 91 of the sequence given in
CC ADO44073 and the E6 polypeptide has no mutations or has mutations at any
CC one or more of the amino acids corresponding to amino acids 63 or 106 of
CC the sequence given in ADO44072. The polypeptides of the invention are

CC useful for treating or preventing human papillomavirus (HPV)-associated
 CC cancers, such as cervical cancer. The fusion proteins and nucleic acids
 CC encoding the fusion proteins are useful for generating immune responses
 CC against HPV. They are also useful for treating lower gastrointestinal
 CC tract cancers, e.g. anal cancer, and other cancers of the reproductive
 CC system, including penile and vulvar cancer.

XX Sequence 747 BP; 247 A; 132 C; 166 G; 202 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 12; Length 747;
 Best Local Similarity 100.0%; Pred. No. 1.8; Mismatches 0; Gaps 0;
 Matches 21; Conservative 0; Indels 0; Gaps 0;

Qy 1 CAGGACACAGTGGCTTTGAC 21
 |||||
 Db 337 CAGGACACAGTGGCTTTGAC 317

RESULT 30
 ADO44063/c
 ID ADO44063 standard; DNA; 747 BP.

XX ADO44063;

DT 15-JUL-2004 (first entry)

XX Nucleotide sequence of a fusion protein designated E6E7TeM.

XX B6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer;
 KM cervical cancer; immune response; lower gastrointestinal tract cancer;
 KM anal cancer; reproductive system cancer; penile cancer; vulvar cancer;
 KM gene; ss.

XX Human papillomavirus type 16.

OS Synthetic.

XX Key Location/Qualifiers
 FT 1..747
 FT CDS /*tag= a
 FT /product= "E6E7TeM fusion protein"

XX MO2004030636-A2.

XX 15-APR-2004.

XX 02-OCT-2003; 2003WO-US031726.

XX 03-OCT-2002; 2002US-0415929P.

XX (AMHP) WYETH HOLDINGS CORP.

XX Smith L, Cassetti MC;

XX WPI, 2004-316328/29.

XX P-PSDB; ADO44062.

XX New polypeptide comprising human papillomavirus E6 and E7 polypeptides,
 PT useful for treating or preventing human papillomavirus (HPV)-associated
 PT cancers, e.g. cervical cancer.

XX Claim 24; Page 70; 101pp; English.

XX The present sequence encodes a fusion protein, comprising E6 and E7
 CC polypeptides from human papillomavirus type 16 (HPV16). The fusion
 CC protein is designated E6E7TeM, and comprises an E6 amino terminus (where
 CC residues 63 and 106 have been replaced with glycine) and an E7 carboxy
 CC terminus (where residues 24 and 26 have been replaced with glycine).
 CC E6E7TeM is representative of fusion proteins of the invention. The
 CC specification describes human papillomavirus E6 and E7 polypeptides,
 CC where the E7 polypeptide has mutations at any one or more of the amino
 CC acids corresponding to amino acids 24, 26 or 91 of the sequence given in
 CC ADO44073 and the E6 polypeptide has no mutations or has mutations at any
 CC one or more of the amino acids corresponding to amino acids 63 or 106 of

CC there sequence given in ADO44072. The polypeptides of the invention are
 CC useful for treating or preventing human papillomavirus (HPV)-associated
 CC cancers, such as cervical cancer. The fusion proteins and nucleic acids
 CC encoding the fusion proteins are useful for generating immune responses
 CC against HPV. They are also useful for treating lower gastrointestinal
 CC tract cancers, e.g. anal cancer, and other cancers of the reproductive
 CC system, including penile and vulvar cancer.

XX Sequence 747 BP; 246 A; 132 C; 170 G; 199 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 12; Length 747;
 Best Local Similarity 100.0%; Pred. No. 1.8; Mismatches 0; Gaps 0;
 Matches 21; Conservative 0; Indels 0; Gaps 0;

Qy 1 CAGGACACAGTGGCTTTGAC 21
 |||||
 Db 337 CAGGACACAGTGGCTTTGAC 317

RESULT 31
 ADO44069/c
 ID ADO44069 standard; DNA; 747 BP.

XX ADO44069;

DT 15-JUL-2004 (first entry)

XX Nucleotide sequence of a fusion protein designated E7E6TeM.

XX B6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer;
 KM cervical cancer; immune response; lower gastrointestinal tract cancer;
 KM anal cancer; reproductive system cancer; penile cancer; vulvar cancer;
 KM gene; ss.

XX Human papillomavirus type 16.

OS Synthetic.

XX Key Location/Qualifiers
 FT 1..747
 FT CDS /*tag= a
 FT /product= "E7E6TeM fusion protein"

XX MO2004030636-A2.

XX 15-APR-2004.

XX 02-OCT-2003; 2003WO-US031726.

XX 03-OCT-2002; 2002US-0415929P.

XX (AMHP) WYETH HOLDINGS CORP.

XX Smith L, Cassetti MC;

XX WPI, 2004-316328/29.

XX P-PSDB; ADO44068.

XX New polypeptide comprising human papillomavirus E6 and E7 polypeptides,
 PT useful for treating or preventing human papillomavirus (HPV)-associated
 PT cancers, e.g. cervical cancer.

XX Claim 24; Page 74-75; 101pp; English.

XX The present sequence encodes a fusion protein, comprising E7 and E6
 CC polypeptides from human papillomavirus type 16 (HPV16). The fusion
 CC protein is designated E7E6TeM, and comprises an E7 amino terminus (where
 CC residues 24 and 26 have been replaced with glycine) and an E6 carboxy
 CC terminus (where residues 63 and 106 have been replaced with glycine).
 CC E7E6TeM is representative of fusion proteins of the invention. The
 CC specification describes human papillomavirus E6 and E7 polypeptides,
 CC where the E7 polypeptide has mutations at any one or more of the amino
 CC acids corresponding to amino acids 24, 26 or 91 of the sequence given in
 CC ADO44073 and the E6 polypeptide has no mutations or has mutations at any

CC one or more of the amino acids corresponding to amino acids 63 or 106 of
 CC there sequence given in ADO44072. The polypeptides of the invention are
 CC useful for treating or preventing human papillomavirus (HPV)-associated
 CC cancers, such as cervical cancer. The fusion proteins and nucleic acids
 CC encoding the fusion proteins are useful for generating immune responses
 CC against HPV. They are also useful for treating lower gastrointestinal
 CC tract cancers, e.g. anal cancer, and other cancers of the reproductive
 CC system, including penile and vulvar cancer.

SO Sequence 747 BP; 246 A; 132 C; 170 G; 199 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 12; Length 747;

Best Local Similarity 100.0%; Pred. No. 1.8;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGACACAGTGGCTTTTGAC 21

DB 628 CAGGACACAGTGGCTTTTGAC 608

RESULT 32

ADO44071/c

ID ADO44071 standard; DNA; 747 BP.

AC ADO44071;

XX 15-UTR-2004 (first entry)

DE Nucleotide sequence of a fusion protein designated E7B6Pentm.

XX E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer;

KW cervical cancer; immune response; lower gastrointestinal tract cancer;

KM anal cancer; reproductive system cancer; penile cancer; vulvar cancer;

KW gene; ss.

XX Human papillomavirus type 16.

OS Synthetic.

FT Key Location/Qualifiers

FT CDS 1..747

PN WO2004030636-A2.

XX 15-APR-2004.

PF 02-OCT-2003; 2003WO-US031726.

PR 03-OCT-2002; 2002US-0415929P.

PA (AMHP) WYETH HOLDINGS CORP.

XX Smith L, Cassetti MC;

PI WPI; 2004-316328/29.

DR P-PSDB; ADO44070.

XX New polypeptide comprising human papillomavirus E6 and E7 polypeptides,

PT useful for treating or preventing human papillomavirus (HPV)-associated

PT cancers, e.g. cervical cancer.

XX Claim 24; Page 76; 101pp; English.

XX The present sequence encodes a fusion protein, comprising E7 and E6

CC polypeptides from human papillomavirus type 16 (HPV16). The fusion

CC protein is designated E7B6Pentm, and comprises an E7 amino terminus

CC (where residues 24, 26 and 91 have been replaced with glycine) and an E6

CC carboxy terminus (where residues 63 and 106 have been replaced with

CC glycine). E7B6Pentm is representative of fusion proteins of the

CC invention. The specification describes human papillomavirus E6 and E7

CC polypeptides, where the E7 polypeptide has mutations at any one or more

CC of the amino acids corresponding to amino acids 24, 26 or 91 of the

CC sequence given in ADO44073 and the E6 polypeptide has no mutations or has
 CC mutations at any one or more of the amino acids corresponding to amino
 CC acids 63 or 106 of there sequence given in ADO44072. The polypeptides of
 CC the invention are useful for treating or preventing human papillomavirus
 CC (HPV)-associated cancers, such as cervical cancer. The fusion proteins
 CC and nucleic acids encoding the fusion proteins are useful for generating
 CC immune responses against HPV. They are also useful for treating lower
 CC gastrointestinal tract cancers, e.g. anal cancer, and other cancers of
 CC the reproductive system, including penile and vulvar cancer.

SO Sequence 747 BP; 246 A; 132 C; 171 G; 198 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 12; Length 747;

Best Local Similarity 100.0%; Pred. No. 1.8;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGACACAGTGGCTTTTGAC 21

DB 628 CAGGACACAGTGGCTTTTGAC 608

RESULT 33

ADR47004/c

ID ADR47004 standard; DNA; 768 BP.

AC ADR47004;

XX 18-NOV-2004 (first entry)

DE Human papillomavirus type 16 E7 gene for Dengue virus vaccine.

XX de; gene; cytotaxtic; virucide; dengue virus; recombinant replicon;

KW deletion; prem protein; C protein; NS1 protein signal; vaccine;

KM cervical cancer; viral disease; antigen; dendritic cell; immune response;

KW human papillomavirus.

XX Human papillomavirus type 16.

OS Synthetic.

FT Key Location/Qualifiers

FT CDS 1..768

PN WO2004072274-A1.

XX 26-AUG-2004.

PF 30-JAN-2004; 2004WO-CN000088.

PR 30-JAN-2003; 2003CN-00115272.

PA 30-JAN-2003; 2003CN-00115273.

PA (SHAN-) SHANGHAI TENGGEN BIOMEDICAL CO LTD.

PA (TENG-) TENGGEN BIOMEDICAL CO.

PA (BEIJ-) BEIJING ORIENTAL TENGGEN TECHNOLOGY DEV C.

XX Pang X;

DR WPI; 2004-625870/60.

DR P-PSDB; ADR47005.

DR GENBANK; AF486352.

XX Virus-like particle vaccines containing dengue virus recombinant replicon

PT as core for carrier, applicable in preventives or/and remedies for tumors

PT like cervical cancer and viral diseases.

XX Example 2; SEQ ID NO 1; 38pp; Chinese.

CC A dengue virus recombinant replicon has a deletion of the complete coding

CC sequence for prem protein of dengue virus and also includes elements of

CC e.g. the non-coding region in the whole of the 5'-end, the coding region

CC of the front 20 amino acids in the C protein, and the coding region of

CC NS1 protein signal; coding regions of all non-structural proteins. The

CC obtained vaccines are useful in producing preventives or/and remedies for
CC cancer like cervical cancer and viral diseases. Such vaccines can
CC efficiently express antigen in infected cells, which is because dengue
CC virus can infect dendritic cells, and can effectively present antigen to
CC provide immunity effect. Different types of dengue virus can be used to
CC repeatedly produce efficient immune response thereby strengthening the
CC body's immune system against the pathogen that contains such antigen.
CC Human papillomavirus (HPV) vaccines were prepared by using a gene-
CC expressing system using of the full-length dengue virus cDNA clone
CC (pRS/FLD2). The recombinant virus vectors were transfected into baby
CC hamster kidney (BHK) cells to enable the screening of BHK-21 Tet-off cell
CC lines. This sequence corresponds to the HPV type 16 E7 gene used as the
CC gene of interest in the recombinant replicon of the invention.

XX
SQ Sequence 768 BP; 255 A; 139 C; 172 G; 202 T; 0 U; 0 Other;

QY Query Match 100.0%; Score 21; DB 13; Length 768;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 652 CAGGACACAGTGGCTTTGAC 632

QY 1 CAGGACACAGTGGCTTTGAC 21
|||||

RESULT 34
ABFA0156/c
ID ABFA0156 standard; DNA; 768 BP.

XX
AC ABFA0156;
XX
DT 23-MAR-2006 (first entry)

XX
DE Human papillomavirus 16 (HPV-16) E7-E6 oncogene.

XX
XX Vaccine; virus-like particle; replicon; therapeutic; cancer; cytostatic;
XX neoplasm; viral infection; virucide; infection; oncogene;
XX coding sequence; ds.

XX
OS Human papillomavirus type 16.

XX
FH Key Location/Qualifiers
FT CDS 1..768
FT /tag= a
FT /partial
FT /product= "Human papillomavirus 16 (HPV-16) E7-E6
FT oncoprotein"
FT /note= "No stop codon"

XX
PN US2006018928-A1.

XX
PD 26-JAN-2006.

XX
PF 29-JUL-2005; 2005US-00192923.

XX
PR 30-JAN-2003; 2003CN-00115272.
PR 30-JAN-2003; 2003CN-00115273.
PR 30-JAN-2004; 2004MO-00072274.

XX
PA (PANG/) PANG X.

XX
PI Pang X;

XX
PI WPI; 2006-109169/11.
DR P-PSDB; ABFA0157.
DR GENBANK; AF486352, AF469197, AF472508.

XX
XX New recombinant DEN replicons with a deletion of prem, useful for
PT producing a drug for the prophylaxis and treatment of cancer or viral
PT infection.
PS Example 2; SEQ ID NO 1; 24pp; English.

CC The present invention provides a virus-like particle (VLP) vaccine which
CC contains dengue virus (DEN) recombinant replicon as its core. The DEN
CC replicon contains exogenous nucleotide sequences such as human
CC papillomavirus (HPV) antigen proteins, immune regulators or combination
CC of HPV antigen and immune regulators. The invention is useful for
CC producing a drug for the prophylaxis and treatment of cancer or viral
CC infection. The present sequence is a human papillomavirus oncogene.

XX
SQ Sequence 768 BP; 255 A; 139 C; 172 G; 202 T; 0 U; 0 Other;

QY Query Match 100.0%; Score 21; DB 15; Length 768;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 652 CAGGACACAGTGGCTTTGAC 632

QY 1 CAGGACACAGTGGCTTTGAC 21
|||||

RESULT 35
AAT14663/c
ID AAT14663 standard; DNA; 776 BP.

XX
AC AAT14663;
XX
DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 10-OCT-1996 (first entry)

XX
DE E6/E7 region of Human Papilloma Virus 16 (HPV 16).

XX
XX Human papilloma virus; HPV; detection; cervical cancer; amplification;
XX hybridisation; diagnosis; transformed cell; E6; E7; ss.

XX
OS Human papillomavirus type 16.

XX
FH Key Location/Qualifiers
FT primer_bind 1..24
FT /tag= a
FT /note= "Primer BB113 binding site."
FT 30..55
FT /tag= b
FT /note= "Primer H16-58 binding site."
FT 37..57
FT /tag= c
FT /note= "Primer BB4 binding site."
FT 454..474
FT /tag= d
FT /note= "Primer BB114 binding site."
FT 480..503
FT /tag= e
FT /note= "Primer BB111 binding site."
FT 591..621
FT /tag= f
FT /note= "Primer BB109 binding site."
FT 658..681
FT /tag= g
FT /note= "Primer H16-686 binding site."
FT 660..683
FT /tag= h
FT /note= "Primer BB112 binding site."
FT 715..738
FT /tag= i
FT /note= "Primer H16-743 binding site."
FT 745..768
FT /tag= j
FT /note= "Primer H16-773 binding site."

XX
PN US5506105-A.

XX
PD 09-APR-1996.

XX
PF 22-MAR-1994; 94US-00216233.

```

XX 10-DEC-1991; 91US-00808456.
XX (DADE-) DADE INT INC.
XX Haydock PV;
XX WPI, 1996-200273/20.
XX Detection of low copy number intracellular markers - by 3SR amplification
XX of target RNA in fixed cells then hybridisation with labelled probe, for
XX detecting human papilloma virus in cervical cells.
XX
XX Example 2; Fig 3; 21pp; English.
XX An in situ hybridisation assay for detecting an intracellular marker of
XX low copy number in cells comprises fixing the cells to a support using
XX paraformaldehyde; treating the cells with a protease to permeabilise them
XX without altering morphology; adding amplification reagents; incubating
XX the cells at below fifty degrees celsius to perform amplification by self
XX sustained sequence replication; adding a labelled probe complementary to
XX the region between the primers; washing cells to remove unhybridised
XX papilloma virus (HPV) 16 is used especially to detect mRNA being
XX transcribed from this region which becomes active in transformed cells.
XX The method can be used for the early diagnosis of cervical cancer.
XX Primers used to amplify fragments of the B6/E7 region are described in
XX AAT14664-T14674. (Updated on 25-MAR-2003 to correct PF field.) (Updated
XX on 27-AUG-2003 to correct OS field.)
XX
XX Sequence 776 BP; 260 A; 139 C; 169 G; 208 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 21; DB 2; Length 776;
XX Best Local Similarity 100.0%; Pred. No. 1.9;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 CAGGACACAGTGGCTTTTGAC 21
XX |||||||||||||||||||
XX 358 CAGGACACAGTGGCTTTTGAC 338
XX
XX RESULT 36
XX AAX89756/C
XX ID AAX89756 standard; DNA; 779 BP.
XX
XX AAX89756;
XX
XX 27-AUG-2003 (revised)
XX 12-OCT-1999 (first entry)
XX
XX Probe sequence for HPV 16 B6/E7.
XX
XX human papilloma virus; infection; gene expression; probe; detection;
XX assay; cancer; virus; HPV; ss.
XX
XX Synthetic.
XX Human papillomavirus.
XX
XX WO9292890-A2.
XX
XX 17-JUN-1999.
XX
XX 11-DEC-1998; 98WO-US026447.
XX
XX 12-DEC-1997; 97US-0069426P.
XX 05-JAN-1998; 98US-0070486P.
XX 17-APR-1998; 98US-0082167P.
XX
XX (DIGE-) DIGENE CORP.
XX
XX Lorincz AT;
XX
XX WPI, 1999-443850/37.

```

```

XX New method for assessing Human Papilloma Virus (HPV) infection by
XX comparison of gene expression levels.
XX
XX Disclosure; Fig 5; 35pp; English.
XX
XX This nucleotide probe is specific for the HPV16 Human Papilloma Virus
XX (HPV) gene. The degree of HPV infection can be assessed, by measuring the
XX levels of expression of genes involved in the diseased state, and
XX comparing the expression to each other or to reference genes. (Updated on
XX 27-AUG-2003 to correct OS field.)
XX
XX Sequence 779 BP; 259 A; 139 C; 170 G; 211 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 21; DB 2; Length 779;
XX Best Local Similarity 100.0%; Pred. No. 1.9;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 CAGGACACAGTGGCTTTTGAC 21
XX |||||||||||||||||||
XX 365 CAGGACACAGTGGCTTTTGAC 345
XX
XX RESULT 37
XX AAQ29389/C
XX ID AAQ29389 standard; DNA; 790 BP.
XX
XX AAQ29389;
XX
XX 24-OCT-2003 (revised)
XX 25-MAR-2003 (revised)
XX 09-MAR-1993 (first entry)
XX
XX DNA encoding HPV 16 B6/E7 proteins obtd. by PCR.
XX
XX Virus vector; vaccinia virus; papillomavirus; HPV; human; amplification;
XX immunotherapeutic; ss.
XX
XX Human papillomavirus type 16.
XX
XX Location/Qualifiers
XX Key 1..789
XX CDS /note= "reading frame 1"
XX /start= 1
XX /end= 790
XX /note= "reading frame 2"
XX /start= 3..788
XX /note= "reading frame 3"
XX /start= 6..482
XX /note= "reading frame 4"
XX /start= 485..781
XX /note= "second reading frame encoding HPV 16 E7"
XX
XX WO9216636-A1.
XX
XX 01-OCT-1992.
XX
XX 10-MAR-1992; 92WO-GB000424.
XX
XX 14-MAR-1991; 91GB-00005383.
XX
XX (IMMU ) IMMUNOLOGY LTD.
XX
XX Bourneil MEG, Inglis SC, Munro AJ;
XX
XX WPI, 1992-349219/42.
XX P-PSDB; AAR27723, AAR27724, AAR27725.
XX
XX Recombinant virus vectors encoding human papillomavirus proteins - for

```

PT treating and vaccinating against HPV infections and conditions caused by
 PT them, such as cervical cancer.
 XX
 PS Disclosure; Fig 1e; 83pp; English.
 CC The fragment of DNA contg. the HPV-16 E6/E7 coding region was prep'd. by
 CC PCR from plasmid pBR322/HPV16 (Durst et al., PNAS, 80: 3812 (1983)) using
 CC oligonucleotides S05 and S06. The DNA prod. has a site for NcoI at the
 CC beginning of the E6 gene and a SmaI site immediately downstream of the
 CC termination codon for E7. The E6 and E7 ORFs are fused together to form a
 CC single continuous ORF via site directed mutagenesis and the immortalising
 CC potential of E7 is removed by altering two key codons of the HPV E7
 CC sequence. The single ORF of HPV-16 E6/E7 may be inserted into CAGGAC
 CC virus DNA at neutral sites (pref. by inserting two sets of the DNA in
 CC opposite orientations to overcome the problem of intertypic
 CC recombination) to make a recombinant virus vector for use
 CC immunotherapeutically to activate cells of the immune system against HPV.
 CC See also AAQ29385-400 and AAQ29450-69. (Updated on 25-MAR-2003 to correct
 CC PN field.) (Updated on 24-OCT-2003 to standardise OS field)
 CC
 SQ Sequence 790 BP; 262 A; 144 C; 175 G; 209 T; 0 U; 0 Other;
 Query Match 100.0%; Score 21; DB 2; Length 790;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAGGACACAGTGGCTTTGAC 21
 DB 363 CAGGACACAGTGGCTTTGAC 343
 RESULT 38
 AAT31833/c
 ID AAT31833 standard; DNA; 801 BP.
 AC AAT31833;
 XX
 DT 27-AUG-2003 (revised)
 DT 10-JAN-1997 (first entry)
 XX
 DE Human papilloma virus E6/E7 protein variant.
 XX
 KW Human papilloma virus; E6; E7; deletion mutant; HPV; immune response;
 KW humoral immune response; cellular immune response; vaccine; ss.
 XX
 OS Human papillomavirus.
 XX
 FT Key Location/Qualifiers
 FT CDS 1..801
 FT /tag= a
 FT /product= "E6/E7 fusion protein."
 XX
 PN MO9619496-A1.
 PD 27-JUN-1996.
 XX
 PF 20-DEC-1995; 95WO-AU000868.
 XX
 PR 20-DEC-1994; 94AU-00000157.
 XX
 PA (CSLC-) CSL LTD.
 PA (UYOU) UNIV QUEENSLAND.
 XX
 PI Edwards SJ, Cox J, Webb BA, Frazer I;
 XX
 DR WPI; 1996-309518/31.
 DR P-PSDB; AAR97561.
 XX
 PT Vaccine variants of human papilloma virus antigens - contain variants of
 PT E6 and/or E7 protein, pref. deletion mutants, and are used to treat or
 PT prevent HPV infection.
 XX
 PS Example 1; Page 15-16; 37pp; English.

XX A variant of the human papilloma virus (HPV) E6 or E7 protein which
 CC elicits a humoral and/or cellular immune response against HPV can be used
 CC in vaccines against HPV or to treat HPV infection. The variant is
 CC preferably a deletion mutant comprising at least half, and preferably two
 CC thirds of full length E6 or E7 protein starting from the N- or C-
 CC terminal, or is a full length E6 moiety fused to a full length E7 moiety.
 CC The variant optionally has a linkage moiety and a foreign protein or
 CC peptide which facilitates the purification of, and enhances the
 CC immunogenicity of, the fusion protein. This sequence encodes a full
 CC length E6/E7 fusion protein. (Updated on 27-AUG-2003 to correct OS
 CC field.)
 CC
 SQ Sequence 801 BP; 266 A; 150 C; 174 G; 211 T; 0 U; 0 Other;
 Query Match 100.0%; Score 21; DB 2; Length 801;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAGGACACAGTGGCTTTGAC 21
 DB 358 CAGGACACAGTGGCTTTGAC 338
 RESULT 39
 AAX78792/c
 ID AAX78792 standard; DNA; 822 BP.
 AC AAX78792;
 XX
 DT 06-SEP-1999 (first entry)
 XX
 DE HPV fusion protein DL/3-E6-His/HPV16 DNA.
 XX
 KW Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour;
 KW immunological fusion partner; CpG oligonucleotide; immune response;
 KW HPV antigen; prevention; treatment; ss.
 XX
 OS Synthetic.
 OS Human papillomavirus.
 XX
 PN WO933868-A2.
 PD 08-JUL-1999.
 XX
 PF 18-DEC-1998; 98WO-EP008563.
 XX
 PR 24-DEC-1997; 97GB-00027262.
 XX
 PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 XX
 PI Dalemans WLJ, Gerard CMG;
 XX
 DR WPI; 1999-405485/34.
 DR P-PSDB; AAY25376.
 XX
 PT Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to
 PT induce immune response to HPV.
 XX
 PS Example II; Page 48; 62pp; English.
 XX
 CC AAX78791-X78801 represent nucleic acid sequences which encode novel
 CC constructs comprising an E6 or E7 protein or E6/E7 fusion protein from
 CC HPV (represented in AAY25375-Y25386). These constructs are optionally
 CC linked to an immunological fusion partner and an immunomodulatory CpG
 CC oligonucleotide. The products of the invention can be used to induce an
 CC immune response in a patient to an HPV antigen. They can also be used for
 CC preventing or treating HPV induced tumours
 CC
 SQ Sequence 822 BP; 277 A; 147 C; 168 G; 230 T; 0 U; 0 Other;
 Query Match 100.0%; Score 21; DB 2; Length 822;
 Best Local Similarity 100.0%; Pred. No. 1.9;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGACACAGTGGCTTTGAC 21
 ||||||||||||||||||
 Db 676 CAGGACACAGTGGCTTTGAC 656

RESULT 40
 AAX29781/c
 ID AAX29781 standard; DNA; 822 BP.
 XX
 AC AAX29781;
 XX
 DT 17-OCT-2003 (revised)
 XX 22-JUN-1999 (first entry)
 XX
 DE Prot. D1/3-E6-His/HPV16 coding sequence.
 XX
 KM Chimeric; E6; E7; fusion protein; protein D; vaccine; immunotherapy;
 XX tumour; lesion; benign; malignant; virus; infection; ss.
 XX
 OS Human papillomavirus.
 OS Haemophilus influenzae.
 OS Chimeric.
 XX
 PN MO9910375-A2.
 XX
 PD 04-MAR-1999.
 XX
 PF 17-AUG-1998; 98MO-EP005285.
 XX
 PR 22-AUG-1997; 97GB-00017953.
 XX
 PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 XX
 PI Bruck C, Cabezon Silva T, Delisse AEF, Gerard CMG;
 PI Lombardo-Bencheikh A;
 PI WPI; 1999-190587/16.
 XX
 DR
 XX
 PT Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for
 XX treatment or prophylaxis of HPV induced lesions.
 XX
 PS Disclosure; Fig 3; 95pp; English.
 XX
 CC This sequence represents the coding region for a chimeric E6 or E7
 CC protein or E6/E7 fusion protein from Human papillomavirus (HPV) linked to
 CC an immunological fusion partner, in this case, a fragment of the
 CC Haemophilus influenzae B protein D. The sequence also contains a
 CC histidine tag at the C-terminus of the encoded protein. The protein can
 CC be used in a vaccine, for immuno-therapeutically treating HPV induced
 CC tumour lesions (benign or malignant) and preventing HPV viral infection.
 CC (Updated on 17-OCT-2003 to standardise OS field)
 CC
 SQ Sequence 822 BP; 277 A; 147 C; 168 G; 230 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 2; Length 822;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGACACAGTGGCTTTGAC 21
 ||||||||||||||||||
 Db 676 CAGGACACAGTGGCTTTGAC 656

RESULT 41
 AED52633/c
 ID AED52633 standard; DNA; 822 BP.
 XX
 AC AED52633;
 XX
 DT 29-DEC-2005 (first entry)
 XX

DE Fusion protein D1/3-E6-His/HPV16, DNA.
 XX
 XX Fusion protein; vaccine; papilloma; cyostatic; papillomavirus infection;
 KM virucide; uterine cervix tumor; E6; ds; gene; D protein.
 XX
 XX Haemophilus influenzae; strain 772.
 OS
 OS Human papillomavirus type 16.
 OS Synthetic.
 OS Chimeric.
 XX
 XX
 FH Key Location/Qualifiers
 FT CDS 1..822
 FT /*tag= a
 FT /product= "Fusion protein D1/3-E6-His/HPV16"
 XX
 PN IN9801903-14.
 XX
 PD 04-MAR-2005.
 XX
 PF 24-AUG-1998; 98IN-CH001903.
 XX
 PR 22-AUG-1997; 97BP-00179535.
 XX
 PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 XX
 PI Tyrrell AMR;
 XX
 DR WPI; 2005-557648/57.
 DR P-PSDB; AED52634.
 XX
 PT Vaccine.
 XX
 PS Example 4; Fig 3; 96pp; English.
 XX
 CC The invention relates to human Papilloma virus (HPV) fusion proteins,
 CC linked to an immunological fusion partner that provides T helper epitopes
 CC to the HPV antigen. Vaccine formulations comprising the fusion proteins
 CC are useful in the treatment or prophylaxis of HPV induced lesions
 CC (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7
 CC proteins (singly, as an E6-E7 fusion or mutated) were fused to either
 CC Haemophilus influenzae D protein (20-127), the C-terminus of
 CC Streptococcus pneumoniae LytA protein (cLYA) or thiorodoxin. The present
 CC sequence encodes an HPV-H. influenzae D protein, fusion protein of the
 CC invention.
 CC
 SQ Sequence 822 BP; 277 A; 147 C; 168 G; 230 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 14; Length 822;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGACACAGTGGCTTTGAC 21
 ||||||||||||||||||
 Db 676 CAGGACACAGTGGCTTTGAC 656

RESULT 42
 AAX78795/c
 ID AAX78795 standard; DNA; 879 BP.
 XX
 AC AAX78795;
 XX
 DT 06-SEP-1999 (first entry)
 XX
 DE HPV fusion protein CLYTA-E6-His/HPV16 DNA.
 XX
 KM Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour;
 KM immunological fusion partner; Cpg oligonucleotide; immune response;
 KM HPV antigen; prevention; treatment; ss.
 XX
 XX Synthetic.
 OS
 OS Human papillomavirus.

```

PN WO933868-A2.
XX
XX 08-JUL-1999.
XX
XX 18-DEC-1998; 98MO-BP008563.
XX
XX 24-DEC-1997; 97GB-00027262.
XX
XX (SMIK ) SMITHKLIN BEERHAM BIOLOGICALS.
XX
XX Dalemans WLJ, Gerard CMG;
XX
XX WPI, 1999-405485/34.
XX
XX P-PSDB; AAY25379.
XX
XX Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to
XX induce immune response to HPV.
XX
XX Example VI, Page 52, 62pp; English.
XX
XX AAY78791-X78801 represent nucleic acid sequences which encode novel
XX constructs comprising an E6 or E7 protein or E6/E7 fusion protein from
XX HPV (represented in AAY25375-Y25386). These constructs are optionally
XX linked to an immunological fusion partner and an immunomodulatory CpG
XX oligonucleotide. The products of the invention can be used to induce an
XX immune response in a patient to an HPV antigen. They can also be used for
XX preventing or treating HPV induced tumours
XX
XX Sequence 879 BP; 289 A; 168 C; 209 G; 213 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 21; DB 2; Length 879;
XX Best Local Similarity 100.0%; Pred. No. 1.9;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 CAGGACACAGTGGCTTTGAC 21
XX 733 CAGGACACAGTGGCTTTGAC 713
XX
XX RESULT 43
XX AAY29784/C
XX ID AAY29784 standard; DNA; 879 BP.
XX
XX AAY29784;
XX
XX 17-OCT-2003 (revised)
XX DT 22-JUN-1999 (first entry)
XX
XX CLYTA-B6-His coding sequence.
XX
XX Chimeric; E6; E7; fusion protein; CLYTA; vaccine; immunotherapy; tumour;
XX lesion; benign; malignant; virus; infection; ss.
XX
XX Human papillomavirus.
XX OS Streptococcus pneumoniae.
XX Chimeric.
XX
XX WO9910375-A2.
XX
XX 04-MAR-1999.
XX
XX 17-AUG-1998; 98MO-BP005285.
XX
XX 22-AUG-1997; 97GB-00017953.
XX
XX (SMIK ) SMITHKLIN BEERHAM BIOLOGICALS.
XX
XX Bruck C, Cabazon Silva T, Delisse ABF, Gerard CMG;
XX Lombardo-Bencheikh A;
XX
XX WPI, 1999-190587/16.
XX
XX P-PSDB; AAY02635.
XX

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PT Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for
XX treatment or prophylaxis of HPV induced lesions.
XX
XX Disclosure; Fig 10; 95pp; English.
XX
XX This sequence represents the coding region for a chimeric E6 or E7
XX protein or E6/E7 fusion protein from Human papillomavirus (HPV) linked to
XX an immunological fusion partner. In this case, a fragment of the
XX Streptococcus pneumoniae CLYTA protein. The sequence also contains a
XX histidine tag at the C-terminus of the encoded protein. The protein can
XX be used in a vaccine, for immuno-therapeutically treating HPV induced
XX tumour lesions (benign or malignant) and preventing HPV viral infection.
XX (Updated on 17-OCT-2003 to standardise OS field)
XX
XX Sequence 879 BP; 289 A; 168 C; 209 G; 213 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 21; DB 2; Length 879;
XX Best Local Similarity 100.0%; Pred. No. 1.9;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 CAGGACACAGTGGCTTTGAC 21
XX 733 CAGGACACAGTGGCTTTGAC 713
XX
XX RESULT 44
XX AED52641/C
XX ID AED52641 standard; DNA; 879 BP.
XX
XX AED52641;
XX
XX 29-DEC-2005 (first entry)
XX DT
XX Fusion protein clyta-B6-His/HPV16, DNA.
XX
XX Fusion protein; vaccine; papilloma; cytostatic; papillomavirus infection;
XX virucide; uterine cervix tumor; E6; de; gene; LyTA.
XX
XX Streptococcus pneumoniae.
XX OS Human papillomavirus type 16.
XX Synthetic.
XX Chimeric.
XX
XX Key Location/Qualifiers
XX FH 1..879
XX CDS /*tag= a
XX FT /product= "Fusion protein clyta-B6-His/HPV16"
XX
XX IN9801903-14.
XX
XX 04-MAR-2005.
XX
XX 24-AUG-1998; 98IN-CH001903.
XX
XX 22-AUG-1997; 97BP-00179535.
XX
XX (SMIK ) SMITHKLIN BEERHAM BIOLOGICALS.
XX
XX Tytrell AMR;
XX
XX WPI, 2005-557648/57.
XX
XX P-PSDB; AED52642.
XX
XX Vaccine.
XX
XX Example 10; Fig 10; 96pp; English.
XX
XX The invention relates to human Papilloma virus (HPV) fusion proteins,
XX linked to an immunological fusion partner that provides T helper epitopes
XX to the HPV antigen. Vaccine formulations comprising the fusion proteins
XX are useful in the treatment or prophylaxis of HPV induced lesions
XX (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7
XX proteins (singly, as an E6-E7 fusion or mutated) were fused to either

```

CC Haemophilus influenzae D protein (20-127), the C-terminus of
CC Streptococcus pneumoniae LytA protein (cLytA) or thiorodoxin. The present
CC sequence encodes an HIV-LytA, fusion protein of the invention.

XX SQ Sequence 879 BP; 289 A; 168 C; 209 G; 213 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 14; Length 879;

Best Local Similarity 100.0%; Pred. No. 1.9;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGACACAGTGGCTTTGAC 21

Db 733 CAGGACACAGTGGCTTTGAC 713

RESULT 45
AAA09477/c

ID AAA09477 standard; DNA; 921 BP.

XX AAA09477;

AC 29-AUG-2000 (first entry)

XX Human papillomavirus type 16 E6 and E7 open reading frames.

XX hINV, involucrin; regulatory region; tissue-specific; promoter; oncogene;
XX Euphrasael; stratified; squamous; epithelial tissue; animal model;
XX neoplasia; papillomavirus 16; E6; E7; blistering; proliferative;
XX Ichthyosis; cancer; ss.

OS Human papillomavirus type 16.

XX Key Location/Qualifiers

FT CDS 170..625

FT /*cag= a

FT /label= E6

FT mat_peptide 628..921

FT /*cag= b

FT /label= E7

XX MO200026343-A2.

XX 11-MAY-2000.

XX 29-OCT-1999; 99WO-US025516.

XX 30-OCT-1998; 98US-0106495P.

XX 29-OCT-1999; 99US-00430201.

XX (UYCA-) UNIV CASE WESTERN RESERVE.

XX Eckert RL, Crish JF;

XX WPI; 2000-365596/31.

XX Transgenic animals that express oncogenes in epithelial tissue, useful as
XX disease models for neoplastic conditions such as psoriasis and melanomas.
XX Disclosure; Fig 13; 86pp; English.

XX The invention concerns transgenic non-human animals that express
XX oncogenes of interest in their epithelial cells, and materials and
XX methods for their production. Expression of the oncogenes is controlled
XX by a sequence from the human involucrin upstream regulatory region (see
XX AAA09476) which targets expression to desired tissues and cells (i.e.
XX supra basal stratified squamous epithelial tissue). The transgenic animals
XX are useful as animal models for studying neoplastic diseases that affect
XX epithelial tissues, such as those caused by the papillomavirus 16
XX oncogene E6 or E7 nucleic acid sequences and including blistering
XX diseases (e.g. epidermolytic hyperkeratosis, Dowling-Meara disease),
XX proliferative diseases (e.g. psoriasis, epidermal cysts and Bulosa
XX simplex), ichthyosis disease (e.g. Ichthyosis bullosa Siemsen and
XX recessive X-linked ichthyosis) and cancers of the skin, breast, lung,

CC colon, cervix and liver. The animal models may also be used to screen
CC candidate agents for the ability to prevent or treat these diseases
CC (claimed)

XX SQ Sequence 921 BP; 308 A; 167 C; 197 G; 249 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 3; Length 921;

Best Local Similarity 100.0%; Pred. No. 1.9;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGACACAGTGGCTTTGAC 21

Db 506 CAGGACACAGTGGCTTTGAC 486

RESULT 46
AAD35101/c

ID AAD35101 standard; DNA; 939 BP.

XX AAD35101;

AC 25-JUL-2002 (first entry)

XX Human papillomavirus enhE6,7 construct DNA.

XX Alphavirus vector system; human papilloma virus; HPV; cervical cancer;
XX therapy; vaccine; virucide; cytostatic; ds.
XX Human papillomavirus.

XX EPI195438-A1.

XX 10-APR-2002.

XX 06-OCT-2000; 2000EP-00203472.

XX 06-OCT-2000; 2000EP-00203472.

XX (UYGR-) RIJSDUNIV GRONINGEN.

XX Regts DG, Wilschut JC, Holtrop M, Daemen CAHH;

XX WPI; 2002-354156/39.

XX 29-OCT-1999; 99WO-US025516.

XX New alphavirus system, useful for genetic immunization against cervical
XX cancer, comprises papilloma virus nucleic acid.

XX Example 2; Fig 19; 45pp; English.

XX The present invention relates to an alphavirus vector system comprising
XX nucleic acid derived from a human papilloma virus (HPV). The invention or
XX cells containing it, are used in treatment and prevention of cervical
XX cancer, particularly as a vaccine. By selecting the nucleic acid that
XX encode E6/E7 proteins without ability to bind to pRB and p53, the risk
XX that cells infected with the alphavirus vector system may become
XX oncogenic is avoided (contrast use of other viral vectors). The present
XX sequence is Human papillomavirus enhE6,7 construct DNA

XX SQ Sequence 939 BP; 284 A; 197 C; 217 G; 241 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 6; Length 939;

Best Local Similarity 100.0%; Pred. No. 1.9;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGACACAGTGGCTTTGAC 21

Db 522 CAGGACACAGTGGCTTTGAC 502

RESULT 47
AAQ08627/c

ID AAQ08627 standard; DNA; 1000 BP.

```

AC AA008627;
XX
XX 24-OCT-2003 (revised)
DT 21-APR-1994 (first entry)
XX
XX HPV-16 fragment.
DE
XX HPV-18; HPV-16; amplification; primer; polymerase chain reaction; PCR;
KM ss.
XX
XX Human papillomavirus type 16.
OS
XX Key Location/Qualifiers
XX FT misc_binding 198..207
XX FT /tag= a
XX FT /note= "primer (AA008628) binding site"
XX FT misc_binding 601..620
XX FT /tag= b
XX FT /note= "primer (AA008629) binding site"
XX FT /tag= c
XX FT /note= "primer (AA008630) binding site"
XX
XX DE3838269-A.
XX
XX PD 17-MAY-1990.
XX
XX PF 11-NOV-1988; 88DE-03838269.
XX
XX PR 11-NOV-1988; 88DE-03838269.
XX
XX PA (BEHW ) BEHRINGER AG.
XX
XX PI Cerutti P, Whitcomb J, Zijlstra J, Devillers EM;
XX WPI, 1990-156905/21.
XX
XX DR Detection of human papilloma virus - by DNA amplification and analysis.
XX
XX PS Example 4b; Page 4; 11pp; German.
XX
XX CC Example 4b describes the results of the amplification of HPV-16 DNA by
XX PCR using primers. (Updated on 24-OCT-2003 to standardise OS field)
XX
XX SQ Sequence 1000 BP; 340 A; 171 C; 230 G; 259 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 21; DB 2; Length 1000;
XX Best Local Similarity 100.0%; Pred. No. 1.9;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CAGGACACAGTGGCTTTTGAC 21
XX |||||||||||||||||||
XX DB 440 CAGGACACAGTGGCTTTTGAC 420
XX
XX RESULT 48
XX AAN91784/c
XX ID AAN91784 standard; DNA; 1005 BP.
XX
XX AC AAN91784;
XX
XX DT 27-AUG-2003 (revised)
XX DT 25-MAR-2003 (revised)
XX DT 16-MAR-1990 (first entry)
XX
XX DB DNA probe complementary to human papilloma virus type 16.
XX
XX KW Cervical cancer.
XX
XX OS Human papillomavirus type 16.
XX
XX PN MO8909940-A.
XX

```

```

PD 19-OCT-1989.
XX
XX PF 04-APR-1989; 89MO-US001318.
XX
XX PR 04-APR-1988; 88US-00177404.
XX PR 31-MAR-1989; 89US-00330381.
XX
XX PA (ONCO-) ONCOR INC.
XX
XX PI George AL, Groff DE;
XX WPI, 1989-324314/44.
XX
XX DR Rapid detection of specific human papilloma virus genotypes - by
XX PT hybridisation of DNA digest with new labelled nucleic acid probes.
XX
XX PS Claim 40; Page 46; 81pp; English.
XX
XX CC Obtd. by cutting HPV16 with BamHI and PvuII. The patent describes probes
XX (DNA or RNA) and their complements capable of detecting one or a
XX combination of HPV types 6, 11, 16, 18, 31, 33 and 35. (Updated on 25-MAR
XX -2003 to correct PR field.) (Updated on 27-AUG-2003 to correct OS field.)
XX
XX SQ Sequence 1005 BP; 325 A; 182 C; 190 G; 308 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 21; DB 1; Length 1005;
XX Best Local Similarity 100.0%; Pred. No. 1.9;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CAGGACACAGTGGCTTTTGAC 21
XX |||||||||||||||||||
XX DB 892 CAGGACACAGTGGCTTTTGAC 872
XX
XX RESULT 49
XX AAX78793/c
XX ID AAX78793 standard; DNA; 1116 BP.
XX
XX AC AAX78793;
XX
XX DT 06-SEP-1999 (first entry)
XX
XX DE HPV fusion protein DI/3-E6E7-His/HPV16 DNA.
XX
XX KM Fusion protein; E6 protein; E7 protein; E6/E7; Immunomodulator; tumour;
XX immunological fusion partner; CPG oligonucleotide; immune response;
XX KM HIV antigen; prevention; treatment; ss.
XX
XX OS Synthetic.
XX OS Human papillomavirus.
XX
XX PN MO9933868-AZ.
XX
XX PD 08-JUL-1999.
XX
XX PF 18-DEC-1998; 98MO-EP008563.
XX
XX PR 24-DEC-1997; 97GB-00027262.
XX
XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX PI Dalemans WLJ, Gerard CMG;
XX
XX DT WPI; 1999-405485/34.
XX DR P-PSDB; AAY25377.
XX
XX PT Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to
XX induce immune response to HPV.
XX
XX PS Example III; Page 49; 62pp; English.
XX
XX CC AAX78791-X78801 represent nucleic acid sequences which encode novel
XX constructs comprising an E6 or E7 protein or E6/E7 fusion protein from

```

CC HPV (represented in AAY25375-Y25386). These constructs are optionally
 CC linked to an immunological fusion partner and an immunomodulatory Cpg
 CC oligonucleotide. The products of the invention can be used to induce an
 CC immune response in a patient to an HPV antigen. They can also be used for
 CC preventing or treating HPV induced tumours
 XX

Db 676 CAGGACACAGTGGCTTTGAC 656
 Search completed: May 24, 2006, 05:56:59
 Job time : 256.028 secs

SQ Sequence 1116 BP; 368 A; 208 C; 235 G; 305 T; 0 U; 0 Other;
 Query Match 100.0%; Score 21; DB 2; Length 1116;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGACACAGTGGCTTTGAC 21
 |||||
 Db 676 CAGGACACAGTGGCTTTGAC 656

RESULT 50
 AAX29782/c
 ID AAX29782 standard; DNA; 1116 BP.
 XX

AC AAX29782;
 XX
 DT 17-OCT-2003 (revised)
 DT 22-JUN-1999 (first entry)
 XX

DE Prot.D1/3-E6-E7-His/HPV16 coding sequence.

XX ChimERIC; E6; E7; fusion protein; protein D; vaccine; immunotherapy;
 KM tumour; lesion; benign; malignant; virus; infection; ss.
 XX

OS Human Papillomavirus.
 OS Haemophilus influenzae.
 OS ChimERIC.
 OS

PN WO910375-A2.

PD 04-MAR-1999.

PF 17-AUG-1998; 98WO-EP005285.

PR 22-AUG-1997; 97GB-00017953.

XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

PI Bruck C, Cabazon Silva T, Delisse AEF, Gerard CMG;
 PI Lombardo-Bencheikh A;
 PI

DR WPI; 1999-190587/16.
 DR P-PSDB; AAY02633.

PT Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for
 PT treatment or prophylaxis of HPV induced lesions.
 XX

PS Disclosure; Fig 6; 95pp; English.

CC This sequence represents the coding region for a chimERIC E6 or E7
 CC protein or E6/E7 fusion protein from Human papillomavirus (HPV) linked to
 CC an immunological fusion partner, in this case, a fragment of the
 CC Haemophilus influenzae B protein D. The sequence also contains a
 CC histidine tag at the C-terminus of the encoded protein. The protein can
 CC be used in a vaccine, for immuno-therapeutically treating HPV induced
 CC tumour lesions (benign or malignant) and preventing HPV viral infection.
 CC (Updated on 17-OCT-2003 to standardise OS field)
 CC

XX Sequence 1116 BP; 368 A; 208 C; 235 G; 305 T; 0 U; 0 Other;
 SQ

Query Match 100.0%; Score 21; DB 2; Length 1116;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGGACACAGTGGCTTTGAC 21
 |||||

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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2006, 05:47:01 ; Search time 1449.58 Seconds
(without alignments)
810.102 Million cell updates/sec

Title: US-10-601-913-85

Perfect score: 21

Sequence: 1 CAGGACACAGTGGCTTTTAC 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_hic:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_g881:*
12: gb_g882:*
13: gb_g883:*
14: gb_g884:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	244	3	BO106475
2	18.4	87.6	229	7	BB333633
3	18.4	87.6	291	7	BB264006
4	18.4	87.6	291	7	BB347346
5	18.4	87.6	534	8	CR538057
6	18.4	87.6	546	9	DA514546
7	18.4	87.6	549	9	DA722798
8	18.4	87.6	583	9	DA906377
9	18.4	87.6	644	7	BB647218
10	18.4	87.6	654	13	C2303586
11	18.4	87.6	660	5	CJ337277
12	18.4	87.6	720	5	CD353955
13	18.4	87.6	2148	14	AY406159
14	18.4	87.6	2400	14	AY406158
15	18.4	87.6	2400	14	AY406160
16	18.4	87.6	2711	6	AK139334
17	18.4	87.6	3161	6	AK044046
18	18.4	87.6	3592	6	AK083092
19	18.4	87.6	3793	6	AK086711

20	17.8	84.8	337	2	BG022939	BG022939 daa81d07.
21	17.8	84.8	357	2	BF771220	BF771220 IL5-IT002
22	17.8	84.8	377	8	CR555978	CR555978 DKFDP4691
23	17.8	84.8	501	4	BY467982	BY467982 BY467982
24	17.8	84.8	507	8	CR429603	CR429603 CR429603
25	17.8	84.8	594	1	AL785427	AL785427 AL785427
26	17.8	84.8	595	9	CK421278	CK421278 JGI_XZG15
27	17.8	84.8	626	14	DR5G15T	AL733484 Danilo rer
28	17.8	84.8	643	11	AQ655517	AO625517 CIRIBI-B1-
29	17.8	84.8	649	1	AL642415	AL642415 AL642415
30	17.8	84.8	683	14	CT346911	CT346911 Sub scrof
31	17.8	84.8	712	14	AG144458	AG144458 Pan trogl
32	17.8	84.8	712	11	A2560569	A2560569 RPCI-23-2
33	17.8	84.8	788	9	CK380870	CK380870 JGI_XZT52
34	17.8	84.8	793	9	CK443805	CK443805 JGI_XZG94
35	17.8	84.8	794	9	CK444795	CK444795 JGI_XZG10
36	17.8	84.8	796	9	CK404457	CK404457 JGI_XZT35
37	17.8	84.8	799	9	CK439900	CK439900 JGI_XZG80
38	17.8	84.8	829	9	CK407260	CK407260 JGI_XZT62
39	17.8	84.8	850	9	CK396192	CK396192 JGI_XZT56
40	17.8	84.8	874	12	CC295265	CC295265 CH261-52A
41	17.8	84.8	883	9	CK418837	CK418837 JGI_XZG65
42	17.8	84.8	895	10	DR897380	DR897380 JGI_XZT42
43	17.8	84.8	895	10	DT398630	DT398630 JGI_CAB12
44	17.8	84.8	896	8	CK333579	CK333579 JGI_XZT69
45	17.8	84.8	906	5	CF222676	CF222676 AGENCOURT
46	17.8	84.8	921	12	CC304636	CC304636 CH261-89N
47	17.8	84.8	2617	6	AK034662	AK034662 Mus muscu
48	17.8	84.8	5736	6	AK157580	AK157580 Mus muscu
49	17.4	82.9	390	12	CE693411	CE693411 C19r-g88-
50	17.4	82.9	430	11	AQ435575	AQ435575 HS_5147 A
51	17.4	82.9	472	4	CB730452	CB730452 AMGNNUC-N
52	17.4	82.9	503	14	CR266963	CR266963 Forward s
53	17.4	82.9	545	1	AJ940900	AJ940900 AJ940900
54	17.4	82.9	602	8	CV429532	CV429532 52239.1 A
55	17.4	82.9	630	8	BG083368	BG083368 H3087B03-
56	17.4	82.9	739	13	C2080667	C2080667 OM_Ba007
57	17.4	82.9	753	1	AJ943303	AJ943303 AJ943303
58	17.4	82.9	792	8	CV450533	CV450533 EST904442
59	17.4	82.9	981	12	CC192876	CC192876 CH261-35F
60	17.4	82.9	1197	12	CC287367	CC287367 CH261-34D
61	17.4	82.9	246	7	BB412072	BB412072 BB412072
62	17.4	82.9	469	10	BP715091	BP715091 BP715091
63	17.4	82.9	480	10	DT926674	DT926674 BMSB10674
64	17.4	82.9	480	10	DT926674	DT926674 BMSB11237
65	17.4	82.9	494	7	BF049136	BF049136 dc04g05.x
66	17.4	82.9	494	2	BG579815	BG579815 dab7ge04.
67	17.4	82.9	497	2	BJ079209	BJ079209 BJO79209
68	17.4	82.9	515	11	AQ318368	AQ318368 RPCI11-10
69	17.4	82.9	542	10	DM550648	DM550648 EST_g881-
70	17.4	82.9	603	3	BP724122	BP724122 BP724122
71	17.4	82.9	635	3	BP724122	BP724122 BP724122
72	17.4	82.9	637	3	BP724451	BP724451 BP724451
73	17.4	82.9	643	3	BP718952	BP718952 BP718952
74	17.4	82.9	652	3	BU448384	BU448384 603213573
75	17.4	82.9	677	2	BT094427	BT094427 BT094427
76	17.4	82.9	678	10	DV868100	DV868100 CRP7832 C
77	17.4	82.9	680	2	BU075913	BU075913 BU075913
78	17.4	82.9	690	2	BP722067	BP722067 BP722067
79	17.4	82.9	700	4	CB600923	CB600923 AGENCOURT
80	17.4	82.9	716	2	BJ632398	BJ632398 BJ632398
81	17.4	82.9	750	2	BT644127	BT644127 BT644127
82	17.4	82.9	757	3	BP701906	BP701906 BP701906
83	17.4	82.9	769	10	DR721880	DR721880 AGENCOURT
84	17.4	82.9	797	3	BP683846	BP683846 BP683846
85	17.4	82.9	798	3	BP721999	BP721999 BP721999
86	17.4	82.9	821	3	BP719880	BP719880 BP719880
87	17.4	82.9	857	4	CB199693	CB199693 AGENCOURT
88	17.4	82.9	861	3	BP733643	BP733643 BP733643
89	17.4	82.9	863	3	BP734862	BP734862 BP734862
90	17.4	82.9	871	4	CB564030	CB564030 AGENCOURT
91	17.4	82.9	896	4	CB561058	CB561058 AGENCOURT
92	17.4	82.9	926	4	CB560615	CB560615 AGENCOURT

93	17	81.0	963	12	CL075720	CL075720 CH216-137	C 166	16.8	80.0	537	11	B2233574	B2233574 CH230-.489
94	16.8	80.0	170	7	AM205371	AM205371 UI-H-B11-	C 167	16.8	80.0	542	4	CA434929	CA434929 UI-H-DH0-
95	16.8	80.0	216	7	BM048216	BM048216	C 168	16.8	80.0	543	5	CD689562	CD689562 EST6085_h
96	16.8	80.0	217	1	AV336599	AV336599	C 169	16.8	80.0	544	9	DA008129	DA008129
97	16.8	80.0	257	8	CN360617	CN360617 170005321	C 170	16.8	80.0	546	8	CN360196	CN360196 170006001
98	16.8	80.0	265	7	BM603540	BM603540	C 171	16.8	80.0	550	9	DA115209	DA115209
99	16.8	80.0	269	1	AA376277	AA376277 EST88732	C 172	16.8	80.0	550	9	DB003754	DB003754
C 100	16.8	80.0	276	2	BI044517	BI044517 CMO-OT021	C 173	16.8	80.0	554	9	DB248688	DB248688
101	16.8	80.0	281	1	AV157995	AV157995	C 174	16.8	80.0	555	9	DA069489	DA069489
102	16.8	80.0	298	1	AV258624	AV258624	C 175	16.8	80.0	555	9	DA283307	DA283307
C 103	16.8	80.0	298	7	BF081693	BF081693 PM-AN008	C 176	16.8	80.0	558	9	DA207522	DA207522
104	16.8	80.0	305	1	AV296599	AV296599	C 177	16.8	80.0	560	8	CN360194	CN360194 170006001
105	16.8	80.0	333	1	AA333907	AA333907 EST38065	C 178	16.8	80.0	560	9	DA459900	DA459900
106	16.8	80.0	341	10	TS7733	TS7733 YC01d01.x1	C 179	16.8	80.0	561	1	DA053159	DA053159
107	16.8	80.0	342	7	AM999666	AM999666 MRO-BN007	C 180	16.8	80.0	564	1	AL704377	AL704377
108	16.8	80.0	345	1	AA010133	AA010133 ze16c11.x	C 181	16.8	80.0	565	2	BI392540	BI392540 PEP11.DK0
109	16.8	80.0	346	1	AA382706	AA382706 EST95944	C 182	16.8	80.0	565	2	DA839844	DA839844
110	16.8	80.0	351	3	BM759109	BM759109 K-EST0039	C 183	16.8	80.0	567	9	DA927289	DA927289
111	16.8	80.0	372	1	AA418923	AA418923 zw01b05.x	C 184	16.8	80.0	568	9	DB245124	DB245124
112	16.8	80.0	373	9	DA419783	DA419783	C 185	16.8	80.0	570	9	DA017534	DA017534
C 113	16.8	80.0	380	7	AM197400	AM197400 xm42e10.x	C 186	16.8	80.0	571	9	DA028941	DA028941
C 114	16.8	80.0	381	1	AA631860	AA631860 np61c10.x	C 187	16.8	80.0	573	9	DB164139	DB164139
115	16.8	80.0	382	11	AZ007632	AZ007632 RPCI-23-2	C 188	16.8	80.0	577	9	DA478562	DA478562
116	16.8	80.0	388	7	AM153502	AM153502 UI-H-B11-	C 189	16.8	80.0	578	9	DA234051	DA234051
C 117	16.8	80.0	389	1	AA702379	AA702379 ze190a10.s	C 190	16.8	80.0	579	9	DA294271	DA294271
118	16.8	80.0	389	1	AA854258	AA854258 a172f11.s	C 191	16.8	80.0	579	9	DA751352	DA751352
119	16.8	80.0	393	2	BI026237	BI026237 CM4-MT028	C 192	16.8	80.0	579	11	AZ977893	AZ977893
C 120	16.8	80.0	395	1	BI368620	BI368620 QV61f06.x	C 193	16.8	80.0	581	3	BP247691	BP247691
121	16.8	80.0	397	7	BE167425	BE167425 CM2-HTD50	C 194	16.8	80.0	581	3	BP872770	BP872770
C 122	16.8	80.0	402	1	AA418826	AA418826 zw01b05.s	C 195	16.8	80.0	581	9	DB040088	DB040088
C 123	16.8	80.0	409	7	AM197285	AM197285 xm41e10.x	C 196	16.8	80.0	582	9	DB233658	DB233658
124	16.8	80.0	416	7	AV740676	AV740676	C 197	16.8	80.0	583	3	BP367165	BP367165
C 125	16.8	80.0	422	5	CD691325	CD691325 EST7848_h	C 198	16.8	80.0	588	7	BE816540	BE816540 RCO-BN022
C 126	16.8	80.0	432	1	AI277364	AI277364 qm54b10.h	C 199	16.8	80.0	594	8	CV030398	CV030398 9506_Pull1
C 127	16.8	80.0	433	1	AA716625	AA716625 zq59g10.s	C 200	16.8	80.0	594	9	DA105744	DA105744
C 128	16.8	80.0	437	1	AI271888	AI271888 q183a06.x	C 201	16.8	80.0	600	13	CM399766	CM399766
129	16.8	80.0	443	8	CN271759	CN271759 170005999	C 202	16.8	80.0	601	3	BU741173	BU741173 UI-E-B20-
C 130	16.8	80.0	444	7	AM629723	AM629723 lh70a06.y	C 203	16.8	80.0	602	1	AA772083	AA772083 a141g10.s
C 131	16.8	80.0	448	14	DE137471	DE137471 Oryz1a8_1	C 204	16.8	80.0	604	11	AQ420138	AQ420138 RPCI-11-1
C 132	16.8	80.0	459	9	DB001106	DB001106	C 205	16.8	80.0	611	8	CO529334	CO529334 3530_1.19
C 133	16.8	80.0	461	9	AA010134	AA010134 ze16c11.s	C 206	16.8	80.0	611	11	AZ996621	AZ996621
134	16.8	80.0	461	9	DB001027	DB001027	C 207	16.8	80.0	614	11	AZ994515	AZ994515
C 135	16.8	80.0	470	9	DA345819	DA345819	C 208	16.8	80.0	614	11	AZ994604	AZ994604 BU-BE000
C 136	16.8	80.0	474	11	AQ512323	AQ512323 HS_5077_A	C 209	16.8	80.0	619	9	BJ303889	BJ303889
137	16.8	80.0	475	9	DA867526	DA867526	C 210	16.8	80.0	619	11	BZ264264	BZ264264 CH230-.420
138	16.8	80.0	476	10	W65363	W65363 zd32b07.x1	C 211	16.8	80.0	621	5	CF131660	CF131660 UI-HF-P00
139	16.8	80.0	477	5	CD931413	CD931413 GR45.114G	C 212	16.8	80.0	623	4	CA118472	CA118472 SCGR109
140	16.8	80.0	479	9	DA677922	DA677922	C 213	16.8	80.0	624	12	CC869562	CC869562 NDL-S2N22
141	16.8	80.0	479	12	CE326627	CE326627 t1gr-g8s-	C 214	16.8	80.0	625	5	CD766933	CD766933 AGNCCORT
C 142	16.8	80.0	480	1	A1669095	A1669095 wb44c12.x	C 215	16.8	80.0	639	11	AZ488738	AZ488738 IM0319J12
143	16.8	80.0	481	4	CA658210	CA658210 w1mo_PK04	C 216	16.8	80.0	645	4	CB433691	CB433691 610091_MA
144	16.8	80.0	489	7	BE670481	BE670481 7e47f04.x	C 217	16.8	80.0	649	11	AZ374230	AZ374230 IM0126O18
145	16.8	80.0	491	9	DA704875	DA704875	C 218	16.8	80.0	652	3	BM726888	BM726888
146	16.8	80.0	494	1	AA424499	AA424499 zve2g07.x	C 219	16.8	80.0	653	7	AM956321	AM956321
C 147	16.8	80.0	497	1	AI150398	AI150398 q140h05.x	C 220	16.8	80.0	659	2	BI032893	BI032893 MR4-NN020
148	16.8	80.0	501	3	BM761791	BM761791 K-EST0042	C 221	16.8	80.0	671	12	CE228956	CE228956 t1gr-g8s-
149	16.8	80.0	502	2	BM512576	BM512576 1f70f01.y	C 222	16.8	80.0	676	3	BU299430	BU299430 603734718
150	16.8	80.0	502	8	CM360195	CM360195 170005325	C 223	16.8	80.0	677	5	CF350424	CF350424 1158e11.y
151	16.8	80.0	506	11	AZ054100	AZ054100 RPCI-23-4	C 224	16.8	80.0	680	5	CK005847	CK005847
152	16.8	80.0	508	2	BI054880	BI054880 PMO-GN040	C 225	16.8	80.0	689	2	BI561623	BI561623
153	16.8	80.0	509	9	DN990354	DN990354 TC101537	C 226	16.8	80.0	691	13	CM155887	CM155887 104_558_1
154	16.8	80.0	515	1	AA397675	AA397675 ze88c06.x	C 227	16.8	80.0	692	13	CM155886	CM155886 104_558_1
C 155	16.8	80.0	516	11	AZ168438	AZ168438 SP_0111_A	C 228	16.8	80.0	693	2	BI561641	BI561641 603256058
156	16.8	80.0	518	9	DB013169	DB013169 DM53d10.x	C 229	16.8	80.0	694	2	BI561006	BI561006 603254396
C 157	16.8	80.0	526	7	AM771170	AM771170	C 230	16.8	80.0	695	2	BI562715	BI562715
C 158	16.8	80.0	528	11	AQ827159	AQ827159 HS_5256_B	C 231	16.8	80.0	704	2	BI220466	BI220466
C 159	16.8	80.0	529	1	AI400621	AI400621 t949g02.x	C 232	16.8	80.0	707	10	DV027885	DV027885
160	16.8	80.0	532	14	CNS07H62	CNS07H62	C 233	16.8	80.0	708	7	BE278775	BE278775
C 161	16.8	80.0	532	14	CNS07H62	CNS07H62	C 234	16.8	80.0	708	9	DN995060	DN995060 TC101013
C 162	16.8	80.0	533	4	CB054297	CB054297 NISG_CM03	C 235	16.8	80.0	715	5	CK023900	CK023900
163	16.8	80.0	533	4	CB298327	CB298327 220018_1e	C 236	16.8	80.0	716	3	BU238985	BU238985 603321987
C 164	16.8	80.0	533	9	DB335333	DB335333	C 237	16.8	80.0	719	7	BB889603	BB889603
165	16.8	80.0	535	9	DA815054	DA815054	C 238	16.8	80.0	720	1	AU125372	AU125372

239	16.8	80.0	727	9	CK751779	AGENCOURT	C 312	16.8	80.0	4610	6	CR857663	CR857663 Pongo pyg
C 240	16.8	80.0	733	14	AG087227	Pan trogl	C 313	16.4	78.1	149	11	AZ097531	AZ097531 RPTCI-23-1
C 241	16.8	80.0	738	14	AG433903	Mus muscu	C 314	16.4	78.1	176	1	AA891581	AA891581 EST195384
C 242	16.8	80.0	738	14	AG538666	Mus muscu	C 315	16.4	78.1	199	4	CE298326	CE298326 220019_7e
C 243	16.8	80.0	739	14	CT162300	Sus scrof	C 316	16.4	78.1	208	1	AA049329	AA049329 EST192096
C 244	16.8	80.0	743	12	CL153855	104_338_1	C 317	16.4	78.1	212	1	AU076937	AU076937 AU076937
C 245	16.8	80.0	755	1	AU125330	AU125330	C 318	16.4	78.1	242	1	A1175801	A1175801 EST219371
C 246	16.8	80.0	755	5	CF348027	AGENCOURT	C 319	16.4	78.1	243	3	BP473182	BP473182 BP473182
C 247	16.8	80.0	759	14	CT080988	Sus scrof	C 320	16.4	78.1	264	1	A1013988	A1013988 EST07543
C 248	16.8	80.0	763	10	DR770718	ILLUMINEN	C 321	16.4	78.1	271	2	B1276870	B1276870 UI-R-CXO-
C 249	16.8	80.0	765	1	AU140332	AU140332	C 322	16.4	78.1	284	12	CE008388	CE008388 t1gr-g8s-
C 250	16.8	80.0	775	3	BU481796	603845164	C 323	16.4	78.1	292	3	BP472115	BP472115 BP472115
C 251	16.8	80.0	782	7	AM106454	um28a06.Y	C 324	16.4	78.1	324	9	DA811247	DA811247 DA811247
C 252	16.8	80.0	783	2	BU309793	BU309793	C 325	16.4	78.1	327	1	A1695540	A1695540 tu27610.X
C 253	16.8	80.0	788	8	COS28007	3530_1_18	C 326	16.4	78.1	332	1	A1008564	A1008564 EST03015
C 254	16.8	80.0	789	2	BG109145	602281341	C 327	16.4	78.1	333	9	DA507386	DA507386 DA507386
C 255	16.8	80.0	790	13	DUI16177	109855344	C 328	16.4	78.1	336	2	B1274411	B1274411 UI-R-CWO-
C 256	16.8	80.0	790	10	DT944937	603006646	C 329	16.4	78.1	353	1	AA333036	AA333036 EST17062
C 257	16.8	80.0	793	1	AT256581	u18C01.X	C 330	16.4	78.1	354	1	AA849643	AA849643 EST192410
C 258	16.8	80.0	793	8	COS54757	AGENCOURT	C 331	16.4	78.1	359	10	DV721281	DV721281 RV112434
C 259	16.8	80.0	797	8	COS54757	AGENCOURT	C 332	16.4	78.1	363	7	BE524577	BE524577 UI-R-AAO-
C 260	16.8	80.0	804	2	BG346245	602573471	C 333	16.4	78.1	369	3	BE605333	BE605333 70204_F0r
C 261	16.8	80.0	804	10	DV173618	ZM_BFPD017	C 334	16.4	78.1	371	7	BE152502	BE152502 CM2-HT032
C 262	16.8	80.0	809	12	BZ756768	PURBM63TD	C 335	16.4	78.1	374	14	DE042998	DE042998 Oryzias 1
C 263	16.8	80.0	812	4	BX883015	BX883015	C 336	16.4	78.1	384	4	CB703307	CB703307 AMGNNUC:M
C 264	16.8	80.0	814	12	CG428187	ZMMBB023	C 337	16.4	78.1	386	2	B1528740	B1528740 1024093B0
C 265	16.8	80.0	817	2	B1765650	603052379	C 338	16.4	78.1	387	2	DA946930	DA946930 DA946930
C 266	16.8	80.0	818	12	CC736566	P0UA88TB	C 339	16.4	78.1	393	4	CB777627	CB777627 AMGNNUC:M
C 267	16.8	80.0	819	14	D0508481	109857427	C 340	16.4	78.1	394	4	CB777228	CB777228 AMGNNUC:M
C 268	16.8	80.0	822	14	DE261252	Oryzias 1	C 341	16.4	78.1	409	1	AA955928	AA955928 UI-R-E0-b
C 269	16.8	80.0	824	10	DR955170	ZM_BFPD04	C 342	16.4	78.1	412	2	BM189830	BM189830 TGEST2574
C 270	16.8	80.0	825	5	CJ488996	CJ488996	C 343	16.4	78.1	416	2	DB187268	DB187268 DB187268
C 271	16.8	80.0	825	10	DR608371	EST998499	C 344	16.4	78.1	417	7	BE099347	BE099347 UI-R-B01-
C 272	16.8	80.0	830	7	CT153755	Sus scrof	C 345	16.4	78.1	419	7	AV858833	AV858833 AV858833
C 273	16.8	80.0	831	7	BB895040	BB895040	C 346	16.4	78.1	420	1	AA900377	AA900377 UI-R-E0-C
C 274	16.8	80.0	833	3	BU928029	BU928029	C 347	16.4	78.1	424	1	AA859625	AA859625 UI-R-E0-b
C 275	16.8	80.0	834	14	CT291757	Sus scrof	C 348	16.4	78.1	424	5	CJ225784	CJ225784 CJ225784
C 276	16.8	80.0	835	6	HSW802099	HSW802099	C 349	16.4	78.1	426	9	DA775436	DA775436 DA775436
C 277	16.8	80.0	836	14	CT328355	Sus scrof	C 350	16.4	78.1	428	2	BF789848	BF789848 602110336
C 278	16.8	80.0	836	3	BQ710462	AGENCOURT	C 351	16.4	78.1	430	1	A1178102	A1178102 EST212161
C 279	16.8	80.0	839	10	DT656389	ZM_BFPD012	C 352	16.4	78.1	431	7	BB875076	BB875076 BB875076
C 280	16.8	80.0	840	2	BG769878	602744743	C 353	16.4	78.1	433	11	AQ188958	AQ188958 HS_3197_B
C 281	16.8	80.0	844	12	CC418659	PURHIF22TB	C 354	16.4	78.1	432	1	A1008089	A1008089 EST302540
C 282	16.8	80.0	855	12	CC418652	PURHIF22TD	C 355	16.4	78.1	432	8	CR735886	CR735886 CR735886
C 283	16.8	80.0	856	14	D0035967	Pan trogl	C 356	16.4	78.1	435	3	BM753692	BM753692 K-EST0027
C 284	16.8	80.0	859	3	BQ878605	AGENCOURT	C 357	16.4	78.1	439	1	A1408022	A1408022 EST136312
C 285	16.8	80.0	859	10	DT838701	LB00445.C	C 358	16.4	78.1	443	1	AA894081	AA894081 EST197884
C 286	16.8	80.0	867	13	DU290502	DU290502	C 359	16.4	78.1	445	1	A1792081	A1792081 ag66C08.Y
C 287	16.8	80.0	872	10	DV515000	ZM_BFPD019	C 360	16.4	78.1	452	9	DA958730	DA958730 DA958730
C 288	16.8	80.0	877	3	BQ881482	AGENCOURT	C 361	16.4	78.1	454	4	CE784680	CE784680 AMGNNUC:M
C 289	16.8	80.0	882	14	BX955738	Reveree B	C 362	16.4	78.1	456	9	DA827941	DA827941 DA827941
C 290	16.8	80.0	884	2	B1765179	603051432	C 363	16.4	78.1	461	9	DA784695	DA784695 DA784695
C 291	16.8	80.0	894	14	CT348149	Sus scrof	C 364	16.4	78.1	465	9	DA705697	DA705697 DA705697
C 292	16.8	80.0	916	12	BZ823687	PURFGB01TB	C 365	16.4	78.1	466	9	DA770486	DA770486 DA770486
C 293	16.8	80.0	918	2	BG687564	602639368	C 366	16.4	78.1	468	9	DA949125	DA949125 DA949125
C 294	16.8	80.0	919	12	CC610026	AGENCOURT	C 367	16.4	78.1	476	9	DA200381	DA200381 DA200381
C 295	16.8	80.0	925	3	BU178807	AGENCOURT	C 368	16.4	78.1	479	2	BG375697	BG375697 UI-R-C80-
C 296	16.8	80.0	935	12	CG116677	PURBHS9TD	C 369	16.4	78.1	481	1	AA965161	AA965161 UI-R-C0-h
C 297	16.8	80.0	968	12	CG116674	PURBHS9TD	C 370	16.4	78.1	481	9	DA090413	DA090413 DA090413
C 298	16.8	80.0	969	12	CG319175	CG319175	C 371	16.4	78.1	481	11	AZ898889	AZ898889 RPTCI-24-1
C 299	16.8	80.0	993	3	BQ707893	AGENCOURT	C 372	16.4	78.1	483	1	A1599265	A1599265 EST350968
C 300	16.8	80.0	1000	4	BX426989	BX426989	C 373	16.4	78.1	484	9	DA371442	DA371442 DA371442
C 301	16.8	80.0	1021	12	CC690836	OGVAs45TV	C 374	16.4	78.1	488	11	AQ665273	AQ665273 HS_2119_B
C 302	16.8	80.0	1064	8	CV477853	57798.1.D	C 375	16.4	78.1	495	1	A1821162	A1821162 ae34d12.Y
C 303	16.8	80.0	1102	5	DQ035966	Homo sapi	C 376	16.4	78.1	504	11	AZ067960	AZ067960 RPTCI-23-4
C 304	16.8	80.0	1120	5	CD359084	AGENCOURT	C 377	16.4	78.1	505	4	CB847218	CB847218 M2PN-2898
C 305	16.8	80.0	1259	10	DT963146	CFW185-C0	C 378	16.4	78.1	512	4	CB327124	CB327124 UI-R-F80-
C 306	16.8	80.0	1321	14	DQ034240	Homo sapi	C 379	16.4	78.1	514	9	DN875454	DN875454 na639G02-
C 307	16.8	80.0	1347	14	DQ049849	Homo sapi	C 380	16.4	78.1	515	3	BQ207889	BQ207889 UI-R-DY1-
C 308	16.8	80.0	1347	14	DQ049850	Pan trogl	C 381	16.4	78.1	517	9	DB267404	DB267404 DB267404
C 309	16.8	80.0	2112	14	DQ036751	Homo sapi	C 382	16.4	78.1	522	9	DB304390	DB304390 DB304390
C 310	16.8	80.0	2567	6	HSW805088	Homo sapi	C 383	16.4	78.1	523	4	BX747093	BX747093 BX747093
C 311	16.8	80.0	2571	14	DQ032195	Homo sapi	C 384	16.4	78.1	523	7	AV866960	AV866960 AV866960

385	16.4	78.1	525	9	DA792831	DA792831	DA792831	458	16.4	78.1	582	3	BP231865	BP231865
C 386	16.4	78.1	529	3	BP471932	BP471932	BP471932	459	16.4	78.1	582	3	BP248499	BP248499
387	16.4	78.1	531	9	DA768153	DA768153	DA768153	460	16.4	78.1	582	3	BP361056	BP361056
388	16.4	78.1	532	9	DA698633	DA698633	DA698633	461	16.4	78.1	582	9	DA723919	DA723919
389	16.4	78.1	532	9	DB021779	DB021779	DB021779	462	16.4	78.1	582	9	DA777225	DA777225
390	16.4	78.1	540	9	DA924363	DA924363	DA924363	463	16.4	78.1	583	3	BP201364	BP201364
391	16.4	78.1	540	9	DA924363	DA924363	DA924363	464	16.4	78.1	583	3	BP231435	BP231435
C 392	16.4	78.1	542	11	AQ771850	AQ771850	AQ771850	465	16.4	78.1	583	3	BP259497	BP259497
393	16.4	78.1	542	9	AM141875	AM141875	AM141875	466	16.4	78.1	583	3	BP341386	BP341386
C 394	16.4	78.1	544	11	AQ980280	AQ980280	AQ980280	467	16.4	78.1	583	3	BP364595	BP364595
395	16.4	78.1	544	9	DB001371	DB001371	DB001371	468	16.4	78.1	583	3	DA445862	DA445862
396	16.4	78.1	545	9	DA505956	DA505956	DA505956	469	16.4	78.1	583	9	DA630941	DA630941
397	16.4	78.1	546	9	DA508648	DA508648	DA508648	470	16.4	78.1	584	3	BP194871	BP194871
398	16.4	78.1	548	9	DA910445	DA910445	DA910445	471	16.4	78.1	587	7	DA734698	DA734698
399	16.4	78.1	550	9	DA626981	DA626981	DA626981	472	16.4	78.1	588	7	AM916852	AM916852
400	16.4	78.1	553	9	DA381889	DA381889	DA381889	473	16.4	78.1	589	9	DA933911	DA933911
401	16.4	78.1	553	9	DA623795	DA623795	DA623795	474	16.4	78.1	589	9	DA937723	DA937723
402	16.4	78.1	554	9	DB104094	DB104094	DB104094	475	16.4	78.1	590	9	DA977060	DA977060
403	16.4	78.1	555	9	DA650490	DA650490	DA650490	476	16.4	78.1	591	9	DA583407	DA583407
404	16.4	78.1	555	9	DA950489	DA950489	DA950489	477	16.4	78.1	593	3	BP310697	BP310697
405	16.4	78.1	556	9	DA691935	DA691935	DA691935	478	16.4	78.1	594	9	DA925401	DA925401
406	16.4	78.1	557	9	DA889406	DA889406	DA889406	479	16.4	78.1	595	3	BP217924	BP217924
407	16.4	78.1	558	3	BP258774	BP258774	BP258774	480	16.4	78.1	602	9	DA528874	DA528874
408	16.4	78.1	558	9	DA498418	DA498418	DA498418	481	16.4	78.1	606	9	DA528976	DA528976
409	16.4	78.1	558	9	DA503987	DA503987	DA503987	C 482	16.4	78.1	607	2	BM488516	BM488516
C 410	16.4	78.1	559	9	DA713778	DA713778	DA713778	483	16.4	78.1	611	9	DA532466	DA532466
C 411	16.4	78.1	559	13	CL420322	CL420322	CL420322	484	16.4	78.1	618	3	BP789225	BP789225
412	16.4	78.1	560	9	DA509509	DA509509	DA509509	485	16.4	78.1	619	1	AA891825	AA891825
413	16.4	78.1	560	9	DA705101	DA705101	DA705101	486	16.4	78.1	623	2	BM487432	BM487432
414	16.4	78.1	560	9	DA876112	DA876112	DA876112	C 487	16.4	78.1	627	11	BM218981	BM218981
415	16.4	78.1	561	9	DA495960	DA495960	DA495960	C 488	16.4	78.1	629	12	CE273665	CE273665
416	16.4	78.1	561	9	DB114581	DB114581	DB114581	C 489	16.4	78.1	634	10	DV714583	DV714583
417	16.4	78.1	561	9	DB174033	DB174033	DB174033	490	16.4	78.1	636	4	CB576913	CB576913
418	16.4	78.1	562	9	DA287038	DA287038	DA287038	C 491	16.4	78.1	637	8	CV798019	CV798019
419	16.4	78.1	562	9	DA514950	DA514950	DA514950	C 492	16.4	78.1	638	2	BM425215	BM425215
C 420	16.4	78.1	562	11	A2113248	A2113248	A2113248	493	16.4	78.1	640	14	AG140667	AG140667
421	16.4	78.1	563	4	CB608993	CB608993	CB608993	C 494	16.4	78.1	645	5	CK842934	CK842934
422	16.4	78.1	563	9	DA888920	DA888920	DA888920	C 495	16.4	78.1	648	4	CB557905	CB557905
423	16.4	78.1	564	9	DA573926	DA573926	DA573926	C 496	16.4	78.1	650	8	CV117086	CV117086
424	16.4	78.1	565	9	DA423450	DA423450	DA423450	C 497	16.4	78.1	651	14	CR194491	CR194491
425	16.4	78.1	565	9	DA521315	DA521315	DA521315	C 498	16.4	78.1	657	2	BM491439	BM491439
426	16.4	78.1	567	9	DA906606	DA906606	DA906606	C 499	16.4	78.1	659	4	EX264641	EX264641
427	16.4	78.1	568	9	DA599325	DA599325	DA599325	500	16.4	78.1	662	4	CB557219	CB557219
428	16.4	78.1	568	9	DA910212	DA910212	DA910212	501	16.4	78.1	663	4	CA039235	CA039235
429	16.4	78.1	569	9	DA064525	DA064525	DA064525	502	16.4	78.1	664	7	BB627612	BB627612
430	16.4	78.1	570	9	DA022462	DA022462	DA022462	503	16.4	78.1	670	9	DN990080	DN990080
431	16.4	78.1	570	9	DA202995	DA202995	DA202995	504	16.4	78.1	671	4	BM833013	BM833013
432	16.4	78.1	571	3	BP265536	BP265536	BP265536	C 505	16.4	78.1	671	4	CA505079	CA505079
433	16.4	78.1	571	9	DA208576	DA208576	DA208576	506	16.4	78.1	679	10	DT651253	DT651253
434	16.4	78.1	571	9	DA655249	DA655249	DA655249	C 507	16.4	78.1	687	11	CV112769	CV112769
435	16.4	78.1	571	9	DA745389	DA745389	DA745389	C 508	16.4	78.1	687	11	A2113970	A2113970
436	16.4	78.1	572	3	BP342841	BP342841	BP342841	509	16.4	78.1	695	5	CK364996	CK364996
437	16.4	78.1	572	9	DA045948	DA045948	DA045948	C 510	16.4	78.1	698	4	CA504797	CA504797
438	16.4	78.1	573	9	DA491815	DA491815	DA491815	511	16.4	78.1	705	14	CT128902	CT128902
439	16.4	78.1	573	9	DA503438	DA503438	DA503438	C 512	16.4	78.1	709	11	A2249416	A2249416
440	16.4	78.1	575	9	DA024655	DA024655	DA024655	513	16.4	78.1	710	14	AX960057	AX960057
441	16.4	78.1	575	9	DA921731	DA921731	DA921731	514	16.4	78.1	712	14	CR132715	CR132715
442	16.4	78.1	576	3	BP341322	BP341322	BP341322	515	16.4	78.1	719	5	CK473502	CK473502
443	16.4	78.1	576	9	DA749024	DA749024	DA749024	516	16.4	78.1	726	14	AG124297	AG124297
444	16.4	78.1	577	9	DA956272	DA956272	DA956272	C 517	16.4	78.1	733	14	AG556303	AG556303
445	16.4	78.1	578	13	DU396069	DU396069	DU396069	518	16.4	78.1	739	5	CK474031	CK474031
446	16.4	78.1	579	9	DA182483	DA182483	DA182483	C 519	16.4	78.1	740	4	CA505151	CA505151
447	16.4	78.1	579	9	DA773171	DA773171	DA773171	520	16.4	78.1	745	9	DR104545	DR104545
448	16.4	78.1	580	3	BP212410	BP212410	BP212410	521	16.4	78.1	747	8	CO566455	CO566455
449	16.4	78.1	580	3	DA814839	DA814839	DA814839	C 522	16.4	78.1	748	3	BU330457	BU330457
450	16.4	78.1	581	3	BP207608	BP207608	BP207608	C 523	16.4	78.1	750	8	CV118913	CV118913
451	16.4	78.1	581	3	BP349019	BP349019	BP349019	524	16.4	78.1	763	8	CO559916	CO559916
452	16.4	78.1	581	9	DA789092	DA789092	DA789092	C 525	16.4	78.1	766	3	BU529678	BU529678
453	16.4	78.1	581	9	DA960607	DA960607	DA960607	526	16.4	78.1	769	5	CK479961	CK479961
454	16.4	78.1	581	9	DA268868	DA268868	DA268868	527	16.4	78.1	782	8	CV116411	CV116411
455	16.4	78.1	582	3	BP194201	BP194201	BP194201	528	16.4	78.1	788	3	BQ215520	BQ215520
456	16.4	78.1	582	3	BP198827	BP198827	BP198827	529	16.4	78.1	793	5	CK461578	CK461578
457	16.4	78.1	582	3	BP212749	BP212749	BP212749	530	16.4	78.1	797	5	CK481874	CK481874

531	16.4	78.1	797	5	CK482101	CK482101	AGENCYCOURT	604	16.2	77.1	434	4	CB139911	CB139911 K-EST0193
532	16.4	78.1	802	5	CK479753	CK479753	SUB SCOTOF	605	16.2	77.1	437	7	CB269298	CB269298 1008205 H
533	16.4	78.1	808	14	CT325336	CT325336	AGENCYCOURT	606	16.2	77.1	441	7	BE505302	BE505302 dc21c09.x
534	16.4	78.1	813	5	CK482490	CK482490	AGENCYCOURT	607	16.2	77.1	443	7	BE159594	BE159594 601769092
535	16.4	78.1	814	4	CB324516	CB324516	UI-R-D20-	608	16.2	77.1	445	9	DA261632	DA261632 DA261632
536	16.4	78.1	814	4	DA647255	DA647255	AGENCYCOURT	609	16.2	77.1	452	11	AZ781035	AZ781035 2M0018H24
537	16.4	78.1	817	5	CK482570	CK482570	AGENCYCOURT	610	16.2	77.1	455	9	DA250697	DA250697 DA250697
538	16.4	78.1	818	5	DN838785	DN838785	AGENCYCOURT	611	16.2	77.1	461	3	BO556749	BO556749 H4041H10-
539	16.4	78.1	822	10	DY318024	DY318024	AGENCYCOURT	612	16.2	77.1	466	7	BE115554	BE115554 UI-R-BJ1-
540	16.4	78.1	827	5	CK472266	CK472266	AGENCYCOURT	613	16.2	77.1	470	10	DT704625	DT704625 B13dPACIA
541	16.4	78.1	828	10	DT238065	DT238065	UI-R-CAAT1	614	16.2	77.1	472	11	AQ060824	AQ060824 CIT-HSP-2
542	16.4	78.1	831	14	CT166491	CT166491	SUB SCOTOF	615	16.2	77.1	474	4	AA166665	AA166665 zq41a07.s
543	16.4	78.1	842	9	DA568086	DA568086	AGENCYCOURT	616	16.2	77.1	474	4	CA578459	CA578459 K0724A12-
544	16.4	78.1	852	13	DUI341736	DUI341736	109831304	617	16.2	77.1	475	1	AV605254	AV605254 AV605254
545	16.4	78.1	857	14	CR203679	CR203679	FORWARD 8	618	16.2	77.1	477	1	AI177938	AI177938 EST21589
546	16.4	78.1	870	7	BE74045	BE74045	602137442	619	16.2	77.1	477	9	DA307093	DA307093 DA307093
547	16.4	78.1	904	12	CC431898	CC431898	PUDHOK25TD	620	16.2	77.1	478	7	BF386117	BF386117 UI-R-CAL-
548	16.4	78.1	914	10	DM088580	DM088580	CLPPI1391	621	16.2	77.1	481	1	AA138618	AA138618 mq79f02.x
549	16.4	78.1	921	3	BP383250	BP383250	BP383250	622	16.2	77.1	485	4	CA573362	CA573362 K0600A05-
550	16.4	78.1	935	2	BF782761	BF782761	602107614	623	16.2	77.1	485	13	CM044951	CM044951 104.281.1
551	16.4	78.1	1103	12	CC276664	CC276664	CH261-149	624	16.2	77.1	487	14	AG933517	AG933517 DROGPHIL
552	16.4	78.1	1121	10	DV075650	DV075650	WT1291191	625	16.2	77.1	488	14	AG269849	AG269849 CYNADIOS
553	16.4	78.1	1151	5	CD506071	CD506071	CDA77-B12	626	16.2	77.1	489	8	CR560701	CR560701 CR560701
554	16.4	78.1	1212	9	DR124657	DR124657	49196059	627	16.2	77.1	490	12	CG502569	CG502569 OST47794
555	16.4	78.1	1326	7	BB899945	BB899945	BB899945	628	16.2	77.1	495	2	BJ097106	BJ097106 BJ097106
556	16.4	78.1	1481	6	AK161883	AK161883	MUS MUSCU	629	16.2	77.1	500	11	AZ142237	AZ142237 SP.0040_B
557	16.4	78.1	1585	6	CP111060	CP111060	SHULTZCOMI	630	16.2	77.1	503	11	AQ701610	AQ701610 HS_2125_A
558	16.4	78.1	2963	6	AK137156	AK137156	MUS MUSCU	631	16.2	77.1	504	4	CA570071	CA570071 K0501B03-
559	16.2	77.1	171	7	BE180286	BE180286	RC3-HT062	632	16.2	77.1	507	11	AQ5311821	AQ5311821 RPT11-10
560	16.2	77.1	182	11	B2223367	B2223367	CH230-361	633	16.2	77.1	507	11	AO3512136	AO3512136 RPT1-11-4
561	16.2	77.1	245	14	DB007248	DB007248	BRANCHLOS	634	16.2	77.1	508	3	BP460438	BP460438 BP460438
562	16.2	77.1	247	11	AZ457494	AZ457494	1M0250A24	635	16.2	77.1	510	1	AL705190	AL705190 DKF2P660
563	16.2	77.1	249	7	AM800556	AM800556	MR2-UM006	636	16.2	77.1	513	5	CD318800	CD318800 STRP538
564	16.2	77.1	251	14	DE253900	DE253900	OXYZ1AB 1	637	16.2	77.1	514	11	BH005231	BH005231 BMEAC09E1
565	16.2	77.1	259	2	BG234958	BG234958	DAB65C05.	638	16.2	77.1	518	3	BP473848	BP473848 BP473848
566	16.2	77.1	271	1	AA694315	AA694315	2147B02.8	639	16.2	77.1	522	1	AI556435	AI556435 UI-R-C2P-
567	16.2	77.1	274	8	CN286269	CN286269	170004245	640	16.2	77.1	522	2	BI995744	BI995744 1031029G1
568	16.2	77.1	278	7	AM813519	AM813519	RC1-ST019	641	16.2	77.1	525	1	AL699675	AL699675 DKF2P66P
569	16.2	77.1	287	7	BE152432	BE152432	BB492040	642	16.2	77.1	525	8	CR539725	CR539725 LIBA216-C
570	16.2	77.1	288	7	BE150014	BE150014	QV3-HT026	643	16.2	77.1	526	8	DA221253	DA221253 DKF2P66P
571	16.2	77.1	290	11	AZ380597	AZ380597	1M0136A08	644	16.2	77.1	527	9	DA221253	DA221253 DA221253
572	16.2	77.1	302	11	CP562475	CP562475	1115075A1	645	16.2	77.1	528	8	CR746528	CR746528 CR746528
573	16.2	77.1	324	5	AZ465302	AZ465302	1M0275F12	646	16.2	77.1	530	3	BO814661	BO814661 1030045A0
574	16.2	77.1	325	11	AQ397091	AQ397091	mq9D0019N	647	16.2	77.1	531	11	B85877	B85877 RPT11-21F1
575	16.2	77.1	328	11	CV427396	CV427396	RC6-FN002	648	16.2	77.1	531	14	CG162445	CG162445 PUTCQ69T
576	16.2	77.1	335	8	BE725688	BE725688	894085G07	649	16.2	77.1	531	12	DE048405	DE048405 OXYZ1AB 1
577	16.2	77.1	336	7	BE725688	BE725688	894085G07	650	16.2	77.1	531	14	DE048405	DE048405 OXYZ1AB 1
578	16.2	77.1	340	10	DR979024	DR979024	SM013387	651	16.2	77.1	533	1	A1048579	A1048579 ud61e11.Y
579	16.2	77.1	345	1	AA452553	AA452553	zx35F08.8	652	16.2	77.1	533	9	DA277293	DA277293 DA277293
580	16.2	77.1	352	12	CG547293	CG547293	OST147858	653	16.2	77.1	539	9	DB172127	DB172127 DB172127
581	16.2	77.1	353	11	AQ903616	AQ903616	G8STC0465	654	16.2	77.1	540	9	DB365009	DB365009 DB365009
582	16.2	77.1	371	12	CG582451	CG582451	OST223646	655	16.2	77.1	542	9	DA628110	DA628110 DA628110
583	16.2	77.1	376	7	BF393678	BF393678	UI-R-CA0-	656	16.2	77.1	547	2	BO375466	BO375466 UI-R-CV1-
584	16.2	77.1	377	7	BF414684	BF414684	UI-R-BJ2-	657	16.2	77.1	548	7	BE101148	BE101148 UI-R-BJ1-
585	16.2	77.1	382	5	CJ296998	CJ296998	CJ296998	658	16.2	77.1	548	11	BH330400	BH330400 CR230-188
586	16.2	77.1	383	12	BZ754860	BZ754860	PUDH122TB	659	16.2	77.1	551	9	DA285216	DA285216 DA285216
587	16.2	77.1	391	11	AZ716895	AZ716895	RPT1-24-8	660	16.2	77.1	551	9	DA360427	DA360427 DA360427
588	16.2	77.1	396	12	BZ754861	BZ754861	PUDH122TD	661	16.2	77.1	555	1	AV612421	AV612421 AV612421
589	16.2	77.1	397	2	BI299726	BI299726	UI-R-CV2-	662	16.2	77.1	556	10	DY206784	DY206784 000705BSP
590	16.2	77.1	401	2	BI298615	BI298615	UI-R-CV2-	663	16.2	77.1	556	11	BH107707	BH107707 RPT1-24-3
591	16.2	77.1	402	2	BG060863	BG060863	10909D08-	664	16.2	77.1	557	2	BI728965	BI728965 1031102P1
592	16.2	77.1	405	5	CJ183817	CJ183817	CJ183817	665	16.2	77.1	557	9	DA299380	DA299380 DA299380
593	16.2	77.1	408	2	BM002325	BM002325	1031102P1	666	16.2	77.1	557	9	DB343857	DB343857 DB343857
594	16.2	77.1	410	7	AW917615	AW917615	EST348919	667	16.2	77.1	558	1	AV640718	AV640718 AV640718
595	16.2	77.1	410	10	DY183335	DY183335	000306BSP	668	16.2	77.1	558	3	BP275894	BP275894 BP275894
596	16.2	77.1	415	2	BI294597	BI294597	UI-R-DKO-	669	16.2	77.1	559	3	BP457311	BP457311 BP457311
597	16.2	77.1	423	1	AI523758	AI523758	HS 3026.B	670	16.2	77.1	559	1	AA452738	AA452738 zx35F08.x
598	16.2	77.1	425	11	AQ094565	AQ094565	HS 3026.B	671	16.2	77.1	559	9	DA288697	DA288697 DA288697
599	16.2	77.1	426	7	BE505329	BE505329	dc21h07.x	672	16.2	77.1	560	9	DA624410	DA624410 DA624410
600	16.2	77.1	429	2	BU035983	BU035983	BU035983	673	16.2	77.1	562	9	DA154710	DA154710 DA154710
601	16.2	77.1	429	11	AQ169855	AQ169855	HS 3181.B	674	16.2	77.1	563	9	DA312379	DA312379 DA312379
602	16.2	77.1	432	4	CB756937	CB756937	AMGNNUC:IS	675	16.2	77.1	564	9	DA255125	DA255125 DA255125
603	16.2	77.1	434	4	CB137840	CB137840	K-EST0190	676	16.2	77.1	566	1	AV605437	AV605437 AV605437

C 677	16.2	77.1	566	9	DB052567	DB052567	750	16.2	77.1	708	5	CK844841	CK844841 UI-R-BU1-
678	16.2	77.1	567	9	DB016191	DB016191	751	16.2	77.1	710	2	B1765823	B1765823 60304736
679	16.2	77.1	569	9	DA872979	DA872979	752	16.2	77.1	712	2	BJ300986	BJ300986 BU300986
680	16.2	77.1	570	9	DA635677	DA635677	753	16.2	77.1	715	1	AJ398260	AJ398260 AJ398260
681	16.2	77.1	573	9	DA250899	DA250899	754	16.2	77.1	722	4	BX849228	BX849228 BX849228
682	16.2	77.1	574	9	DA363747	DA363747	755	16.2	77.1	722	4	DU305883	DU305883 109844834
C 683	16.2	77.1	574	11	A2080747	DA2080747 RPTC1-23-3	756	16.2	77.1	723	13	CM242330	CM242330 104_702_1
684	16.2	77.1	575	9	DA621554	DA621554	C 757	16.2	77.1	725	13	C2267913	C2267913 bee09_LBI
685	16.2	77.1	576	9	DA363755	DA363755	C 758	16.2	77.1	730	12	B2628245	B2628245 1hs5810_L
686	16.2	77.1	577	13	C2450603	C2450603 MCF731G02	C 759	16.2	77.1	735	11	AG894886	AG894886 HS_3072_B
C 687	16.2	77.1	578	14	DX227822	DX227822 OR_ABA010	C 760	16.2	77.1	737	12	CG271176	CG271176 OQDB90TH
C 688	16.2	77.1	579	9	DA435581	DA435581	C 761	16.2	77.1	739	8	CY089075	CY089075 est_C_v1r
689	16.2	77.1	580	9	DA577702	DA577702	762	16.2	77.1	739	10	DT143197	DT143197 UGI_ANN02
C 690	16.2	77.1	580	13	DA634019	DA634019	763	16.2	77.1	739	14	AG593353	AG593353 Mus muscu
691	16.2	77.1	580	13	CM911220	CM911220 RPTC142_15	764	16.2	77.1	740	14	AG469616	AG469616 Mus muscu
C 692	16.2	77.1	585	1	AL710792	AL710792 DKP686G	C 765	16.2	77.1	741	3	BU622955	BU622955 UI-H-FL1-
C 693	16.2	77.1	586	2	BM179592	BM179592 da109f12.	C 766	16.2	77.1	743	8	CO394871	CO394871
C 694	16.2	77.1	588	7	BR614243	BR614243 de03g09.Y	C 767	16.2	77.1	746	10	DR624986	DR624986 BSR101511
C 695	16.2	77.1	593	3	BQ814662	BQ814662 1030045A0	C 768	16.2	77.1	747	14	CR077565	CR077565 Forward B
C 696	16.2	77.1	596	13	AQ275003	AQ275003 RPTC1-5-84	C 769	16.2	77.1	749	4	CA050418	CA050418 BSR102163
C 697	16.2	77.1	596	11	AQ275003	AQ275003 RPTC1-5-84	C 770	16.2	77.1	748	5	CD650278	CD650278 CVG110098
C 698	16.2	77.1	598	13	CA408418	CA408418 1004121.R	C 771	16.2	77.1	749	4	CA050418	CA050418 BSR102163
C 699	16.2	77.1	599	5	CF793403	CF793403 888787.MA	C 772	16.2	77.1	752	5	CE547419	CE547419 AGENCOURT
C 700	16.2	77.1	599	7	BR041844	BR041844 BP250024B	C 773	16.2	77.1	755	5	CD650417	CD650417 CVG110112
C 701	16.2	77.1	600	11	BH005033	BH005033 BMBAC08P1	C 774	16.2	77.1	755	12	CC993589	CC993589 ZDNEK43TV
C 702	16.2	77.1	601	8	CV088809	CV088809 est_C_v1r	C 775	16.2	77.1	755	13	DU361353	DU361353 109831300
C 703	16.2	77.1	601	11	AQ601492	AQ601492 HS_2110_A	C 776	16.2	77.1	756	10	DT818286	DT818286 LB0169_CR
C 704	16.2	77.1	603	1	AL779866	AL779866 AL779866	C 777	16.2	77.1	758	13	CZ898496	CZ898496 216_1_123
C 705	16.2	77.1	603	7	AM850315	AM850315 IL3-CR021	C 778	16.2	77.1	760	10	BG919927	BG919927 602821428
C 706	16.2	77.1	608	13	CL459651	CL459651 PHCRC-GT-	C 779	16.2	77.1	760	10	DT107950	DT107950 UGI_ANN08
C 707	16.2	77.1	614	1	AL645354	AL645354 AL645354	C 780	16.2	77.1	761	11	AZ265840	AZ265840 RPTC1-23-1
C 708	16.2	77.1	614	2	BI274618	BI274618 UI-R-CX0-	C 781	16.2	77.1	761	14	AG413343	AG413343 Mus muscu
C 709	16.2	77.1	614	5	CF947217	CF947217 UI-D-GC1-	C 782	16.2	77.1	763	11	AZ793244	AZ793244 2M0046N18
C 710	16.2	77.1	616	4	CA515561	CA515561 622654_NC	C 783	16.2	77.1	766	1	A1596599	A1596599 ml62e01.Y
C 711	16.2	77.1	617	11	AZ783281	AZ783281 2M0024P18	C 784	16.2	77.1	766	5	CK488008	CK488008 BSR777323
C 712	16.2	77.1	617	11	BH262549	BH262549 CR230_121	C 785	16.2	77.1	766	5	CK488069	CK488069 AGENCOURT
C 713	16.2	77.1	622	11	AZ874790	AZ874790 2M0189105	C 786	16.2	77.1	774	12	BZ989319	BZ989319 PUBKH54TD
C 714	16.2	77.1	623	2	BI296464	BI296464 UI-R-CV2-	C 787	16.2	77.1	777	14	DE098393	DE098393 Oryzias 1
C 715	16.2	77.1	627	13	CM120091	CM120091 104_497_1	C 788	16.2	77.1	778	10	DT115785	DT115785 JGI_ANN03
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C 718	16.2	77.1	630	5	CP774683	CP774683 UI-D-GC1-	C 791	16.2	77.1	782	10	DT161764	DT161764 JGI_ANN03
C 719	16.2	77.1	631	3	BQ082434	BQ082434 K-BST0108	C 792	16.2	77.1	783	4	CB596299	CB596299 AGENCOURT
C 720	16.2	77.1	631	5	CK433824	CK433824 UI-D-GC1-	C 793	16.2	77.1	784	2	BG208478	BG208478 RST77980
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C 722	16.2	77.1	637	1	AL641336	AL641336 AL641336	C 795	16.2	77.1	787	8	CV121517	CV121517 AGENCOURT
C 723	16.2	77.1	640	11	AQ316243	AQ316243 RPTC11-10	C 796	16.2	77.1	788	11	BZ227672	BZ227672 CH230-305
C 724	16.2	77.1	644	14	BX224959	BX224959 Danilo rer	C 797	16.2	77.1	789	8	BM967393	BM967393 est_C_v1r
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C 873	16.2	77.1	1029	14	DU749262	DU749262	AGENCOURT	C 946	15.8	75.2	312	3	BU736497	BU736497 UI-E-CL1-
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ORIGIN

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REFERENCE 1 (bases 1 to 229)
AUTHORS  Kono,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T.,
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TITLE JOURNAL COMMENT	
	<p>Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Saito, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shingawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomimaga, N., Toyota, T., Tsunoda, Y., Wachihi, A., Watanabe, S., Yamamura, T., Yamaneke, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.</p> <p>RIKEN Mouse ESTs (Kono, H., et al.)</p> <p>Unpublished (2000)</p> <p>Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216</p> <p>Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/ Carinci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Thermosensitization and thermoactivation of thermostable enzymes by trehalose and its application for the synthesis of full length cDNA. <i>Proc. Natl. Acad. Sci. U.S.A.</i> 95 (2), 520-524 (1998)</p> <p>Itoh, M., Kitsuai, T., Akiyama, J., Shibata, K., Iwawa, M., Kawai, J., Tomaru, Y., Carinci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y., and Hayashizaki, Y. Automated filtration-based high-throughput plasmid preparation system. <i>Genome Res.</i> 9 (5), 463-470 (1999)</p> <p>Carinci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning. <i>Methods Enzymol.</i> 303, 13-44 (1999)</p> <p>Please visit our web site (http://genome.riken.go.jp) for further details.</p>

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 GAGAGAGAGAGATCCAGAGCTTTTCTTTTCTTTTCTTTT 3', cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGATTCCTGAGTTATTTATTTATCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pluescript KS(+) after bulk excision from Lambda FLC I."

ORIGIN

Query Match 87.6%; Score 18.4; DB 7; Length 229;
 Best Local Similarity 95.0%; Pred. No. 6.6e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AGGACACAGTGGCTTTGAC 21
 Db 93 AGGACACAGTGGCTTTGAC 112

RESULT 3
 BB264006 291 bp mRNA linear EST 07-JUL-2000
 LOCUS BB264006 RIKEN full-length enriched, 10 days neonate cortex Mus
 DEFINITION musculus cDNA clone A830013L24 3' similar to X95600 M.musculus mRNA for cadherin-8, mRNA sequence.

ACCESSION BB264006.1 GI:8960462
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.

1 (bases 1 to 291)
 Komno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koyu, S., Kurihara, C., Kuwabara, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomioka, N., Toyota, T., Tsunoda, Y., Watabiki, A., Watanabe, S., Yamamura, T., Yamane, K., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

RIKEN Mouse ESTs (Komno, H., et al.)
 Unpublished (2000)

TITLE JOURNAL
 COMMENT Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suenho-cho, Tsunumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/

FEATURES

source

Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Thermo-stabilization and thermolysis of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
 Itoh, M., Katsunari, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
 Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
 Please visit our web site (http://genome.rtc.riken.go.jp) for further details.

Location/Qualifiers

1..291

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="A830013L24"

/tissue_type="cortex"

/dev_stage="10 days neonate"

/lab_host="DH10B"

/clone_lib="RIKEN full-length enriched, 10 days neonate cortex"

/note="Site 1: SalI; Site 2: BamHI. cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5']
 GAGAGAGAGAGATCCAGAGCTTTTCTTTTCTTTTCTTTT 3', cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGATTCCTGAGTTATTTATTTATCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pluescript KS(+) after bulk excision from Lambda FLC I."

ORIGIN

Query Match 87.6%; Score 18.4; DB 7; Length 291;
 Best Local Similarity 95.0%; Pred. No. 6.8e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AGGACACAGTGGCTTTGAC 21
 Db 150 AGGACACAGTGGCTTTGAC 169

RESULT 4
 BB347346 291 bp mRNA linear EST 12-JUL-2000
 LOCUS BB347346 RIKEN full-length enriched, 10 days neonate cerebellum Mus
 DEFINITION musculus cDNA clone B930065F09 3' similar to X95600 M.musculus mRNA for cadherin-8, mRNA sequence.

ACCESSION BB347346.1 GI:9059174
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.

1 (bases 1 to 291)
 Komno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,

Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M., Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A., Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S. Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes

JOURNAL PUBMED
Genome Res. 16 (1), 55-65 (2006)
16344560

COMMENT

Contact: Takao Isogai
FLJ Project (HRI Team)
Helix Research Institute
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Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: flj-cdna@nifty.com
NEO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.
Location/Qualifiers

FEATURES

source

1..546
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="FEBRA2002360"
/tissue_type="brain"
/dev_stage="fetal"
/clone_1lb="FEBRA2"
/note="Vector: pME18SFL3"

ORIGIN

Query Match 87.6%; Score 18.4; DB 9; Length 546;
Best Local Similarity 95.0%; Pred. No. 7.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 1 CAGGACAGCTGCGCTTTGA 20
|||||
Db 220 CAGGACTCAGTGGCTTTGA 239

RESULT 7

LOCUS

DA722798 549 bp mRNA linear EST 15-NOV-2005
DEFINITION DA722798 NT2R13 Homo sapiens cDNA clone NT2R13003688 5', mRNA sequence.

ACCESSION

VERSION

DA722798.1 GI:82437260

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo
1 (bases 1 to 549)

REFERENCE

AUTHORS

Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T., Yamashita, R., Yamamoto, J., Sekine, M., Teurillac, K., Wakaguri, H., Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushiida, N., Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M., Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A., Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S. Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes

TITLE

JOURNAL PUBMED
Genome Res. 16 (1), 55-65 (2006)
16344560

COMMENT

Contact: Takao Isogai
FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986

Email: flj-cdna@nifty.com
NEO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.
Location/Qualifiers

FEATURES

source

1..549
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2R13003688"
/cell_type="teratocarcinoma"
/cell_line="NT2"
/clone_1lb="NT2R13"
/note="Vector: pME18SFL3; majorly NT2 neuron; mRNA from NT2 neuronal precursor cells treated 2-weeks mitotic inhibitor after 5-weeks retinoic acid (RA) induction"

ORIGIN

Query Match 87.6%; Score 18.4; DB 9; Length 549;
Best Local Similarity 95.0%; Pred. No. 7.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 1 CAGGACAGCTGCGCTTTGA 20
|||||
Db 220 CAGGACTCAGTGGCTTTGA 239

RESULT 8

LOCUS

DA906377 583 bp mRNA linear EST 03-DEC-2005
DEFINITION DA906377 SKNMC2 Homo sapiens cDNA clone SKNMC2007458 5', mRNA sequence.

ACCESSION

VERSION

DA906377.1 GI:83037875

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo
1 (bases 1 to 583)

REFERENCE

AUTHORS

Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T., Yamashita, R., Yamamoto, J., Sekine, M., Teurillac, K., Wakaguri, H., Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushiida, N., Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M., Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A., Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S. Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes

TITLE

JOURNAL PUBMED
Genome Res. 16 (1), 55-65 (2006)
16344560

COMMENT

Contact: Takao Isogai
FLJ Project (HRI Team)
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2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
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Fax: 81-438-52-3986
Email: flj-cdna@nifty.com
NEO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.
Location/Qualifiers

FEATURES

source

1..583
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 87.6%; Score 18.4; DB 9; Length 583;
 Best Local Similarity 95.0%; Pred. No. 7.5e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 CAGGACACAGTGGCTTTGA 20
 217 CAGGACTCAGTGGCTTTGA 236

RESULT 9
 BB647218 644 bp mRNA linear EST 26-OCT-2001
 LOCUS BB647218 RIKEN full-length enriched, 10 days neonate cerebellum Mus
 DEFINITION BB647218 musculus cDNA clone B930077M09 5', mRNA sequence.
 BB647218
 VERSION BB647218.1 GI:16481547
 KEYWORDS EST.
 ORGANISM Mus musculus (house mouse)
 SOURCE Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 644)
 Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T.,
 Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,
 Kono, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,
 Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K.,
 Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,
 Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
 Takeda, Y., Tanaka, T., Toyama, T., Muramatsu, M. and Hayashizaki, Y.
 RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
 Unpublished (2001)
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gscc.riken.jp, URL: http://genome.gsc.riken.jp/
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 Wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, B.,
 Watanuki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,
 Matsuda, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A.
 and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,
 Sugahara, Y. and Hayashizaki, Y.
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 Kondo, S., Shingawa, A., Saito, T., Kiyosawa, H., Yamakata, I.,
 Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
 Hayashizaki, Y.
 Computational Analysis of Full-length Mouse cDNAs Compared with
 Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
 Please visit our web site (http://genome.gsc.riken.go.jp) for
 further details.
 e mouse tissues.
 Location/Qualifiers

source

1. 644
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="B930077M09"
 /sex="mixed"
 /tissue_type="cerebellum"
 /dev_stage="10 days neonate"
 /lab_host="DHI0B"
 /clone_lib="RIKEN full-length enriched, 10 days neonate
 cerebellum"
 /note="Site 1: SalI; Site 2: BamHI; cDNA library was
 prepared and sequenced in Mouse Genome Encyclopedia
 Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN. Division of Experimental Animal Research in Riken
 contributed to prepare mouse tissues. 1st strand cDNA was
 primed with a primer [5'
 GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTT 3']. cDNA was
 prepared by using trehalose thermo-activated reverse
 transcriptase and subsequently enriched for full-length by
 cap-trapper. cDNA went through one round of normalization
 to Rot = 10.0 and subtraction to Rot = 100.0. Second
 strand cDNA was prepared with the primer adaptor of
 sequence [5' GAGAGAGAGATTCGATTCGATTAATTAATCCCCCCCC
 3']. cDNA was cloned into the XhoI and BamHI sites.
 Vector: a modified pBluescript KS(+) after bulk excision
 from Lambda phage I. Cloning sites, 5' end: SalI, 3' end:
 BamHI"

ORIGIN

Query Match 87.6%; Score 18.4; DB 7; Length 644;
 Best Local Similarity 95.0%; Pred. No. 7.6e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 CAGGACACAGTGGCTTTGA 20
 83 CAGGACTCAGTGGCTTTGA 102

RESULT 10
 CZ303586 654 bp DNA linear GSS 23-MAR-2005
 LOCUS CZ303586 ZMMBF0080F02c ZMMBF Zea mays genomic clone ZMMBF0080F02 3', genomic
 DEFINITION survey sequence.
 CZ303586
 VERSION CZ303586.1 GI:61729764
 KEYWORDS GSS.
 ORGANISM Zea mays
 Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoidae; Andropogoneae; Zea.
 1 (bases 1 to 654)
 Bharti, A.K., Nelson, A.B., Young, S., Keiser, G., Zohovetz, V., Fuks, G.
 and Messing, J.
 Construction, Sequencing and Characterization of a Fosmid Library
 of the B73 Maize Genome
 Unpublished (2005)
 Contact: Bharti, A.K.
 Dr. Joachim Messing's lab
 The Plant Genome Research Initiative at Rutgers, Waksman Institute, Rutgers
 University
 190 Frelinghuysen Road, Piscataway, NJ 08854, USA
 Tel: 732 445 3801
 Fax: 732 445 5735
 Email: bharti@waksman.rutgers.edu
 Seq primer: Fos R
 Class: fosmid ends.
 Location/Qualifiers

FEATURES
 source
 1. 654
 /organism="Zea mays"

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/mo1_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="ZMABF0080F02"
/lab_host="EPI100-T1"
/clone_1ib="ZMABF"
/note="Vector: pBg1FOS-5; Site_1: Eco72I"

ORIGIN

Query Match      87.6%; Score 18.4; DB 13; Length 654;
Best Local Similarity 95.0%; Pred. No. 7.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 AGGACACAGTGGCTTTGAC 21
    |||||
Db 579 AGGACACAGTGGCTTTGAC 598

RESULT 11
LOCUS C333727 660 bp mRNA linear EST 14-JUN-2005
DEFINITION C333727 Molgula tectiformis unpublished cDNA library Molgula
tectoformis cDNA clone mtbh004d21 3', mRNA sequence.
ACCESSION C333727
VERSION C333727.1 GI:67744326
KEYWORDS EST
SOURCE Molgula tectiformis
ORGANISM Molgula tectiformis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
Stolidobranchia; Molgulidae; Molgula.
REFERENCE 1 (bases 1 to 660)
AUTHORS Gyoja,F., Satou,Y. and Satoh,N.
TITLE Expressed genes in Molgula tectiformis
JOURNAL Unpublished (2005)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp
When you want to obtain this EST clone, please send an e-mail to
Nori Satoh (natosat@acidian.zool.kyoto-u.ac.jp) and its cc to Yutaka
Satou (yutaka@acidian.zool.kyoto-u.ac.jp).
FEATURES
Location/Qualifiers
1..660
/organism="Molgula tectiformis"
/mol_type="mRNA"
/db_xref="taxon:30286"
/clone="mtbh004d21"
/tissue_type="whole animal"
/dev_stage="embryo just before hatching"
/clone_1ib="Molgula tectiformis unpublished cDNA library"

ORIGIN

Query Match      87.6%; Score 18.4; DB 5; Length 660;
Best Local Similarity 95.0%; Pred. No. 7.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CAGGACACAGTGGCTTTGA 20
    |||||
Db 43 CAGGACACAGTGGCTTTGA 62

RESULT 12
LOCUS CD353955 720 bp mRNA linear EST 15-JUL-2003
DEFINITION UT-M-GMO-gga-j-04-0-UI.r1 NIH_BMAP_GMO Mus musculus cDNA clone
IMAGE:30360123 5', mRNA sequence.
ACCESSION CD353955
VERSION CD353955.1 GI:31146456
KEYWORDS EST.
SOURCE Mus musculus (house mouse)

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ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 720)
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA library preparation: Dr. M. Bento Soares, University of Iowa
cDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mouse1.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

Seq primer: PYX-5.
FEATURES
Location/Qualifiers
1..720
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30360123"
/tissue_type="whole brain"
/dev_stage="1, 5 and 15 days newborn"
/lab_host="DH10B (T1 phage resistant)"
/clone_1ib="NIH BMAP GM0"
/note="Organ: Brain; Vector: pYX-Asc; Site 1: Scor I;
Site 2: Not I; The library was constructed according
to Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was size
selected according to mRNA size fraction. Ligated with Scor
I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGACTGAT. This library was created for the University
of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chn, Ph.D.,
program coordinator."

ORIGIN

Query Match      87.6%; Score 18.4; DB 5; Length 720;
Best Local Similarity 95.0%; Pred. No. 7.8e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 AGGACACAGTGGCTTTGAC 21
    |||||
Db 495 AGGACACAGTGGCTTTGAC 514

RESULT 13
LOCUS AY406159 2148 bp DNA linear GSS 15-DEC-2003
DEFINITION Pan troglodytes CDH8 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY406159
VERSION AY406159.1 GI:39762133
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Pan.
REFERENCE 1 (bases 1 to 2148)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tenenbaum,D.M., Civallo,D.R., Lu,P., Murphy,B.,
Fertiera,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.D.,

```

TITLE Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

REFERENCE PUBMED 14671302

AUTHORS 2 (bases 1 to 2148)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tenenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,
Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.

FEATURES Location/Qualifiers

source 1..2148
/organism="Pan troglodytes"
/mol_type="genomic DNA"
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/gene="CDH8"
/locus_tag="HCM2464"

ORIGIN

Query Match 87.6%; Score 18.4; DB 14; Length 2148;
Best Local Similarity 95.0%; Pred. No. 9.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AGGACACAGTGGCTTTGAC 21
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Db 1772 AGGACACAGAGCTTTGAC 1791

RESULT 14

LOCUS AY406158 2400 bp DNA linear GSS 15-DEC-2003

DEFINITION Homo sapiens CDH8 gene, VIRUTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.

ACCESSION AY406158

VERSION AY406158.1 GI:39762132

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo
1 (bases 1 to 2400)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tenenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,
Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

REFERENCE PUBMED 14671302

AUTHORS 2 (bases 1 to 2400)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tenenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,
Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.

FEATURES Location/Qualifiers

source 1..2400
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
<1..>2400
/gene="CDH8"

gene

ORIGIN /locus_tag="HCM2464"

Query Match 87.6%; Score 18.4; DB 14; Length 2400;
Best Local Similarity 95.0%; Pred. No. 9.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AGGACACAGTGGCTTTGAC 21
|||||
Db 2024 AGGACACAGAGCTTTGAC 2043

RESULT 15

LOCUS AY406160 2400 bp DNA linear GSS 15-DEC-2003

DEFINITION Mus musculus CDH8 gene, VIRUTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.

ACCESSION AY406160

VERSION AY406160.1 GI:39762134

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 2400)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tenenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,
Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

REFERENCE PUBMED 14671302

AUTHORS 2 (bases 1 to 2400)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tenenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,
Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.

FEATURES Location/Qualifiers

source 1..2400
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
<1..>2400
/gene="CDH8"
/locus_tag="HCM2464"

gene

ORIGIN

Query Match 87.6%; Score 18.4; DB 14; Length 2400;
Best Local Similarity 95.0%; Pred. No. 9.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AGGACACAGTGGCTTTGAC 21
|||||
Db 2024 AGGACACAGAGCTTTGAC 2043

RESULT 16

LOCUS AK139334 2711 bp mRNA linear HTC 21-SEP-2005

DEFINITION Mus musculus 10 days neonate cortex cDNA, RIKEN full-length
enriched library, clone:A830013124 product:cadherin 8, full insert
sequence.

ACCESSION AK139334

VERSION AK139334.1 GI:74228151

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.
AUTHORS	1 Carninci, P. and Hayashizaki, Y.
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
PUBMED	10349636
REFERENCE	2
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
PUBMED	11042159
REFERENCE	3
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE	RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
PUBMED	11076861
REFERENCE	4
AUTHORS	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Kono, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kato, K., Matsuda, H., Ashburner, M., Batelov, S., Casavant, T., Flatschmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schiml, L.M., Staudli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Botelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.P., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Guelinich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seta, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Whitaker, C., Wilming, L., Wyshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, H., Kohzuki, S. and Hayashizaki, Y.
CONSTRM	RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409 (6821), 685-690 (2001)
PUBMED	11217851
REFERENCE	5
AUTHORS	Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Mikaido, I., Otsu, N., Saito, R., Suzuki, H., Yamana, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schiml, L.M., Kanapin, A., Matwuda, H., Batelov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chochois, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Fraser, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grivomont, S., Guetion, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedierski, R.M., King, B.L., Konagaya, A., Kurachin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., MacLott, D.R., Malate, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Perce, G., Pesole, G., Petrovsky, N., Pillai, R., Portius, U.V., Q.D., Kamachandran, S., Ravasi, T., Reed, D.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sadelin, A., Schneider, C., Semp, J., Setou, M., Shinada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verdardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wyshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirokawa, N., Sato, K., Shiraki, T., Waki, K., Kawai, T., Aizawa, K., Sakazume, N., Fukuda, S., Hara, A., Hashizume, W., Imochi, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.
CONSTRM	PANTOM Consortium
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420 (6915), 563-573 (2002)
PUBMED	12468851
REFERENCE	6
AUTHORS	Carninci, P., Kasukawa, T., Katayama, S., Gough, J., Frith, M.C., Maeda, N., Oyama, R., Ravasi, T., Lenhard, B., Wells, C., Kodzius, R., Shimokawa, K., Bajic, V.B., Bremner, S.E., Batelov, S., Forrest, A.R., Zavolan, M., Davis, M.J., Wilming, L.G., Aldred, V., Allen, J.E., Ambesi-Imbimbato, A., Apweiler, R., Aturaliya, R.N., Bailey, T.L., Banerji, M., Baxter, L., Beisel, K.W., Bersano, T., Bono, H., Chalk, A.M., Chiu, K.P., Choudhary, V., Christoffel, A., Clutterbuck, D.R., Crome, M.L., Dalla, E., Dalrymple, B.P., de Bono, B., Della Gatta, G., di Bernardo, D., Down, T., Engstrom, P., Fagiolini, M., Faulkner, G., Fletcher, C.F., Fukushima, T., Furuno, M., Fukui, S., Gariboldi, M., Georgii-Hemming, P., Gingeras, T.R., Gojobori, T., Green, R.E., Guetion, S., Harbers, M., Hayashizaki, Y., Hensch, T.K., Hirokawa, N., Hill, D., Hummichek, L., Iacono, M., Ieko, K., Iwama, A., Ishikawa, T., Jakt, M., Kanapin, A., Katoh, M., Kawasawa, Y., Kelso, J., Kitano, H., Kitano, H., Kollas, G., Krishnan, S.P., Kruger, A., Kummerfeld, S.K., Kurochkin, I.V., Lareau, L.F., Lazarevic, D., Lipovich, L., Liu, J., Llunsi, S., McMillan, S., Madan, B., Mader, M., Madera, M., Marchionni, L., Matsuda, H., Matsuzawa, S., Miki, H., Mignone, F., Miyake, S., Morita, K., Mottaz, T., Muller, N., Nakano, N., Nakachi, H., Ng, P., Nilsson, R., Nishiguchi, S., Nishikawa, S., Nori, F., Ohara, O., Okazaki, Y., Orlando, V., Pang, K.C., Pavan, W.J., Pavoni, G., Pesole, G., Petrovsky, N., Piazza, S., Reed, J., Reid, J.F., Ring, B.Z., Ringwald, M., Ros, B., Ruan, Y., Salzberg, S.L., Sandelin, A., Schneider, C., Schonbach, C., Sekiguchi, K., Semp, C.A., Seno, S., Sessa, L., Sheng, Y., Shibata, Y., Shimada, H., Shimada, K., Silva, D., Sinclair, B., Sperling, S., Stupka, S., Sugita, K., Sultana, R., Takenaka, Y., Taki, K., Tammoja, K., Tan, S.L., Tang, S., Taylor, M.S., Tegner, J., Teichmann, S.A., Ueda, H.R., van Nimwegen, E., Verdardo, R., Wei, C.L., Yagi, K., Yamashita, H., Zaslavsky, E., Zhu, S., Zimmer, A., Hide, W., Bult, C., Grimmond, S.M., Teasdale, R.D., Liu, E.T., Brusic, V., Quackenbush, J., Wahlestedt, C., Wietick, J.S., Hume, D.A., Kai, C., Sasaki, D., Tomaru, Y., Fukuda, S., Kanamori, Katayama, M., Suzuki, M., Aoki, J., Arakawa, T., Iida, J., Imamura, K., Itoh, M., Kato, T., Kawaji, H., Kawagashira, N., Kawashima, T., Kojima, M., Kondo, S., Kono, H., Nakano, K., Niimura, N., Nishio, T., Okada, M., Plessey, C., Shibata, K., Shiraki, T., Suzuki, S., Tagami, M., Waki, K., Watanabe, A., Okamura-Oho, Y., Suzuki, H., Kawai, J. and Hayashizaki, Y.
CONSTRM	PANTOM Consortium
TITLE	The transcriptional landscape of the mammalian genome
JOURNAL	Science 309 (5740), 1559-1563 (2005)
PUBMED	16141072
REFERENCE	7
AUTHORS	Katayama, S., Tomaru, Y., Kasukawa, T., Waki, K., Nakamichi, M., Nakamura, M., Nishida, H., Yap, C.C., Suzuki, M., Kawai, J., Suzuki, H., Carninci, P., Hayashizaki, Y., Wells, C., Frith, M., Ravasi, T., Pang, K.C., Hallinan, J., Matick, J., Hume, D.A., Lipovich, L., Batelov, S., Engstrom, P.G., Mizuno, Y., Faghihi, M.A., Sadelin, A., Chalk, A.M., Mottaz, T., Tabar, S., Liang, Z., Lenhard, B. and Wahlestedt, C.
CONSTRM	RIKEN Genome Exploration Research Group
TITLE	Antisense transcription in the mammalian transcriptome
JOURNAL	Science 309 (5740), 1564-1566 (2005)
PUBMED	16141073
REFERENCE	8 (bases 1 to 2711)
AUTHORS	Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hori, F., Iida, J., Imamura, K., Imochi, K., Itoh, M., Kanagawa, S., Kawai, J., Kojima, M., Kono, H., Murata, K., Itoh, M., Nakamura, N., Nishiguchi, H., Nomura, K., Ohno, M., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shiraki, T., Tagami, M., Tagami, Y., Waki, K., Watanabe, A.,

TITLE
JOURNAL
 Muramatsu, M. and Hayashizaki, Y.
 Direct Submission
 Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration and Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa, 230-0045, Japan (E-mail: genome-res@gscc.riken.jp,
 URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
 Fax: 81-45-503-9216)
COMMENT
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in Riken.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.jp/
 URL: http://fantom.gsc.riken.jp/
FEATURES
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 QKQEVYLPVIYSDSGNPPLSTSTLTIRVCGCSNDGVQSCVRAAYVLPIGLMGAL

Query Match
 87.6%; Score 18.4; DB 6; Length 2711;
 Best Local Similarity 95.0%; Pred. No. 9,4e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OR
 2 AGGACACAGTGCGCTTGGAC 21
 |||||
Db
 2570 AGGACACAGAGCGCTTTGAC 2589

RESULT 17
AK044046
LOCUS
DEFINITION
 Mus musculus 10 days neonate cortex cDNA, RIKEN full-length
 enriched library, clone:A830083P13 product:cadherin 8, full insert
 sequence.
ACCESSION
 AK044046
VERSION
 AK044046.1 GI:26336131
KEYWORDS
 HTC, CAP trapper.
SOURCE
 Mus musculus (house mouse)
ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
 1 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning

JOURNAL
PUBMED
 10349636
REFERENCE
AUTHORS
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL
PUBMED
 11042159
REFERENCE
AUTHORS
 Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P.,
 Kono, H., Akiyama, U., Nishi, K., Kitahara, T., Teshiro, H., Itoh, M.,
 Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
 Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matshiki, M.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer
JOURNAL
 Genome Res. 10 (11), 1757-1771 (2000)
TITLE
 The RIKEN Genome Exploration Research Group Phase II Team and the
 PANTOM Consortium.
REFERENCE
AUTHORS
 Functional annotation of a full-length mouse cDNA collection
 Nature 409, 685-690 (2001)
TITLE
 The PANTOM Consortium, the RIKEN Genome Exploration Research Group
 Phase I and II Team.
REFERENCE
AUTHORS
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
JOURNAL
PUBMED
 11076861
REFERENCE
AUTHORS
 The RIKEN Genome Exploration Research Group Phase II Team and the
 PANTOM Consortium.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409, 685-690 (2001)
TITLE
 The PANTOM Consortium, the RIKEN Genome Exploration Research Group
 Phase I and II Team.
REFERENCE
AUTHORS
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
JOURNAL
PUBMED
 11076861
REFERENCE
AUTHORS
 The RIKEN Genome Exploration Research Group, Genome Science Group
 (Genome Network Core Team) and the PANTOM Consortium.
 Antisense Transcription in the Mammalian Transcriptome
 Science 309, 1564-1566 (2005)
TITLE
 The PANTOM Consortium, Riken Genome Exploration Research Group and
 Genome Science Group (Genome Network Project Core Group).
REFERENCE
AUTHORS
 The Transcriptional Landscape of the Mammalian Genome
 Science 309, 1559-1563 (2005)
TITLE
 8 (bases 1 to 3161)
JOURNAL
PUBMED
 11076861
REFERENCE
AUTHORS
 Adachi, J., Aizawa, K., Akimura, T., Arikawa, T., Bono, H., Carninci, P.,
 Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T.,
 Horii, F., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
 Kato, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Koude, M.,
 Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
 Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
 Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
 Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
 Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takahashi, S.,
 Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
 Muramatsu, M. and Hayashizaki, Y.
TITLE
 Direct Submission
JOURNAL
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration and Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa, 230-0045, Japan (E-mail: genome-res@gscc.riken.jp,
 URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
 Fax: 81-45-503-9216)
COMMENT
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in Riken.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.jp/
 URL: http://fantom.gsc.riken.jp/
FEATURES
source
 1. 3161
 Location/Qualifiers

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polya_site
polya_signal

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Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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2 AGGACACAGGCGCTTTTGAC 21
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RESULT 18

LOCUS	AKO83092	3592 bp	mRNA	linear	HTC 02-SEP-2005
DEFINITION	Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched library, clone:C630002D14 product:cadherin 8, full insert sequence.				
ACCESSION	AKO83092				
VERSION	AKO83092.1	GI:26350236			
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murideae; Murinae; Mus.				
AUTHORS	Carninci,P. and Hayashizaki,Y.				
TITLE	High-efficiency full-length cDNA cloning				
JOURNAL	Mech. Enzymol. 303, 19-44 (1999)				
PUBMED	10349636				
REFERENCE	2				
AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Kono,H., Okasaki,Y., Muramatsu,M. and Hayashizaki,Y.				
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)				
PUBMED	11042159				
REFERENCE	3				
AUTHORS	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,				

TITLE	JOURNAL	PUBLISHED	REFERENCE	AUTHORS
4	THE RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.		Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)	Komori, H., Akiyama, J., Nishii, K., Katsunuma, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishize, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujikawa, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matakaki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
5	THE PANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I and II Team.		Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)	RIKEN Genome Exploration Research Group, Genome Science Group (Genome Network Core Team) and the PANTOM Consortium.
6	RIKEN Genome Exploration Research Group, Genome Science Group		Antisense Transcription in the Mammalian Transcriptome Science 309, 1564-1566 (2005)	
7	THE PANTOM Consortium, Riken Genome Exploration Research Group and Genome Science Group (Genome Network Project Core Group).		The Transcriptional Landscape of the Mammalian Genome Science 309, 1559-1563 (2005)	
8	(bases 1 to 3592)		Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Horii, F., Imclat, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Ohnato, N., Okazaki, Y., Saito, R., Saitoh, K., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Saeki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.	
	Direct Submission		Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 220-0045, Japan (E-mail: genome-res@gs.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)	
	CNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.		Please visit our web site for further details. URL: http://genome.gsc.riken.jp/	
	Location/Qualifiers			
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ORIGIN

Query Match 87.6%; Score 18.4; DB 6; Length 3592;
Best Local Similarity 95.0%; Pred. No. 9.8e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

2 AGGACACAGTGGCTTTGAC 21
|||||
2581 AGGACACAGAGGCTTTGAC 2600

Db

RESULT 19
AK086711
LOCUS

AK086711 3793 bp mRNA linear HTC 02-SEP-2005
Mus musculus 15 days embryo head cDNA, RIKEN full-length enriched
library, clone:DB30046N17 product:cadherin 8, full insert sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AK086711.1 GI:26352174
HTC; CAP trapper.
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED

Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)

REFERENCE
AUTHORS

TITLE

2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)

JOURNAL
PUBMED

11042159
1076861

REFERENCE
AUTHORS

3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Kono, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M.,
Sun, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yanamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Harada, A.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanuki, K.,
Okazaki, Y., Ishikawa, T., Ozawa, K., Tanaka, K., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)

JOURNAL
PUBMED

11076861

REFERENCE
AUTHORS

4
The RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 403, 685-690 (2001)

JOURNAL
PUBMED

11076861

REFERENCE
AUTHORS

5
Nature 403, 685-690 (2001)

AUTHORS

The PANTOM Consortium, the RIKEN Genome Exploration Research Group
Phase I and II Team.

TITLE

Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs

JOURNAL

Nature 420, 563-573 (2002)

REFERENCE
AUTHORS

6
RIKEN Genome Exploration Research Group, Genome Science Group
(Genome Network Core Team) and the PANTOM Consortium.
Antisense Transcription in the Mammalian Transcriptome
Science 309, 1564-1566 (2005)

JOURNAL

7
The PANTOM Consortium, Riken Genome Exploration Research Group and
Genome Science Group (Genome Network Project Core Group).
The transcriptional landscape of the mammalian genome
Science 309, 1559-1563 (2005)

REFERENCE
AUTHORS

8
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T.,
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Kato, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M.,
Koyama, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
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Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toyé, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.

TITLE

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa, 230-0045, Japan (E-mail: genome-rs@gsr.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/.

FEATURES

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ORIGIN
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 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 DB 2583 AGGACACAGAGGCTTTGAC 2602

RESULT 20
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ACCESSION BG022939.1 GI:12479018
 VERSION BG022939.1
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 ORGANISM Xenopus laevis

REFERENCE 1 (bases 1 to 337)
 AUTHORS Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L.,
 Pape,D., Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y.,
 Person,B., Gibbons,M., Harvey,N., Ritter,B., Jackson,Y., McCann,R.,
 Waterston,R. and Wilson,R.
 Washu Xenopus EST project, 1999
 Unpublished (1999)

TITLE Contact: Sandy Clifton, Ph.D.
 JOURNAL Washu Xenopus EST project, 1999
 COMMENT Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 Library constructed by C. Hashimoto, Ph.D. in the laboratory of K.
 Cho, Ph.D. DNA Sequencing by: Washington University Genome
 Sequencing Center

FEATURES
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 by C. Hashimoto, Ph.D., in the laboratory of K. Cho, Ph.D.
 (Department of Developmental and Cell Biology, University
 of California, Irvine)."

ORIGIN

Query Match 84.8%; Score 17.8; DB 2; Length 337;
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 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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DB 25 CAGGACAAAGAGGCTTTGAC 5

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 VERSION EST.
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE 1 (bases 1 to 357)
 AUTHORS Dias Neto,B., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
 Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V.,
 O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 10737800
 CONTACT: Simpson A.J.G.
 JOURNAL Laboratory of Cancer Genetics
 PUBMED Ludwig Institute for Cancer Research
 COMMENT Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?cl=IL5&f2=IL5-IT0027-
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 High quality sequence stop: 302.
 location/Qualifiers
 1..357

FEATURES
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 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the puc 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

ORIGIN

Query Match 84.8%; Score 17.8; DB 2; Length 357;
 Best Local Similarity 90.5%; Pred. No. 1.4e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CAGGACACAGTGGCTTTGAC 21
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 DB 56 CAGGACACAGTGGCTTTGAC 36

RESULT 22

CR555978 377 bp mRNA linear EST 12-JUL-2004
 LOCUS DKR2p4691192.r1 469 (synonym: pklid1) Pongo pygmaeus cDNA clone
 DEFINITION DKR2p4691192 5', mRNA sequence.
 ACCESION CR555978
 VERSION CR555978.1 GI:50249580
 KEYWORDS EST.

SOURCE
ORGANISM Pongo pygmaeus (orangutan)

REFERENCE
AUTHORS Pongo pygmaeus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Pongo.
1 (bases 1 to 377)

TITLE
JOURNAL Bloecker, H., Boecher, M., Brandt, P., Mewes, H. W., Weill, B., Amdt, C.,
Osaenger, A., Fobö, G., Han, M., and Wiemann, S.
Pongo pygmaeus mRNA (Bloecker, H., Boecher, M., Brandt, P., et al.)
Unpublished (2004)

COMMENT
MIPS
Contact: MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert Clone from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKFZ);
Email s.wiemann@dkfz-heidelberg.de; sequenced by GBF (National
Research Centre for Biotechnology Ltd., Braunschweig/Germany)
within the cDNA sequencing consortium of the German Genome Project.
This clone (DKFZp4691192) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at <http://mips.gsf.de/projects/cdna/>.
Location/Qualifiers
1..377
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ORIGIN

Query Match 84.8%; Score 17.8; DB 8; Length 377;
Best Local Similarity 90.5%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAGGACACAGTGGCTTTGAC 21
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54 CAGGACACAGTGGCTTTGAC 74

Db

RESULT 23
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DEFINITION BY467982 RIKEN full-length enriched, melanocyte Mus musculus cDNA
ACCESSION BY467982
VERSION BY467982.1 GI:26802361
KEYWORDS Bst.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 501)
Okazaki, Y., Furuno, M., Kaenaka, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Otsu, N., Saito, R., Suzuki, H., Yamakata, T.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C.,
Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Macnude, H.,
Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V.,
Chothia, C., Corbani, L. E., Cousine, S., Della, B., Dragani, T. A.,
Fletcher, C. F., Forrest, A., Frazer, K. S., Gasterland, T.,
Gatibordi, M., Gissi, C., Godzik, A., Gough, J., Grilmond, S.,
Guelincich, S., Hirokawa, N., Jackson, I. J., Jarvis, B. D., Kanai, A.,
Kawaji, H., Kawasawa, Y., Kedzierzki, R. M., King, B. L., Kung, A.,
Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R.,
Matsuda, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W. J., Petca, G., Peeole, G.,

FEATURES
source
1..501
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="G270040C21"
/cell_type="melanocyte"
/clone_1lb="RIKEN full-length enriched, melanocyte"

ORIGIN

Query Match 84.8%; Score 17.8; DB 4; Length 501;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAGGACACAGTGGCTTTGAC 21
|||||
186 CAGGACACAGTGGCTTTGAC 206

Db

COMMENT
JOURNAL
PUBMED
TITLE
Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Saitama-cho, Tsukuba-shi, Ibaraki, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gs.c.riken.jp, URL: <http://genome.gsc.riken.jp/>
Aizawa, K., Akimura, T., Aizawa, T., Carninci, P., Fukuda, S.,
Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Kono, H.,
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numata, K.,
Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
Shiraki, T., Tagami, M., Waki, K., Watanabe, A., Muramatsu, M. and
Hayashizaki, Y. Direct Subdivision
Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Cells were provided by Drs. William J Pavan, Stacie Loftus, and
Denise Larson (Division of Intramural Research Genetic Disease
Research Branch National Human Genome Research Institute, National
Institutes of Health (NIH) Building: 49, Room 4A82 49 Convent Drive
MSC 4472 Bethesda, Maryland U.S.A) whose assistance we gratefully
acknowledge
Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.
Location/Qualifiers
1..501
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="G270040C21"
/cell_type="melanocyte"
/clone_1lb="RIKEN full-length enriched, melanocyte"

RESULT 24
 CR429603/c 507 bp mRNA linear EST 17-JUN-2004
 LOCUS CR429603 XGC-tailbud Xenopus tropicalis cDNA clone TtBA075007 5',
 DEFINITION mRNA sequence.
 CR429603
 ACCESSION CR429603.1 GI:48923012
 VERSION EST.
 SOURCE Xenopus tropicalis (western clawed frog)
 ORGANISM Xenopus tropicalis
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 Xenopodinae; Xenopus; Silurana.
 1 (bases 1 to 507)
 Croining,M.D.R., Ashurst,J.L., Taylor,R., Garrett,N. and Rogers,J.
 Sanger Xenopus tropicalis EST project 2001 (2004)
 JOURNAL Unpublished (2004)
 COMMENT Contact: Croining MDR
 Sanger Institute
 Hinxton, Cambridgeshire, CB10 1SA, UK
 Email: trop@sanger.ac.uk
 Sanger Xenopus tropicalis EST project 2001
 TROPICALIS_SEQUENCE_ID: TtBA075007.p1ksp6
 This sequence is from a Xenopus Gene Collection (XGC) library
 constructed by Nigel Garrett.
 Seq primer: SP6.
 Location/Qualifiers
 1..507
 /organism="Xenopus tropicalis"
 /mol_type="mRNA"
 /db_xref="taxon:8364"
 /clone="TtBA075007"
 /dev_stage="tailbud (stage 28-30)"
 /lab_host="Escherichia coli DH10B."
 /clone_lib="XGC-tailbud"
 /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
 was oligo dt primed from 5ug of poly A+ RNA from tailbud.
 EcoRI-NotI cut cDNA was then ligated into pCS107 with
 EcoRI at the 5' end and NotI at the 3' end."
 ORIGIN
 Query Match 84.8%; Score 17.8; DB 8; Length 507;
 Best Local Similarity 90.5%; Pred. No. 1.5e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 1 CAGGACAGGTGGCTTTGAC 21
 |||||
 Db 340 CAGGACAGGTGGCTTTGAC 320
 RESULT 25
 AL785427/c 594 bp mRNA linear EST 13-NOV-2003
 LOCUS AL785427 XGC-neurula Xenopus tropicalis cDNA clone TNeu072e23 5',
 DEFINITION mRNA sequence.
 AL785427
 ACCESSION AL785427.2 GI:38308397
 VERSION EST.
 SOURCE Xenopus tropicalis (western clawed frog)
 ORGANISM Xenopus tropicalis
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 Xenopodinae; Xenopus; Silurana.
 1 (bases 1 to 594)
 Croining,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
 Sanger Xenopus tropicalis EST project 2001 (11_2003)
 JOURNAL Unpublished (2003)
 COMMENT On Jun 25, 2002 this sequence version replaced gi:21571131.
 Contact: Taylor R
 Sanger Institute
 Hinxton, Cambridgeshire, CB10 1SA, UK

Email: trop@sanger.ac.uk
 This sequence is from a Xenopus Gene Collection (XGC) library
 constructed by Aaron M. Zorn.
 cDNA was oligo dt primed from 5ug of poly A+ RNA from neurula.
 EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
 5' end and NotI at the 3' end.
 Vector: pCS107; Site_1: EcoRI; Site_2: NotI
 Host: Escherichia coli DH10B
 Sanger Xenopus tropicalis EST project 2001
 TROPICALIS_SEQUENCE_ID: TNeu072e23.p1ksp6
 Sequencing primer: SP6.
 Location/Qualifiers
 1..594
 /organism="Xenopus tropicalis"
 /mol_type="mRNA"
 /db_xref="taxon:8364"
 /clone="TNeu072e23"
 /dev_stage="neurula"
 /lab_host="Escherichia coli DH10B"
 /clone_lib="XGC-neurula"
 /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
 was oligo dt primed from 5ug of poly A+ RNA from neurula.
 EcoRI-NotI cut cDNA was then ligated into pCS107 with
 EcoRI at the 5' end and NotI at the 3' end."
 ORIGIN
 Query Match 84.8%; Score 17.8; DB 1; Length 594;
 Best Local Similarity 90.5%; Pred. No. 1.5e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 1 CAGGACAGGTGGCTTTGAC 21
 |||||
 Db 426 CAGGACAGGTGGCTTTGAC 406
 RESULT 26
 CX421278/c 595 bp mRNA linear EST 24-AUG-2005
 LOCUS CX421278 XGI-XZG15551.fwd NIH_XGC_tropgas7 Xenopus tropicalis cDNA clone
 DEFINITION IMAGE:7531609 5', mRNA sequence.
 CX421278
 ACCESSION CX421278.2 GI:73751990
 VERSION EST.
 SOURCE Xenopus tropicalis (western clawed frog)
 ORGANISM Xenopus tropicalis
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 Xenopodinae; Xenopus; Silurana.
 1 (bases 1 to 595)
 Richardson,P., Lucas,S., Rohhar,D., Dettler,J.C., Ng,D.C.,
 Brokstein,P. and Lindquist,E.A.
 DOE Joint Genome Institute Xenopus tropicalis EST project
 Unpublished (2004)
 On Jan 6, 2005 this sequence version replaced gi:57201981.
 Other ESTs: JGI XZG15551.rev
 Contact: Lindquist,E.A., Richardson,P.
 DOE Joint Genome Institute
 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 Tel: 925 296 5600
 Fax: 925 296 5710
 Email: cdna@jgi-psf.org
 Tissue Procurement: Richard M. Harland laboratory, University of
 California, Berkeley; http://tropicalis.berkeley.edu/home
 cDNA Library Preparation: Richard M. Harland Laboratory, University
 of California, Berkeley
 DNA Sequencing: DOE Joint Genome Institute; http://www.jgi.doe.gov
 Clone Distribution: I.M.A.G.E. Consortium/LNLN:
 http://image.llnl.gov
 Naming Conventions: EST name is generated by the concatenation of
 the JGI Clone Id and the direction of sequencing. The suffix '.fwd'
 indicates a forward sequencing read of the insert. It does not
 necessarily reflect the orientation of the insert.
 Plate: XZG 0161 row: n column: 23

High quality sequence stop: 528.

FEATURES
source

1..595
Location/Qualifiers
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="IMAGE:7531609"
/tissue_type="whole embryo"
/dev_stage="Gastrula (st. 10.5-12.5)"
/lab_host="E. coli XL1-Blue derivative, Stratagene Electropen-Blue"
/clone_lib="NH_XGC_tropcas7"
/note="Vector: PCS108; Site_1: SalI; Site_2: NotI; Gastrula library constructed by Russell B. Fletcher in R. Harland's lab using poly A RNA and oligo dt primers (Invitrogen Superscript Plasmid System for cDNA Synthesis and Cloning). SalI (5' end) -NotI (3' end) cDNA was inserted into vector PCS108 (http://mcb.berkeley.edu/labs/harland/pages/plasmids.html)."

ORIGIN

Query Match 84.8%; Score 17.8; DB 9; Length 595;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAGGACACAGTGGCTTTGAC 21
|||||
Db 166 CAGGACACAGTGGCTTTGAC 146

RESULT 27

DR5G15T 626 bp DNA linear GSS 22-NOV-2002
LOCUS Dantio rerio genomic clone DKX1-5G15, genomic survey sequence.
ACCESSION AT733484
VERSION AT733484.1 GI:21350492
KEYWORDS GSS.
SOURCE Dantio rerio (zebrafish)
ORGANISM Dantio rerio

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 626)
Humphrey,S.J., Huckle,E. and Hunt,S.R.
TITLE Direct Submision
JOURNAL Submitted (06-JUN-2002) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact: humphrey@sanger.ac.uk Unpublished

COMMENT This sequence was generated from the T7 end of BAC 5G15. 5G15 is part of the Dantiokey BAC Library created by R. Plasterk and N.V. Kyegee.
Further details: http://www.sanger.ac.uk/Projects/D_rerio/
Location/Qualifiers

FEATURES
source

1..626
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKX1-5G15"
/tissue_type="Testis"
/note="vector pIndigoBAC-536"

ORIGIN

Query Match 84.8%; Score 17.8; DB 14; Length 626;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAGGACACAGTGGCTTTGAC 21
|||||
Db 398 CAGGACACAGTGGCTTTGTC 418

RESULT 28

A0625517/c A0625517 643 bp DNA linear GSS 16-JUN-1999
LOCUS CITR1-B1-2653J24.TR CITR1-B1 Homo sapiens genomic clone 2653J24,
DEFINITION genomic survey sequence.

ACCESSION A0625517
VERSION A0625517.1 GI:5087909
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 643)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shiyaya,H., Simon,M. and Venter,J.C.

TITLE Use of BAC End Sequences from Caltech Libraries for Sequence-Ready Map Building
JOURNAL Unpublished (1997)
COMMENT Other GSSs: CITR1-B1-2653J24.TF
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org

Clones are available from Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/cdb/hungen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.
Location/Qualifiers

FEATURES
source

1..643
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="2653J24"
/sex="male"
/cell_type="sperm"
/clone_lib="CITR1-B1"
/note="Vector: pBel0BAC11; Site_1: EcoRI; Site_2: EcoRI; Caltech Human BAC Library D"

ORIGIN

Query Match 84.8%; Score 17.8; DB 11; Length 643;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAGGACACAGTGGCTTTGAC 21
|||||
Db 494 CAGGACACAGTGGCTTATGAC 474

RESULT 29

AL642415/c AL642415 649 bp mRNA linear EST 07-NOV-2003
LOCUS AL642415 XGC-neurula Xenopus tropicalis cDNA clone TNeu025k14.5,
DEFINITION mRNA sequence.

ACCESSION AL642415
VERSION AL642415.2 GI:38221123
KEYWORDS EST.
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae; Xenopus; Silurana.

1 (bases 1 to 649)
Croning,M.D.R., Ashurel,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
TITLE Sanger Xenopus tropicalis EST project 2001 (11_2003)
JOURNAL Unpublished (2003)
COMMENT On Nov 7, 2001 this sequence version replaced gi:16794540.
Contact: Huckle E
Sanger Institute

Hinxton, Cambridgeshire, CB10 1SA, UK
 Email: trop@sanger.ac.uk
 This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
 cDNA was oligo dt primed from 5ug of poly A+ RNA from neurula. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end.
 Vector: pCS107; Site_1: EcoRI; Site_2: NotI
 Host: Escherichia coli DH10B
 Sanger Xenopus tropicalis EST project 2001
 TROPICALIS SEQUENCE ID: TNeu025K14.plkSp6
 Sequencing primer: SP6.
 Location/Qualifiers
 1..649
 /organism="Xenopus tropicalis"
 /mol_type="mRNA"
 /db_xref="taxon:8364"
 /clone="TNeu025K14"
 /dev_stage="neurula"
 /lab_host="Escherichia coli DH10B"
 /clone_lib="XGC-neurula"
 /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA was oligo dt primed from 5ug of poly A+ RNA from neurula. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end."
 ORIGIN
 Query Match 84.8%; Score 17.8; DB 1; Length 649;
 Best Local Similarity 90.5%; Pred. No. 1.5e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CAGGACACAGTGGCTTTGAC 21
 |||||
 Db 420 CAGGACACAGTGGCTTTGAC 400
 |||||
 RESULT 30
 CT346911/c 683 bp DNA 1linear GSS 03-NOV-2005
 LOCUS CT346911
 DEFINITION Sus scrofa genomic clone CH242-42B24, genomic survey sequence.
 ACCESSION CT346911
 VERSION CT346911.1 GI:79916515
 KEYWORDS GSS.
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.
 1 (bases 1 to 683)
 Humphray, S.J., Plumb, R.W. and Durham, J.L.
 Direct Submission
 Submitted (01-NOV-2005) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humphray@sanger.ac.uk Unpublished
 This sequence was generated from the T7 end of BAC 42B24. 42B24 is part of the CHORI-242 BAC library created by P. de Jong. Further details: http://www.sanger.ac.uk/Projects/S_scrofa/.
 Location/Qualifiers
 1..683
 /organism="Sus scrofa"
 /mol_type="genomic DNA"
 /db_xref="taxon:9623"
 /clone="CH242-42B24"
 /tissue_type="White blood cells"
 /note="Vector pTARBAC1.3_BamHI sex female"
 ORIGIN
 Query Match 84.8%; Score 17.8; DB 14; Length 683;
 Best Local Similarity 90.5%; Pred. No. 1.5e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CAGGACACAGTGGCTTTGAC 21

Db 228 CAGGACACAGAGGCTTTGTC 208
 |||||
 RESULT 31
 AG144458/c 710 bp DNA 1linear GSS 08-JAN-2002
 LOCUS AG144458
 DEFINITION Pan troglodytes DNA, clone: RP43-005H09.TU, genomic survey sequence.
 ACCESSION AG144458
 VERSION AG144458.1 GI:16674136
 KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Pan.
 1
 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Torok, Y., Watanabe, H. and Sakaki, Y.
 BAC end sequences of Library RP43-005H09
 2 (bases 1 to 710)
 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Torok, Y., Watanabe, H. and Sakaki, Y.
 Direct Submission
 Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suicho-chou, Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: chimbee@gsc.riken.go.jp, URL: <http://hgp-gsc.riken.go.jp/>, Tel:81-45-503-9111, Fax:81-45-503-9170)
 Clones are derived from the chimpanzee BAC library RP43-005H09 and was generated during the R&D process and may have higher chance of clone tracking errors.
 PRIMERS
 Sequencing: TU
 LIBRARY
 Vector : pBACe3.6
 R.Site 1 : EcoRI
 R.Site 2 : EcoRI.
 Location/Qualifiers
 1..710
 /organism="Pan troglodytes"
 /mol_type="genomic DNA"
 /db_xref="taxon:9598"
 /clone="RP43-005H09.TU"
 /sex="male"
 /cell_type="lymphocytes"
 /clone_lib="RP43-005H09 Chimpanzee Male BAC Library"
 ORIGIN
 Query Match 84.8%; Score 17.8; DB 14; Length 710;
 Best Local Similarity 90.5%; Pred. No. 1.5e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CAGGACACAGTGGCTTTGAC 21
 |||||
 Db 539 CAGGACACAGTGGCTTTATGAC 519
 |||||
 RESULT 32
 AZ560569 712 bp DNA 1linear GSS 20-NOV-2000
 LOCUS AZ560569
 DEFINITION RP43-23-206G21.TU RP43-23 Mus musculus genomic clone
 ACCESSION AZ560569
 VERSION AZ560569.1 GI:11240389
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.
 1

REFERENCE 1 (bases 1 to 712)
 AUTHORS Zhao, S., Nierman, W., Feldblum, T., Malek, J., Shatman, S., Akniet, B., Levins, M., McGinn, S., Tesgaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.
 TITLE Mouse BAC End Sequences from Library RPCI-23
 JOURNAL Unpublished (1999)
 COMMENT Other: GSSs: RPCI-23-206G21.TV
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhaoc@igr.org
 Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/cdb/bac_ends/mouse/bac_end_intro.html
 Plate: 206 row: G column: 21
 Seq primer: SP6
 Class: BAC ends.

FEATURES
 source Location/Qualifiers
 1..712
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPCI-23-206G21"
 /sex="Female"
 /lab_host="DH10B"
 /clone_id="RPCI-23"
 /note="Organ: Kidney/Brain; Vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBAC3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."

ORIGIN
 Query Match 84.8%; Score 17.8; DB 11; Length 712;
 Best Local Similarity 90.5%; Pred. No. 1.5e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAGGACACAGTGGCTTTGAC 21
 |||||
 Db 645 CAGGACACAGTGGCTTTGAC 665

RESULT 33
 CX380870 788 bp mRNA linear EST 08-SEP-2005
 LOCUS JGI_XZT52439.fwd NIH_XGC_tropTad5 Xenopus tropicalis cDNA clone
 DEFINITION IMAGE:7627184 5', mRNA sequence.
 ACCESSION CX380870
 VERSION CX380870.2 GI:74291806
 KEYWORDS EST.
 ORGANISM Xenopus tropicalis (western clawed frog)
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae; Xenopus; Silurana.
 1 (bases 1 to 788)
 Richardson, P., Lucas, S., Rokhsar, D., Dettter, J.C., Ng, D.C., Brokstein, P. and Lindquist, E.A.
 DOE Joint Genome Institute Xenopus tropicalis EST project
 Unpublished (2004)
 On Jan 5, 2005 this sequence version replaced gi:57149427.
 Other ESTs: JGI_XZT52439.rev
 Contact: Lindquist, E.A., Richardson, P.
 DOE Joint Genome Institute

2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 Tel: 925 296 5600
 Fax: 925 296 5710
 Email: cdna@jgi-psf.org
 Tissue Procurement: Richard M. Harland Laboratory, University of California, Berkeley: http://ctropicalis.berkeley.edu/home
 cDNA Library Preparation: Richard M. Harland Laboratory, University of California, Berkeley
 DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
 Clone Distribution: I.M.A.G.E. Consortium/LNL:
 http://image.lnl.gov
 Naming Conventions: EST name is generated by the concatenation of the JGI Clone Id and the direction of sequencing. The suffix '.fwd' indicates a forward sequencing read of the insert. It does not necessarily reflect the orientation of the insert.
 Plate: XZT 0545 row: m column: 6
 High quality sequence stop: 786.

FEATURES
 source Location/Qualifiers
 1..788
 /organism="Xenopus tropicalis"
 /mol_type="mRNA"
 /db_xref="taxon:8364"
 /clone="IMAGE:7627184"
 /tissue_type="whole embryo"
 /dev_stage="Tadpole (st. 36-41)"
 /lab_host="E. coli XL1-Blue derivative, Stratagene Electrogen-Blue"
 /clone_id="NIH_XGC_tropTad5"
 /note="Vector: pCS108; Site 1: SalI; Site 2: NotI; Tadpole library constructed by Russell B. Fletcher in R. Harland's lab using poly A RNA and oligo dt primers (invitrogen SuperScript Plasmid System for cDNA Synthesis and Cloning). SalI (5' end) -NotI (3' end) cDNA was inserted into vector pCS108
 (http://mb.berkeley.edu/labs/harland/pages/plasmids.html)."

ORIGIN
 Query Match 84.8%; Score 17.8; DB 9; Length 788;
 Best Local Similarity 90.5%; Pred. No. 1.5e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAGGACACAGTGGCTTTGAC 21
 |||||
 Db 764 CAGGACACAGTGGCTTTGAC 744

RESULT 34
 CX443805 793 bp mRNA linear EST 07-JAN-2005
 LOCUS JGI_XZG9472.fwd NIH_XGC_tropCas7 Xenopus tropicalis cDNA clone
 DEFINITION IMAGE:7526634 5', mRNA sequence.
 ACCESSION CX443805
 VERSION CX443805.1 GI:57259637
 KEYWORDS EST.
 ORGANISM Xenopus tropicalis (western clawed frog)
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae; Xenopus; Silurana.
 1 (bases 1 to 793)
 Richardson, P., Lucas, S., Rokhsar, D., Dettter, J.C., Ng, D.C., Brokstein, P. and Lindquist, E.A.
 DOE Joint Genome Institute Xenopus tropicalis EST project
 Unpublished (2004)
 Contact: Lindquist, E.A., Richardson, P.
 DOE Joint Genome Institute
 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 Tel: 925 296 5600
 Fax: 925 296 5710
 Email: cdna@jgi-psf.org
 Tissue Procurement: Richard M. Harland Laboratory, University of California, Berkeley: http://ctropicalis.berkeley.edu/home

CDNA Library Preparation: Richard M. Harland Laboratory, University of California, Berkeley
 DNA Sequencing: DOE Joint Genome Institute: <http://www.jgi.doe.gov>
 Clone Distribution: I.M.A.G.E. Consortium/LNLN:
<http://image.llnl.gov>

Naming Conventions: EST name is generated by the concatenation of the JGI Clone id and the direction of sequencing. The suffix '.fwd' indicates a forward sequencing read of the insert. It does not necessarily reflect the orientation of the insert.
 Plate: XZG 0097 row: 0 column: 16
 High quality sequence stop: 756.
 Location/Qualifiers

FEATURES

source

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1..793
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="IMAGE:7526634"
/tissue_type="whole embryo"
/dev_stage="Gastrula (st. 10.5-12.5)"
/lab_host="E. coli XL1-Blue derivative, Stratagene Electropen-Blue"
/clone_lib="NIH_XGC_tropcas7"
/notes="vector: PCS108; Site 1: SalI; Site 2: NotI; Gastrula library constructed by Russell B. Fletcher in R. Harland's lab using poly A RNA and oligo dt primers (Invitrogen Superscript Plasmid System for cDNA Synthesis and Cloning). SalI (5' end) -NotI (3' end) cDNA was inserted into vector PCS108 (http://mcb.berkeley.edu/labs/harland/pages/plasmids.html)"
"
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ORIGIN

Query Match 84.8%; Score 17.8; DB 9; Length 793;
 Best Local Similarity 90.5%; Pred. No. 1.6e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CAGGACACAGTGGCTTTGAC 21
 |||||
 Db 732 CAGGACACAGTGGCTTTGAC 712

RESULT 35
 CX444795/c 794 bp mRNA linear EST 07-JAN-2005
 LOCUS JGI_XZG10768.fwd NIH_XGC_tropcas7 Xenopus tropicalis cDNA clone
 DEFINITION IMAGE:7527773 5', mRNA sequence.
 ACCESSION CX444795
 VERSION CX444795.1 GI:57260627
 KEYWORDS EST.
 SOURCE Xenopus tropicalis (western clawed frog)
 ORGANISM Xenopus tropicalis
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae; Xenopus; Silurana.
 1 (bases 1 to 794)
 Richardson, P., Lucas, S., Rohrer, D., Dettler, J.C., Ng, D.C., Brockstein, P., and Lindquist, E.A.
 DOE Joint Genome Institute Xenopus tropicalis EST project
 Unpublished (2004)
 CONTACT Contact: Lindquist, E.A., Richardson, P.
 DOE Joint Genome Institute
 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 Tel: 925 296 5600
 Fax: 925 296 5710
 Email: cdna@jgi-psf.org
 Tissue Procurement: Richard M. Harland Laboratory, University of California, Berkeley: <http://tropicalis.berkeley.edu/home>
 CDNA Library Preparation: Richard M. Harland Laboratory, University of California, Berkeley
 DNA Sequencing: DOE Joint Genome Institute: <http://www.jgi.doe.gov>
 Clone Distribution: I.M.A.G.E. Consortium/LNLN:
<http://image.llnl.gov>
 Naming Conventions: EST name is generated by the concatenation of

the JGI Clone id and the direction of sequencing. The suffix '.fwd' indicates a forward sequencing read of the insert. It does not necessarily reflect the orientation of the insert.
 Plate: XZG 0113 row: 0 column: 3
 High quality sequence stop: 707.
 Location/Qualifiers

FEATURES

source

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1..794
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="IMAGE:7527773"
/tissue_type="whole embryo"
/dev_stage="Gastrula (st. 10.5-12.5)"
/lab_host="E. coli XL1-Blue derivative, Stratagene Electropen-Blue"
/clone_lib="NIH_XGC_tropcas7"
/notes="vector: PCS108; Site 1: SalI; Site 2: NotI; Gastrula library constructed by Russell B. Fletcher in R. Harland's lab using poly A RNA and oligo dt primers (Invitrogen Superscript Plasmid System for cDNA Synthesis and Cloning). SalI (5' end) -NotI (3' end) cDNA was inserted into vector PCS108 (http://mcb.berkeley.edu/labs/harland/pages/plasmids.html)"
"
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ORIGIN

Query Match 84.8%; Score 17.8; DB 9; Length 794;
 Best Local Similarity 90.5%; Pred. No. 1.6e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CAGGACACAGTGGCTTTGAC 21
 |||||
 Db 776 CAGGACACAGTGGCTTTGAC 756

RESULT 36
 CX404457/c 796 bp mRNA linear EST 01-SEP-2005
 LOCUS JGI_XZT5930.fwd NIH_XGC_tropTads Xenopus tropicalis cDNA clone
 DEFINITION IMAGE:7611970 5', mRNA sequence.
 ACCESSION CX404457
 VERSION CX404457.2 GI:74091209
 KEYWORDS EST.
 SOURCE Xenopus tropicalis (western clawed frog)
 ORGANISM Xenopus tropicalis
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae; Xenopus; Silurana.
 1 (bases 1 to 796)
 Richardson, P., Lucas, S., Rohrer, D., Dettler, J.C., Ng, D.C., Brockstein, P., and Lindquist, E.A.
 DOE Joint Genome Institute Xenopus tropicalis EST project
 Unpublished (2004)
 CONTACT Contact: JGI_XZT5930.rev
 DOE Joint Genome Institute
 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 Tel: 925 296 5600
 Fax: 925 296 5710
 Email: cdna@jgi-psf.org
 Tissue Procurement: Richard M. Harland Laboratory, University of California, Berkeley: <http://tropicalis.berkeley.edu/home>
 CDNA Library Preparation: Richard M. Harland Laboratory, University of California, Berkeley
 DNA Sequencing: DOE Joint Genome Institute: <http://www.jgi.doe.gov>
 Clone Distribution: I.M.A.G.E. Consortium/LNLN:
<http://image.llnl.gov>
 Naming Conventions: EST name is generated by the concatenation of

the JGI Clone id and the direction of sequencing. The suffix '.fwd' indicates a forward sequencing read of the insert. It does not necessarily reflect the orientation of the insert.
 Plate: XZT 0373 row: c column: 8

High quality sequence stop: 789.

FEATURES
source
1..796
Location/Qualifiers

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/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="IMAGE:7611970"
/tissue_type="whole embryo"
/dev_stage="Tadpole (st. 36-41)"
/lab_host="E. coli XL1-Blue derivative, Stratagene
Electroten-Blue"
/clone_idb="NIH_XGC_tropTad5"
/note="Vector: pCS108; Site 1: SalI; Site 2: NotI; Tadpole
library constructed by Russell B. Fletcher in R. Harland's
lab using poly A RNA and oligo dt primers (Invitrogen
SuperScript Plasmid System for cDNA Synthesis and
Cloning). SalI (5' end) -NotI (3' end) cDNA was inserted
into vector pCS108
(http://mcb.berkeley.edu/labs/harland/pages/plasmids.html)"
```

ORIGIN

Query Match 84.8%; Score 17.8; DB 9; Length 796;
Best Local Similarity 90.5%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CAGGACACAGTGGCTTTGAC 21
|||||
Db 429 CAGGACACAGTGGCTTTGAC 409

RESULT 37
LOCUS CX439900 799 bp mRNA linear EST 07-JAN-2005
DEFINITION JGI XZG8004 fwd NIH XGC_tropGast7 Xenopus tropicalis cDNA clone
IMAGE:7524924 5', mRNA sequence.
ACCESSION CX439900
VERSION CX439900.1 GI:57255732
KEYWORDS EST.

SOURCE
ORGANISM Xenopus tropicalis (western clawed frog)

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 799)
Richardson, P., Lucas, S., Rokhsar, D., Dettler, J.C., Ng, D.C.,
Brokstein, P. and Lindquist, E.A.
DOI Joint Genome Institute Xenopus tropicalis EST project
Unpublished (2004)

TITLE
JOURNAL Contact: Lindquist, E.A., Richardson, P.
COMMENT DOE Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 296 5600
Fax: 925 296 5710

Email: cdna@jgi-psf.org
Tissue Procurement: Richard M. Harland Laboratory, University of
California, Berkeley: http://tropicals.berkeley.edu/home
cDNA Library Preparation: Richard M. Harland Laboratory, University
of California, Berkeley
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
Clone Distribution: I.M.A.G.E. Consortium/LLNL:
http://image.llnl.gov
Naming Conventions: EST name is generated by the concatenation of
the JGI clone id and the direction of sequencing. The suffix '.fwd'
indicates a forward sequencing read of the insert. It does not
necessarily reflect the orientation of the insert.
Plate: XZG 0081 row: h column: 10
High quality sequence stop: 791.

FEATURES

source
1..799
Location/Qualifiers
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"

ORIGIN

Query Match 84.8%; Score 17.8; DB 9; Length 799;
Best Local Similarity 90.5%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CAGGACACAGTGGCTTTGAC 21
|||||
Db 778 CAGGACACAGTGGCTTTGAC 758

RESULT 38
LOCUS CX407260 829 bp mRNA linear EST 08-SEP-2005
DEFINITION JGI XZT62721 fwd NIH XGC_tropTad5 Xenopus tropicalis cDNA clone
IMAGE:7637291 5', mRNA sequence.
ACCESSION CX407260
VERSION CX407260.2 GI:74301053
KEYWORDS EST.

SOURCE
ORGANISM Xenopus tropicalis (western clawed frog)

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 829)
Richardson, P., Lucas, S., Rokhsar, D., Dettler, J.C., Ng, D.C.,
Brokstein, P. and Lindquist, E.A.
DOI Joint Genome Institute Xenopus tropicalis EST project
Unpublished (2004)

TITLE
JOURNAL On Jan 6, 2005 this sequence version replaced gi:57187960.
COMMENT Other ESTs: JGI XZT62721.rev
Contact: Lindquist, E.A., Richardson, P.
DOI Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 296 5600
Fax: 925 296 5710

Email: cdna@jgi-psf.org
Tissue Procurement: Richard M. Harland Laboratory, University of
California, Berkeley: http://tropicals.berkeley.edu/home
cDNA Library Preparation: Richard M. Harland Laboratory, University
of California, Berkeley
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
Clone Distribution: I.M.A.G.E. Consortium/LLNL:
http://image.llnl.gov
Naming Conventions: EST name is generated by the concatenation of
the JGI clone id and the direction of sequencing. The suffix '.fwd'
indicates a forward sequencing read of the insert. It does not
necessarily reflect the orientation of the insert.
Plate: XZT 0653 row: b column: 9
High quality sequence stop: 828.

FEATURES

source
1..829
Location/Qualifiers
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="IMAGE:7637291"
/tissue_type="whole embryo"
/dev_stage="Tadpole (st. 36-41)"
/lab_host="E. coli XL1-Blue derivative, Stratagene

Electroten-Blue"
/clone.lib="NIH XGC tropoBads"
/note="Vector: pCS108; Site 1: SalI; Site 2: NotI; Tadpole
library constructed by Russell B. Fletcher in R. Harland's
lab using poly A RNA and oligo dt primers (Invitrogen
SuperScript Plasmid System for cDNA Synthesis and
cloning). SalI (5' end) -NotI (3' end) cDNA was inserted
into vector pCS108
(http://mcb.berkeley.edu/labs/harland/pages/plasmids.html)

ORIGIN

Query Match 84.8%; Score 17.8; DB 9; Length 829;
Best Local Similarity 90.5%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 CAGGACACAGTGGCTTTGAC 21
|||||
381 CAGGACACAGTGGCTTTGAC 361

RESULT 39 850 bp mRNA linear EST 08-SEP-2005
CX396192/c
LOCUS JGI XZT56263.fwd NIH XGC tropoBads Xenopus tropicalis cDNA clone
DEFINITION IMAGE:7631020 5', mRNA sequence.

ACCESSION CX396192 GI:74295269
VERSION CX396192
KEYWORDS EST.
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoes; Pipidae;
Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 850)
Richardson, P., Lucas, S., Rokhsar, D., Dettler, J.C., Ng, D.C.,
Brooks, P., and Lindquist, B.A.
DOE Joint Genome Institute Xenopus tropicalis EST project
Unpublished (2004)
On Jan 6, 2005 this sequence version replaced gi:57176876.
Other ESTs: JGI XZT56263.rev
Contact: Lindquist, B.A., Richardson, P.
DOE Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 296 5600
Fax: 925 296 5710
Email: cdna@jgi-psf.org
Tissue Procurement: Richard M. Harland Laboratory, University of
California, Berkeley: http://tropicalis.berkeley.edu/home
cDNA library Preparation: Richard M. Harland Laboratory, University
of California, Berkeley
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
Clone Distribution: I.M.A.G.E. Consortium/LINL:
http://imgc.llnl.gov
Naming Conventions: EST name is generated by the concatenation of
the JGI Clone Id and the direction of sequencing. The suffix ".fwd"
indicates a forward sequencing read of the insert. It does not
necessarily reflect the orientation of the insert.
Plate: XZT 0585 row: m column: 2
High quality sequence stop: 829.
Location/Qualifiers
1..850
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="IMAGE:7631020"
/tissue_type="whole embryo"
/dev_stage="Tadpole (st. 36-41)"
/lab_host="E. coli XL1-Blue derivative, Stratagene
Electroten-Blue"
/note="Vector: pCS108; Site 1: SalI; Site 2: NotI; Tadpole
library constructed by Russell B. Fletcher in R. Harland's

lab using poly A RNA and oligo dt primers (Invitrogen
SuperScript Plasmid System for cDNA Synthesis and
cloning). SalI (5' end) -NotI (3' end) cDNA was inserted
into vector pCS108
(http://mcb.berkeley.edu/labs/harland/pages/plasmids.html)

ORIGIN

Query Match 84.8%; Score 17.8; DB 9; Length 850;
Best Local Similarity 90.5%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 CAGGACACAGTGGCTTTGAC 21
|||||
129 CAGGACACAGTGGCTTTGAC 109

RESULT 40 874 bp DNA linear GSS 13-MAY-2003
CC295265/c
LOCUS CH261-52A19_RML.1 CH261 Gallus gallus genomic clone CH261-52A19,
DEFINITION genomic survey sequence.
ACCESSION CC295265
VERSION CC295265.1 GI:3066706
KEYWORDS GSS.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 874)
Kremetzki, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J.,
Warren, W., Graves, T., Wardis, R., and Wilson, R.
Gallus gallus BAC End Reads
Unpublished (2003)
Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 182000 Std Error: 0.00
Seq primer: RML YACGACTCAGTATGAGGAGA
Class: BAC ends
High quality sequence start: 33
High quality sequence stop: 589.
Location/Qualifiers
1..874
/organism="Gallus gallus"
/mol_type="genomic DNA"
/strain="Red Jungle Fowl"
/db_xref="taxon:9031"
/clone="CH261-52A19"
/sex="female"
/cell_line="UCD001, inbred 256"
/clone.lib="CH261"
/note="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;
CH261 Female Chicken library - for library and clone
ordering information: http://www.chori.org/bacpac"

ORIGIN

Query Match 84.8%; Score 17.8; DB 12; Length 874;
Best Local Similarity 90.5%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 CAGGACACAGTGGCTTTGAC 21
|||||
593 CTGACACAGTGGCTTTGTC 573

RESULT 41 883 bp mRNA linear EST 07-SEP-2005
CX418837/c
LOCUS JGI XZ665774.fwd NIH XGC tropoBads Xenopus tropicalis cDNA clone
DEFINITION IMAGE:757925 5', mRNA sequence.

ACCESSION CX418837
 VERSION CX418837.2 GI:74266898
 KEYWORDS EST.
 SOURCE Xenopus tropicalis (western clawed frog)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae; Xenopus; Silurana.

REFERENCE 1 (bases 1 to 883)
 AUTHORS Richardson,P., Lucas,S., Rokhsar,D., Dettler,J.C., Ng,D.C., Brokstein,P. and Lindquist,E.A.
 TITLE DOB Joint Genome Institute Xenopus tropicalis EST project
 JOURNAL Unpublished (2004)
 COMMENT On Jan 6, 2005 this sequence version replaced gi:57199540.
 Contact: Lindquist,E.A., Richardson,P.
 DOE Joint Genome Institute
 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 Tel: 925 296 5600
 Fax: 925 296 5710
 Email: cdna@jgi-psf.org
 Tissue Procurement: Richard M. Harland Laboratory, University of California, Berkeley: <http://tropicalis.berkeley.edu/home>
 cDNA Library Preparation: Richard M. Harland Laboratory, University of California, Berkeley
 DNA Sequencing: DOE Joint Genome Institute: <http://www.jgi.doe.gov>
 Clone Distribution: I.M.A.G.E. Consortium/LLNL: <http://image.llnl.gov>
 Naming Conventions: EST name is generated by the concatenation of the JGI Clone Id and the direction of sequencing. The suffix '.fwd' indicates a forward sequencing read of the insert. It does not necessarily reflect the orientation of the insert.
 Plate: XZG 0685 row: 1 column: 3
 High quality sequence stop: 827.
 Location/Qualifiers
 1..883
 /organism="Xenopus tropicalis"
 /mol_type="mRNA"
 /db_xref="taxon:8364"
 /clone="IMAGE:7579925"
 /tissue_type="whole embryo"
 /dev_stage="Gastrula (st. 10.5-12.5)"
 /lab_host="E. coli XL1-Blue derivative, Stratagene Electrotren-Blue"
 /clone_1ib="NIH XGC tropGa87"
 /note="Vector: PCS108; Site 1: SalI; Site 2: NotI; Gastrula library constructed by Russell B. Fletcher in R. Harland's lab using poly A RNA and oligo dt primers (Invitrogen Superscript Plasmid System for cDNA Synthesis and Cloning). SalI (5' end) -NotI (3' end) cDNA was inserted into vector PCS108 (<http://mcb.berkeley.edu/labs/harland/pages/plasmids.html>)".

ORIGIN
 Query Match 84.8%; Score 17.8; DB 9; Length 883;
 Best Local Similarity 90.5%; Pred. No. 1.6e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAGGACACAGTGGCTTTGAC 21
 |||||
 Db 789 CAGGACACAGTGGCTTTGAC 769

RESULT 42
 LOCUS DR897380 895 bp mRNA linear EST 01-AUG-2005
 DEFINITION JGI_XZT42063.fwd NIH XGC tropTads Xenopus tropicalis cDNA clone
 IMAGE:7617582 5', mRNA sequence.
 ACCESSION DR897380
 VERSION DR897380.1 GI:71586632
 KEYWORDS EST.
 SOURCE Xenopus tropicalis (western clawed frog)
 ORGANISM Xenopus tropicalis

REFERENCE 1 (bases 1 to 895)
 AUTHORS Richardson,P., Lucas,S., Rokhsar,D., Dettler,J.C., Ng,D.C., Brokstein,P. and Lindquist,E.A.
 TITLE DOB Joint Genome Institute Xenopus tropicalis EST project
 JOURNAL Unpublished (2004)
 COMMENT Other ESTs: JGI_XZT42063.rev
 Contact: Lindquist,E.A., Richardson,P.
 DOE Joint Genome Institute
 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 Tel: 925 296 5600
 Fax: 925 296 5710
 Email: cdna@jgi-psf.org
 Tissue Procurement: Richard M. Harland Laboratory, University of California, Berkeley: <http://tropicalis.berkeley.edu/home>
 cDNA Library Preparation: Richard M. Harland Laboratory, University of California, Berkeley
 DNA Sequencing: DOE Joint Genome Institute: <http://www.jgi.doe.gov>
 Clone Distribution: I.M.A.G.E. Consortium/LLNL: <http://image.llnl.gov>
 Naming Conventions: EST name is generated by the concatenation of the JGI Clone Id and the direction of sequencing. The suffix '.fwd' indicates a forward sequencing read of the insert. It does not necessarily reflect the orientation of the insert.
 Plate: XZT 0437 row: m column: 4
 High quality sequence stop: 827.
 Location/Qualifiers
 1..895
 /organism="Xenopus tropicalis"
 /mol_type="mRNA"
 /db_xref="taxon:8364"
 /clone="IMAGE:7617582"
 /tissue_type="whole embryo"
 /dev_stage="Tadpole (st. 36-41)"
 /lab_host="E. coli XL1-Blue derivative, Stratagene Electrotren-Blue"
 /clone_1ib="NIH XGC tropTads"
 /note="Vector: PCS108; Site 1: SalI; Site 2: NotI; Tadpole library constructed by Russell B. Fletcher in R. Harland's lab using poly A RNA and oligo dt primers (Invitrogen Superscript Plasmid System for cDNA Synthesis and Cloning). SalI (5' end) -NotI (3' end) cDNA was inserted into vector PCS108 (<http://mcb.berkeley.edu/labs/harland/pages/plasmids.html>)".

ORIGIN
 Query Match 84.8%; Score 17.8; DB 10; Length 895;
 Best Local Similarity 90.5%; Pred. No. 1.6e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAGGACACAGTGGCTTTGAC 21
 |||||
 Db 461 CAGGACACAGTGGCTTTGAC 441

RESULT 43
 LOCUS DT398630 895 bp mRNA linear EST 25-AUG-2005
 DEFINITION JGI CAB12333.fwd NIH XGC tropOv11 Xenopus tropicalis cDNA clone
 IMAGE:7855953 5', mRNA sequence.
 ACCESSION DT398630
 VERSION DT398630.1 GI:73784827
 KEYWORDS EST.
 SOURCE Xenopus tropicalis (western clawed frog)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae; Xenopus; Silurana.

REFERENCE 1 (bases 1 to 895)
 AUTHORS Richardson,P., Lucas,S., Rokhsar,D., Dettler,J.C., Ng,D.C.,

TITLE
JOURNAL
COMMENT

Brokslein, P. and Lindquist, E.A.
DOE Joint Genome Institute Xenopus tropicalis EST project
Unpublished (2004)
Other ESTs: JGI CAB12333.rev
Contact: Lindquist, E.A., Richardson, P.
DOE Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 296 5600
Fax: 925 296 5710
Email: cdna@jgi-psf.org
Tissue Procurement: Robert M. Grainger
CDNA Library Preparation: Bruce Blumberg Laboratory, University of California, Irvine
CDNA Library Arrayed by: DOE Joint Genome Institute:
http://www.jgi.doe.gov
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
Clone Distribution: I.M.A.G.E. Consortium/LNL:
http://image.llnl.gov

Naming Conventions: EST name is generated by the concatenation of the JGI Clone Id and the direction of sequencing. The suffix '.fwd' indicates a forward sequencing read of the insert. It does not necessarily reflect the orientation of the insert.
Plate: CAB1 0025 row: 1 column: 7
High quality sequence stop: 842.

FEATURES
source

1. 895
Location/Qualifiers
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/strain="N6 (Nigerian 6th generation inbred)"
/db_xref="taxon:8364"
/clone="IMAGE:7855953"
/sex="female"
/tissue_type="Oviduct"
/dev_stage="Adult"
/lab_host="ElectroMAX DH10B T1 Phage Resistant cells"
/clone_1fb="NIH XGC tropov11"
/note="Vector: pCS107; Site 1: EcoRI; Site 2: XhoI; The library was prepared from 5 ug of poly A+ RNA by oligo-dT priming (5'-ACTAGTGGCGCCCTAGAGCTCGAGTTTCTTTTCTTTT-3') and Stratascript reverse transcriptase. After ligation of EcoRI adapters (5'-AATTCGACGACG-3') followed by kinasing adapters and by XhoI digestion, the cDNA was size selected by chromatography on Sepharose CL-2B columns and fractions containing cDNAs larger than 1000 bp were ligated into EcoRI/XhoI-digested pCS107. Reference for library construction: Current Genomics 4, 635-644. Library constructed by Michelle Tabb and Bruce Blumberg (Dept of Developmental and Cell Biology, University of California, Irvine)."

ORIGIN

Query Match 84.8%; Score 17.8; DB 10; Length 895;
Best Local Similarity 90.5%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAGGACACAGTGGCTTTGAC 21
|||||
Db 476 CAGGACACAGTGGCTTTGAC 456

RESULT 44
CX333579 896 bp mRNA linear EST 08-SEP-2005
LOCUS JGI XZT69314.fwd NIH XGC cTropTads Xenopus tropicalis cDNA clone
DEFINITION IMAGE:7788320 5', mRNA sequence.
ACCESSION CX333579
VERSION CX333579
KEYWORDS EST.
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 896)
Richardson, P., Lucas, S., Rohrer, D., Deter, J.C., Ng, D.C.,
Brokslein, P., and Lindquist, E.A.
DOE Joint Genome Institute Xenopus tropicalis EST project
Unpublished (2004)
On Jan 4, 2005 this sequence version replaced gi:57070051.
Other ESTs: JGI XZT69314.rev
Contact: Lindquist, E.A., Richardson, P.
DOE Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 296 5600
Fax: 925 296 5710
Email: cdna@jgi-psf.org

Tissue Procurement: Richard M. Harland Laboratory, University of California, Berkeley: http://tropicalis.berkeley.edu/home
CDNA Library Preparation: Richard M. Harland Laboratory, University of California, Berkeley
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
Clone Distribution: I.M.A.G.E. Consortium/LNL:
http://image.llnl.gov
Naming Conventions: EST name is generated by the concatenation of the JGI Clone Id and the direction of sequencing. The suffix '.fwd' indicates a forward sequencing read of the insert. It does not necessarily reflect the orientation of the insert.
Plate: XZT 0721 row: c column: 2
High quality sequence stop: 803.

FEATURES
source

1. 896
Location/Qualifiers
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="IMAGE:7788220"
/tissue_type="whole embryo"
/dev_stage="Tadpole (st. 36-41)"
/lab_host="B. coli XLI-Blue derivative, Stratagene Electrogen-Blue"
/clone_1fb="NIH XGC tropTads"
/note="Vector: pCS108; Site 1: SalI; Site 2: NotI; Tadpole library constructed by Russell B. Fletcher in R. Harland's lab using poly A RNA and oligo dT primers (Invitrogen SuperScript Plasmid System for cDNA Synthesis and cloning). SalI (5' end) -NotI (3' end) cDNA was inserted into vector pCS108 (http://mcb.berkeley.edu/labs/harland/pages/plasmids.html)"

ORIGIN

Query Match 84.8%; Score 17.8; DB 8; Length 896;
Best Local Similarity 90.5%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAGGACACAGTGGCTTTGAC 21
|||||
Db 785 CAGGACACAGTGGCTTTGAC 765

RESULT 45
CF222676 906 bp mRNA linear EST 04-AUG-2003
LOCUS AGENCOURT 15066211 NICHD XGC Embs Xenopus tropicalis cDNA clone
DEFINITION IMAGE:6981253 5', mRNA sequence.
ACCESSION CF222676
VERSION CF222676.1 GI:33423384
KEYWORDS EST.
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 906)
NIH-MGC http://mhc.mcl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL COMMENT
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NCI
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgsbbs-remail.nih.gov
Tissue Procurement: Robert M. Grainger
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM14642 row: c column: 12
High quality sequence start: 4
High quality sequence stop: 715.
Location/Qualifiers

FEATURES
source
1..906
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="IMAGE:6981253"
/tissue_type="gastrula"
/dev_stage="embryo, stages 10-13"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NICHD XGC Emb5"
/note="Vector: pCMV-SF0R6.1; Site 1: NotI; Site 2: EcoRV;
cloned unidirectionally. Primer: Oligo dT. Average insert
size 2.0 kb. Constructed by Invitrogen. Note: This is a
Xenopus Gene Collection (XGC) library."

ORIGIN
Query Match 84.8%; Score 17.8; DB 5; Length 906;
Best Local Similarity 90.5%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAGGACACAGTGGCTTTGAC 21
|||||
Db 755 CAGGACACAGTGGCTTTGAC 735
|||||

RESULT 46
CC304636 971 bp DNA linear GSS 13-MAY-2003
LOCUS CH261-89N15.RM1.1 CH261 Gallus gallus genomic clone CH261-89N15,
DEFINITION genomic survey sequence.
ACCESSION CC304636
VERSION CC304636.1 GI:30676077
KEYWORDS GSS.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archaeopteryx; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 971)
AUTHORS Kremitzki,C., Higgsibotham,J., Wylie,K., Carter,J., McPherson,J.,
Warren,M., Graves,T., Mardis,E. and Wilson,R.
JOURNAL Gallus gallus BAC End Reads
COMMENT Unpublished (2003)
Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submis@wustl.edu
Insert length: 182000 Std Error: 0.00
Seq primer: RM1 TACGACTGACTATAGGAGGA
Class: BAC ends
High quality sequence start: 34
High quality sequence stop: 713.
Location/Qualifiers

FEATURES
source
1..971
/organism="Gallus gallus"
/mol_type="genomic DNA"
/strain="Red Jungle Fowl"

/db_xref="taxon:9031"
/clone="CH261-89N15"
/sex="female"
/cell_line="UCD001, inbred 256"
/clone_1ib="CH261"
/note="Vector: pTRAC2.1; Site 1: EcoRI; Site 2: EcoRI;
CH261 Female Chicken library - for library and clone
ordering information: http://www.chori.org/bacpac"

ORIGIN
Query Match 84.8%; Score 17.8; DB 12; Length 971;
Best Local Similarity 90.5%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAGGACACAGTGGCTTTGAC 21
|||||
Db 125 CAGGACACAGTGGCTTTGAC 145
|||||

RESULT 47
AK034662 2617 bp mRNA linear HTC 02-SEP-2005
LOCUS Mus musculus 12 days embryo embryonic body between diaphragm region
DEFINITION and neck cDNA, RIKEN full-length enriched library, clone:1943002A14
product:hypothetical protein, full insert sequence.
ACCESSION AK034662
VERSION AK034662.1 GI:26330096
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.

REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagao,K., Sasaki,N., Carninci,P.,
Kono,H., Akiyama,U., Nishi,K., Kikunishi,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishino,T., Harada,A.,
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Matsubuchi,M.,
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuyama,S., Kawai,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
PUBMED 11076861
REFERENCE 5
AUTHORS The FANTOM Consortium, the RIKEN Genome Exploration Research Group
Phase I and II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
PUBMED 11076861
REFERENCE 6
AUTHORS RIKEN Genome Exploration Research Group, Genome Science Group
(Genome Network Core Team) and the PANTOM Consortium.
TITLE Antisense Transcription in the Mammalian Transcriptome
JOURNAL Science 309, 1564-1566 (2005)

REFERENCE
AUTHORS
TITLE
JOURNAL
AUTHORS

7
The FANTOM Consortium, Riken Genome Exploration Research Group and
Genome Science Group (Genome Network Project Core Group).
The Transcriptional Landscape of the Mammalian Genome
Science 309, 1559-1563 (2005)
8 (bases 1 to 2617)
Adachi, J., Alizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T.,
Hori, P., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kaubawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takaishi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M., and Hayashizaki, Y.

TITLE
JOURNAL

Submitted (16-JUN-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
URI:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)

COMMENT
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URI:http://genome.gsc.riken.jp/
URI:http://fantom.gsc.riken.jp/
Location/Qualifiers

FEATURES
source

1. 2617
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:9430022A14"
/db_xref="taxon:10090"
/clone="9430022A14"
/tissue_type="embryonic body between diaphragm region and
neck"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="12 days embryo"
/dev_1624
/note="unnamed protein product; hypothetical protein
(evidence: Procrest,decoder, longest-ORF)
putative"
/codon_start=1
/protein_id="BAC28787.1"
/db_xref="GI:26330097"
/translation="MRPAPGAPRCLTSMASLFCASASTLPGPMAAKWKEPFLTL
KTASRRARPGAGKGRKNSGTGAAPRGAATGAGKNSAGLGSASGPPDSRSD
SLQITLAAAGKGRKNSGTGAAPRGAATGAGKNSAGLGSASGPPDSRSD
AYPGGGSSTSSSSSSSSSSSSSSSSSSSGPELDRAKIRQDDTYIIEDYADPDAKRTG
QRDAERLVGENDGYMEPYDAQMTIEIRKGSADPLVKALQLIDSGSEGEVYKVAATA
KRQSSKDLGRPEQLYTPPEBSGQVAVKTRPAPSRLEBEDRPAEAEQPEW
KREQIALSLVQPEBSRPGEDRPHHOKTKPLTSLDGHGDEDPGALAEKOP
WYHGISRAEASRLQPCKEAYLVAVRNSGSKSYIALTKTSGCVHIIIVQTKONKY
TLNQTSAVFDSIPRYVHYHYSNAKLPRKGAEMHTLHPHKLH"

ORIGIN

Query Match 84.8%; Score 17.8; DB 6; Length 2617;
Best Local Similarity 90.5%; Pired. No. 1.8e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAGGACACAGTGGCTTTGAC 21
|||||
DB 1756 CAGGACACAGTGGCTTTGAC 1776
|||||

RESULT 48
AC157580
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AK157580 5736 bp mRNA linear HNC 21-SRP-2005
Mus musculus activated spleen cDNA, RIKEN full-length enriched
library, clone: F830224M15 product: hypothetical protein, full insert
sequence.
AK157580.1 GI:74185930
HNC, CAP trapper.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED

Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
10349636

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
11042159

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED

Shibata, K., Itoh, M., Alizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P.,
Kono, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M.,
Sun, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Maehachi, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multichipillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
11076861

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED

Kawai, J., Shingawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
Arakawa, T., Hara, A., Fukunishi, Y., Kono, H., Adachi, J., Fukuda, S.,
Alizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I.,
Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kaubawa, T., Saito, R.,
Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
Pletschmann, W., Gaasterland, T., Gissi, C., King, B., Kochiya, H.,
Kuehl, P., Lewis, S., Matsuo, Y., Nikaio, T., Pesole, G.,
Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M.,
Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,
Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,
Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C.,
Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P.,
Marchionni, L., Mashima, J., Mazzei, L., Mombauts, P., Nordone, P.,
Rising, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
Sato, K., Schonbach, C., Sessa, T., Shibata, Y., Storch, K.F., Suzuki, H.,
Tayo-Oka, K., Wang, K.H., Weitz, C., Whiteaker, C., Williams, L.,
Wyshaw-Borja, A., Yoshida, K., Haegawa, Y., Kawaji, H., Kortsch, S.,
and Hayashizaki, Y.
RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
11217851

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED

Okazaki, Y., Furuno, M., Kaubawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Ohsato, N., Saito, R., Suzuki, H., Yamana, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Haegawa, Y., Nogami, A.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,
Hume, D.A., Quackenbush, J., Schriml, L.M., Kamapin, A., Matsuda, H.,
Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,
Chotia, C., Corbani, L.R., Cousins, S., Dalia, B., Dragan, T.A.,
Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,

CONSRM	Guatincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kurochi, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konegaya, A., Kuvshinov, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, M.J., Petrea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sanderlin, A., Schneider, C., Sempile, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Velardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.
JOURNAL	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
PUBMED	Nature 420 (6915), 563-573 (2002)
REFERENCE	12466851
AUTHORS	6
CONSRM	Carninci, P., Kasukawa, T., Katayama, S., Gough, J., Frith, M.C., Maeda, N., Oyama, R., Ravasi, T., Lenhard, B., Wells, C., Kodzius, R., Shinkawa, K., Bail, V.B., Brenner, S.B., Batalov, S., Forrest, A.R., Zavolan, M., Davis, M.J., Wilming, L.G., Aidinis, V., Allen, J.E., Ambesi-Impolato, A., Apweiler, R., Aurali, R.N., Bailey, T.L., Barnes, M., Baxter, L., Beisel, K.W., Bersano, T., Bono, H., Chalk, A.M., Chiu, K.P., Choudhary, V., Chistol, A., Clutterbuck, D.R., Crowe, M.L., Dalla, E., Dalrymple, B.P., de Bonis, D., Della Gatta, G., di Bernardo, D., Down, T., Engstrom, P., Fagiolini, M., Faulkner, G., Fletcher, C.F., Fukushima, T., Furum, M., Fukui, S., Gariboldi, M., Georgi-Hemming, P., Gingeras, T.R., Gojovic, T., Green, R.B., Guettich, S., Harbers, M., Hayashi, Y., Hensch, T.K., Hirokawa, N., Hill, D., Hummel, L., Iacono, M., Ikeo, K., Iwama, A., Ishikawa, T., Jakt, M., Kanapin, A., Katoh, M., Kawasawa, Y., Kelso, J., Kitamura, H., Kitano, H., Koike, G., Krishnan, S.P., Kruger, A., Kummerfeld, S.K., Kurochkin, I.V., Lareau, L.F., Lazarevic, D., Lipovich, L., Liu, J., Ljun, S., McWilliam, S., Madan Babu, M., Madera, M., Marchionni, L., Matsuda, H., Matsuzawa, S., Miki, H., Mignone, F., Miyake, S., Morita, K., Mottagui-Tabar, S., Mulder, N., Nakano, N., Nakachi, H., Ng, P., Nilsson, R., Nishiguchi, S., Nishikawa, S., Nori, F., Ohara, O., Okazaki, Y., Orlando, V., Pang, K.C., Pavan, M.J., Pavoni, G., Pesole, G., Petrovsky, N., Piazza, S., Reed, J., Reid, J.F., Ring, B.Z., Ringwald, M., Rost, B., Ruan, Y., Salzberg, S.L., Sanderlin, A., Schneider, C., Schonbach, C., Sekiguchi, K., Sempile, C.A., Seno, S., Sessa, L., Sheng, Y., Shibata, Y., Shimada, H., Shimada, K., Silva, D., Sincalir, B., Sperling, S., Stupka, R., Sugitani, K., Sultana, R., Takenaka, Y., Taki, K., Tammo, K., Tan, S.L., Tang, S., Taylor, M.S., Teener, J., Teichmann, S.A., Ueda, H.R., van Nimwegen, E., Verardo, R., Wei, C.L., Yang, K., Yamashita, H., Zabarovsky, E., Zhu, S., Zimmer, A., Hilde, W., Bul, C., Grimmond, S.M., Teasdale, R.D., Liu, E.T., Brune, V., Quackenbush, J., Wahlestedt, C., Mattick, J.S., Hume, D.A., Kai, C., Sasaki, D., Tomaru, Y., Fukuda, S., Kanamori, K., Katayama, M., Suzuki, M., Aoki, J., Arakawa, T., Iida, J., Imamura, K., Itoh, M., Kato, T., Kawaji, H., Kawagashira, N., Kawashima, T., Kojima, M., Kondo, S., Konno, H., Nakano, K., Ninomiya, N., Nishio, T., Okada, M., Plessey, C., Shibata, K., Shiraki, T., Suzuki, S., Tagami, M., Waki, K., Watanabe, A., Okamura-Oho, Y., Suzuki, H., Kawai, J. and Hayashizaki, Y.
JOURNAL	The transcriptional landscape of the mammalian genome
PUBMED	Science 309 (5740), 1559-1563 (2005)
REFERENCE	16141072
AUTHORS	7
CONSRM	Katayama, S., Tomaru, Y., Kasukawa, T., Waki, K., Nakashima, M., Nakamura, M., Nishida, H., Yap, C.C., Suzuki, M., Kawai, J., Suzuki, H., Carninci, P., Hayashizaki, Y., Wells, C., Frith, M., Ravasi, T., Pang, K.C., Hallinan, J., Mattick, J., Hume, D.A., Lipovich, L., Batalov, S., Engstrom, P.G., Mizuno, Y., Faghihi, M.A., Sanderlin, A., Chalk, A.M., Mottagui-Tabar, S., Liang, Z., Lenhard, B. and Wahlestedt, C.

CONSRM	RIKEN Genome Exploration Research Group
JOURNAL	Antisense transcription in the mammalian transcriptome
PUBMED	Science 309 (5740), 1554-1566 (2005)
REFERENCE	16141073
AUTHORS	8 (bases 1 to 5736)
CONSRM	Arkawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hori, F., Iida, J., Imamura, K., Imotani, K., Itoh, M., Kanagawa, S., Kawai, J., Kojima, M., Konno, H., Murata, M., Nakamura, M., Ninomiya, N., Nishiyori, H., Nomura, K., Ohno, M., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shiraki, T., Tagami, M., Tagami, Y., Waki, K., Watanabe, A., Muramatsu, M. and Hayashizaki, Y.
JOURNAL	Direct Submission
PUBMED	Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Science Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suenho-cho, Tsunumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gscc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge. Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/. location/Qualifiers
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DB	1745 CAGGACACAGTGGCTTTTGCAC 1765
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DEFINITION	t1gr-gss-dog-17000368649375 Dog Library Canis familiaris genomic,
ACCESSION	CE693411
VERSION	CE693411.1 GI:37012481

KEYWORDS	GSS.
SOURCE	Canis familiaris (dog)
ORGANISM	Canis familiaris
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.
AUTHORS	1 (bases 1 to 390) Kirkness, B.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Ruesch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.
TITLE	The dog genome: survey sequencing and comparative analysis
JOURNAL	Science 301 (5641), 1898-1903 (2003)
PUBMED	14512627
COMMENT	Contact: Kirkness EF The Institute for Genomic Research Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-0200 Fax: 301-838-0208 Email: ekirkness@tigr.org Class: shotgun. Location/Qualifiers
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Db	
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DEFINITION	HS_5147_A1_A10_SPE6 RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=723 Col=19 Row=A, genomic library sequence.
ACCESSION	AQ435575
VERSION	AQ435575.1 GI:4546914
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SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.	
1 (bases 1 to 430)	
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.	
Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome	
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)	
10449764	
Contact: Mahairas GG, Wallace JC, Hood L	
High Throughput Sequencing Center	
University of Washington	
401 Queen Anne Avenue North, Seattle, WA 98109, USA	
Tel: (206) 616-3618	
Fax: (206) 616-3887	
Email: jwallace@u.washington.edu	
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)	
TITLE	
JOURNAL	
PUBMED	
COMMENT	

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FEATURES
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EcoRI Methylase. Size selected DNA was cloned into the
pBACe3.6 vector at EcoRI sites"

ORIGIN

Query Match      82.9%; Score 17.4; DB 11; Length 430;
Best Local Similarity 94.7%; Prod. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 24, 2006, 05:34:58 ; Search time 300.037 Seconds
(without alignments)
650.664 Million cell updates/sec

Title: US-10-601-913-5

Perfect score: 28

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 1000 summaries

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2: geneseqn1980s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002as:*

7: geneseqn2002bs:*

8: geneseqn2003as:*

9: geneseqn2003bs:*

10: geneseqn2003cs:*

11: geneseqn2003ds:*

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13: geneseqn2004bs:*

14: geneseqn2005s:*

15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	28	100.0	28	2	AAT72300 Human pap
3	28	100.0	28	2	AAT72335 Human pap
4	28	100.0	28	2	AAT72299 Human pap
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7	28	100.0	456	2	ABO76223 Human pap
8	28	100.0	459	10	ADG37149 HPV
9	28	100.0	477	10	ADP09607 Human pap
10	28	100.0	477	10	AAL54430 B6 gRNA
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C	95	19	67.9	450	12	ADO44104	Ado44104 Nucleotid	C 168	18.4	65.7	12880	11	ADN39609	Adn39609 Cancer/an
C	96	19	67.9	453	4	AAI15124	AAI15124 Probe #50	C 169	18.4	65.7	13202	4	AAK51828	Aak51828 Human pol
C	97	19	67.9	453	4	ABAS6878	Abas6878 Human foe	C 170	18.4	65.7	13202	4	AAK51828	Adz42284 Human K10
C	98	19	67.9	453	4	AAI36460	AAI36460 Probe #51	C 171	18.2	65.0	131	4	AAI26845	AAI26845 Probe #16
C	99	19	67.9	453	4	ABAA6321	Abaa6321 Human bre	C 172	18.2	65.0	131	4	ABAA7508	Abaa7508 Human foe
C	100	19	67.9	453	4	AAK04982	AAK04982 Human bra	C 173	18.2	65.0	131	4	AAI55634	AAI55634 Probe #24
C	101	19	67.9	453	5	AAI04876	AAI04876 Probe #48	C 174	18.2	65.0	131	4	AAK49738	AAK49738 Human bon
C	102	19	67.9	533	4	AAK42809	AAK42809 Human G P	C 175	18.2	65.0	131	4	AAK23614	AAK23614 Human bra
C	103	19	67.9	534	4	ABAA69015	ABAA69015 Human foe	C 176	18.2	65.0	131	4	ABSA49367	ABSA49367 Human liv
C	104	19	67.9	534	4	AAI49205	AAI49205 Probe #17	C 177	18.2	65.0	131	6	ABSA23230	ABSA23230 Human gen
C	105	19	67.9	534	4	ABAA51025	ABAA51025 Human bre	C 178	18.2	65.0	417	6	ABN95008	ABN95008 Gene #150
C	106	19	67.9	534	4	AAK43128	AAK43128 Human bon	C 179	18.2	65.0	467	10	ADBS81762	Adbs81762 Arabidops
C	107	19	67.9	534	4	ABSA42760	ABSA42760 Human liv	C 180	18.2	65.0	514	4	AAI17640	AAI17640 Probe #75
C	108	19	67.9	534	5	AAI09498	AAI09498 Probe #94	C 181	18.2	65.0	514	4	ABAA62577	ABAA62577 Human foe
C	109	19	67.9	924	4	AAI24453	AAI24453 Probe #14	C 182	18.2	65.0	514	4	AAI42565	AAI42565 Probe #11
C	110	19	67.9	924	4	ABAA51552	ABAA51552 Human bre	C 183	18.2	65.0	514	4	AAK36788	AAK36788 Human bon
C	111	19	67.9	924	4	ABAA36526	ABAA36526 Probe #14	C 184	18.2	65.0	514	4	AAK10934	AAK10934 Human bra
C	112	19	67.9	924	6	ABSA17863	ABSA17863 Human gen	C 185	18.2	65.0	514	4	ABSA36451	ABSA36451 Human liv
C	113	19	67.9	1033	6	AAQ48575	AAQ48575 HPV B6/77	C 186	18.2	65.0	514	6	ABSA10792	ABSA10792 Human gen
C	114	19	67.9	1069	12	ADBS0784	ADBS0784 Porcine e	C 187	18.2	65.0	531	6	ABV95791	ABV95791 Human pan
C	115	19	67.9	1961	4	AAI15278	AAI15278 Probe #52	C 188	18.2	65.0	534	6	ABV95677	ABV95677 Human pan
C	116	19	67.9	1961	4	ABAA46452	ABAA46452 Human bre	C 189	18.2	65.0	534	6	ABV95677	ABV95677 Arabidops
C	117	19	67.9	1961	4	ABAA26658	ABAA26658 Probe #51	C 190	18.2	65.0	632	3	AAK38756	AAK38756 Arabidops
C	118	19	67.9	1961	6	ABSA05364	ABSA05364 Human gen	C 191	18.2	65.0	1239	12	ADBS5282	Adbs5282 HPTP-1 co
C	119	19	67.9	2353	4	AAI19563	AAI19563 Probe #94	C 192	18.2	65.0	1239	12	ADBS5282	AAV29126 HPTP-1 co
C	120	19	67.9	2353	4	ABAA64582	ABAA64582 Human foe	C 193	18.2	65.0	1239	2	AAV29126	AAV29126 HPTP-1 co
C	121	19	67.9	2353	4	AAI44754	AAI44754 Probe #13	C 194	18.2	65.0	1695	3	AAK34705	AAK34705 Arabidops
C	122	19	67.9	2353	4	ABAA6708	ABAA6708 Human bre	C 195	18.2	65.0	2200	6	ABL63311	ABL63311 Breast ca
C	123	19	67.9	2353	4	ABAA31710	ABAA31710 Probe #10	C 196	18.2	65.0	2200	6	ABL62890	ABL62890 Human pro
C	124	19	67.9	2353	4	AAK38756	AAK38756 Human bon	C 197	18.2	65.0	2200	6	ABK64351	ABK64351 Human CDN
C	125	19	67.9	2353	4	AAK33028	AAK33028 Human bra	C 198	18.2	65.0	2200	6	ABN96871	ABN96871 Gene #336
C	126	19	67.9	2353	4	ABSA38334	ABSA38334 Human liv	C 199	18.2	65.0	2441	3	AAK98926	AAK98926 Human pan
C	127	19	67.9	2353	5	AAI05284	AAI05284 Probe #52	C 200	18.2	65.0	2853	8	ACAA37230	ACAA37230 Prokaryot
C	128	19	67.9	2353	5	ABSA12830	ABSA12830 Human gen	C 201	18.2	65.0	2916	10	ADBS97788	Adbs97788 Human pro
C	129	19	67.9	4230	8	ADBS69573	ADBS69573 C. neofo	C 202	18.2	65.0	2916	15	ABE86404	ABE86404 Human pro
C	130	19	67.9	4230	8	ABX12953	ABX12953 DNA encod	C 203	18.2	65.0	3357	10	ADBS98075	ADBS98075 Hepatic s
C	131	19	67.9	4230	8	ADBS6265	ADBS6265 DNA encod	C 204	18.2	65.0	4342	3	AAZ51564	AAZ51564 Human hyp
C	132	19	67.9	4352	14	ABED22627	ABED22627 Human mut	C 205	18.2	65.0	4342	8	ABSA6338	ABSA6338 Human gen
C	133	19	67.9	4895	10	ADBS62900	ADBS62900 Human MLH	C 206	18.2	65.0	4394	12	ADBS03661	ADBS03661 Antipso
C	134	19	67.9	4895	12	ADBS44520	ADBS44520 Human PRO	C 207	18.2	65.0	4394	12	ADBS20794	ADBS20794 Human pro
C	135	19	67.9	4895	12	ADBS66691	ADBS66691 Human mls	C 208	18.2	65.0	4394	14	ADBS08167	ADBS08167 Cyclin-de
C	136	19	67.9	4895	14	ADBS3442	ADBS3442 Human MLH	C 209	18.2	65.0	4626	8	ACCA6213	ACCA6213 Human dit
C	137	19	67.9	4895	14	ABSA23877	ABSA23877 Human PRO	C 210	18.2	65.0	5099	14	ADBS80561	ADBS80561 Protein t
C	138	19	67.9	4895	14	ABED22625	ABED22625 Human mut	C 211	18.2	65.0	5289	5	ADBS3192	ADBS3192 Human ova
C	139	19	67.9	4895	14	ABED22626	ABED22626 Human mut	C 212	18.2	65.0	110000	14	ABSA39175_04	ABSA39175_04 Cont
C	140	19	67.9	4895	14	ADBS69212	ADBS69212 C. neofo	C 213	18.2	65.0	243335	14	ABSA42401_04	ABSA42401_04 Cont
C	141	19	67.9	5130	11	ACNA4919	ACNA4919 Human mRN	C 214	18.2	65.0	256294	13	ABBS33020	ABBS33020 Mouse can
C	142	19	67.9	5210	11	ACNA91621	ACNA91621 Breast ca	C 215	18.2	65.0	295644	14	ABBS35721	ABBS35721 L. pneumo
C	143	19	67.9	5212	3	AAK76356	AAK76356 Human ORF	C 216	18.2	65.0	295644	14	ABBS35721	ABBS35721 L. pneumo
C	144	19	67.9	8307	6	ABK90804	ABK90804 DNA encod	C 217	18.2	65.0	298667	12	AAK39173	AAK39173 L. pneumo
C	145	19	67.9	32134	4	AAI03615	AAI03615 Human rep	C 218	18.2	64.3	18	2	AAK40319	AAK40319 Primer fo
C	146	19	67.9	32134	4	ABAA07813	ABAA07813 Human ova	C 219	18.2	64.3	289	2	AAK40091	AAK40091 PCR prime
C	147	19	67.9	32134	4	AAI03616	AAI03616 Human rep	C 220	18.2	64.3	918	8	ACAA29376	ACAA29376 Prokaryot
C	148	19	67.9	32134	4	ABAA07814	ABAA07814 Human ova	C 221	18.2	64.3	918	8	ACAA29376	ACAA29376 Prokaryot
C	149	19	67.9	55114	11	ACNA4918	ACNA4918 Human gen	C 222	18.2	64.3	3001	14	ADBS61200	ADBS61200 Mxine Yth
C	150	19	67.9	110000	11	ADBS1651_1	ADBS1651_1 Cont	C 223	18.2	64.3	21921	4	ABLO5352	ABLO5352 Cont
C	151	19	67.9	110000	14	ADBS1651_2	ADBS1651_2 Cont	C 224	18.2	64.3	110000	11	ACNA44150_3	ACNA44150_3 Cont
C	152	19	67.9	110000	14	ADBS1651_2	ADBS1651_2 Cont	C 225	18.2	64.3	110000	13	ABDS32921_0	ABDS32921_0 Cont
C	153	19	67.9	110000	14	ADBS1651_2	ADBS1651_2 Cont	C 226	18.2	64.3	110000	13	ABDS32921_1	ABDS32921_1 Cont
C	154	19	67.9	144723	11	ACNA4898	ACNA4898 Human gen	C 227	18.2	64.3	142299	10	ADBS0651	ADBS0651 BAC seque
C	155	19	67.9	276276	11	ACNA4350	ACNA4350 Human gen	C 228	18.2	64.3	142299	14	ADBS77909	ADBS77909 Human BAC
C	156	19	67.9	276276	11	ADBS9380	ADBS9380 Human can	C 229	18.2	64.3	349981	10	ADBS7619	ADBS7619 Human GPC
C	157	19	67.9	276276	11	ADBS9380	ADBS9380 Human can	C 230	18.2	64.3	349981	10	ADBS7619	ADBS7619 Human GPC
C	158	18.6	66.4	912	5	ABAS8414	ABAS8414 Bacterial	C 231	17.8	63.6	421	4	AAK5167	AAK5167 Human imm
C	159	18.6	66.4	32184	5	ABAS20589	ABAS20589 Human ner	C 232	17.8	63.6	25461	11	ACNA45168	ACNA45168 Human pro
C	160	18.6	66.4	32184	5	ABAS20589	ABAS20589 Human ner	C 233	17.8	63.6	104514	5	ABV47896	ABV47896 Human col
C	161	18.6	66.4	38272	4	AAK4952	AAK4952 Human imm	C 234	17.6	62.9	589	14	AAZ50946	AAZ50946 Photo
C	162	18.6	66.4	38272	4	AAK4952	AAK4952 Human imm	C 235	17.6	62.9	781	3	AAZ50946	AAZ50946 Photo
C	163	18.6	66.4	70435	14	ABBS32384	ABBS32384 Human gen	C 236	17.6	62.9	781	3	AAZ50946	AAZ50946 Photo
C	164	18.6	66.4	100696	14	ABBS32384	ABBS32384 Human gen	C 237	17.6	62.9	1190	3	AAZ50946	AAZ50946 Photo

C 238	17.6	62.9	1206	3	AAZ50948	Aaz50948 luxRV fu	311	17.4	62.1	2842	4	ABL28100	Ab128100 Drosophila
C 239	17.6	62.9	1487	13	ADX27604	Adx27604 Plant ful	312	17.4	62.1	3250	3	AAA64292	AAa64292 Nucleoid
C 240	17.6	62.9	1489	13	AD062673	Ad062673 Transcript	313	17.4	62.1	3579	3	ABL14708	Ab114708 Drosophila
C 241	17.6	62.9	1504	12	ADM28734	Adm28734 Bacterial	314	17.4	62.1	4643	13	ADT05451	Adt05451 Haemophil
C 242	17.6	62.9	1513	12	ADM28738	Adm28738 Bacterial	315	17.4	62.1	4751	4	ABL16318	Ab116318 Drosophila
C 243	17.6	62.9	1537	5	AAF57764	Aaf57764 Oligonuc	316	17.4	62.1	4816	10	ADD46187	Add46187 Rat gene
C 244	17.6	62.9	1537	14	AED33577	Aed33577 Expressio	317	17.4	62.1	4839	4	ADBE62381	Adbe62381 Rat gene
C 245	17.6	62.9	1545	3	AAA69452	Aaa69452 Plasmid p	318	17.4	62.1	4939	10	ABL14642	Ab114642 Drosophila
C 246	17.6	62.9	1546	2	AAV04373	Aav04373 Sequence	319	17.4	62.1	4993	2	AAO12994	Aao12994 HincII fr
C 247	17.6	62.9	1546	5	AAV57768	Aav57768 Oligonuc	320	17.4	62.1	4993	2	AAO73385	Aao73385 HincII fr
C 248	17.6	62.9	1546	6	ABK24112	Abk24112 Expressio	321	17.4	62.1	5268	4	ABL16316	Ab116316 Drosophila
C 249	17.6	62.9	1546	6	ABL35769	Ab135769 Plasmid p	322	17.4	62.1	5660	5	ABAI9013	Abai9013 Human ner
C 250	17.6	62.9	1546	10	ABT33898	Abt33898 pCFM1656	323	17.4	62.1	6439	13	ADT95948	Adt95948 Human imm
C 251	17.6	62.9	1546	14	ABE19733	Aeb19733 pMG21 ex	324	17.4	62.1	6439	13	ADT95948	Adt95948 Human imm
C 252	17.6	62.9	1546	14	AED33581	Aed33581 Expressio	325	17.4	62.1	7529	6	AAV66694	Aav66694 Arabidops
C 253	17.6	62.9	1548	14	ABE19862	Aeb19862 pMG21 ex	326	17.4	62.1	8580	6	AAV66694	Aav66694 Arabidops
C 254	17.6	62.9	1731	13	ADT63920	Adt63920 Cotton CD	327	17.4	62.1	8580	11	ADM39547	Adm39547 DW7 polyn
C 255	17.6	62.9	1731	13	ADT63920	Adt63920 Cotton CD	328	17.4	62.1	9128	15	ABE40104	Abe40104 HIV1 RF v
C 256	17.6	62.9	1731	13	ADT63920	Adt63920 Cotton CD	329	17.4	62.1	10478	4	AAV42059	Aav42059 Arabidops
C 257	17.6	62.9	1731	13	ADT63920	Adt63920 Cotton CD	330	17.4	62.1	10478	4	AAV42059	Aav42059 Arabidops
C 258	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	331	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 259	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	332	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 260	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	333	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 261	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	334	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 262	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	335	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 263	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	336	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 264	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	337	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 265	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	338	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 266	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	339	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 267	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	340	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 268	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	341	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 269	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	342	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 270	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	343	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 271	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	344	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 272	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	345	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 273	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	346	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 274	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	347	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 275	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	348	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 276	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	349	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 277	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	350	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 278	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	351	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 279	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	352	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 280	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	353	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 281	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	354	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 282	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	355	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 283	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	356	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 284	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	357	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 285	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	358	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 286	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	359	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 287	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	360	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 288	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	361	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 289	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	362	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 290	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	363	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 291	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	364	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 292	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	365	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 293	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	366	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 294	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	367	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 295	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	368	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 296	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	369	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 297	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	370	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 298	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	371	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 299	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	372	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 300	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	373	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 301	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	374	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 302	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	375	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 303	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	376	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 304	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	377	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 305	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	378	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 306	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	379	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 307	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	380	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 308	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	381	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 309	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	382	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops
C 310	17.6	62.9	19371	4	AAV05706	Aav05706 Human rep	383	17.4	62.1	11453	4	AAV42060	Aav42060 Arabidops

C 384	17	60.7	528	4	AAK67947	AAK67947 Human imm	457	17	60.7	3800	12	AD035541	AD035541 Novel mou
C 385	17	60.7	528	4	AAK67946	AAK67946 Human imm	458	17	60.7	3952	4	ABL02940	ABL02940 Drosophi1
C 386	17	60.7	597	2	AAE68028	AAE68028 H. pylori	459	17	60.7	4044	4	ABL02942	ABL02942 Drosophi1
C 387	17	60.7	601	13	ADV15561	ADV15561 Human oet	460	17	60.7	4224	5	AA594229	AA594229 DNA encod
C 388	17	60.7	601	14	ABR33554	ABR33554 Human DNA	461	17	60.7	4224	5	AA592704	AA592704 DNA encod
C 389	17	60.7	700	14	AAH92940	AAH92940 Human int	462	17	60.7	4224	5	AA588559	AA588559 DNA encod
C 390	17	60.7	877	5	ABV22831	ABV22831 Human pro	463	17	60.7	4350	2	ACA12252	ACA12252 Neteeria
C 391	17	60.7	877	5	ABV28661	ABV28661 Human pro	464	17	60.7	4350	8	ACA11657	ACA11657 Prokaryot
C 392	17	60.7	894	4	AAH06922	AAH06922 Human CDN	465	17	60.7	4350	14	ABR94960	ABR94960 M. mening
C 393	17	60.7	921	14	ACI65551	ACI65551 M. xanthu	466	17	60.7	4350	14	ABR91910	ABR91910 DNA encod
C 394	17	60.7	1083	8	ABX06440	ABX06440 S. pneumo	467	17	60.7	4355	3	AAZ38917	AAZ38917 Neisseria
C 395	17	60.7	1086	8	ACA49832	ACA49832 Prokaryot	468	17	60.7	4378	6	ABQ70913	ABQ70913 Listeria
C 396	17	60.7	1086	13	ADK43557	ADK43557 Streptococ	469	17	60.7	4399	10	AD555113	AD555113 Human gen
C 397	17	60.7	1095	13	ADK93568	ADK93568 Novel S.	470	17	60.7	5558	2	AAV52266	AAV52266 Streptococ
C 398	17	60.7	1095	14	AEA57438	AEA57438 Streptococ	471	17	60.7	5573	2	AAV54058	AAV54058 Drosophi1
C 399	17	60.7	1317	12	AD007229	AD007229 Human org	472	17	60.7	15572	14	ACI64668	ACI64668 M. xanthu
C 400	17	60.7	1317	14	ABR93649	ABR93649 Human tra	473	17	60.7	28486	9	ADD56096	ADD56096 Mouse Ccn
C 401	17	60.7	1410	6	ABQ68821	ABQ68821 Listeria	474	17	60.7	28486	9	ADA02458	ADA02458 Mouse Ccn
C 402	17	60.7	1536	6	ABN93116	ABN93116 Staphyloc	475	17	60.7	28486	10	ADB72197	ADB72197 Mouse Ccn
C 403	17	60.7	1536	13	AD502384	AD502384 Staphyloc	476	17	60.7	28486	10	AD582929	AD582929 Mouse Ccn
C 404	17	60.7	1566	14	ABE67765	ABE67765 Rice geno	477	17	60.7	29695	6	ABO78853	ABO78853 Human PPM
C 405	17	60.7	1611	9	ACD40273	ACD40273 Human bre	478	17	60.7	29871	13	ADS36480	ADS36480 Human aut
C 406	17	60.7	1611	9	ADM56404	ADM56404 Human CDN	479	17	60.7	31960	14	ABR44604	ABR44604 Sleep dis
C 407	17	60.7	1611	11	ADM56404	ADM56404 Human CDN	480	17	60.7	33231	14	ABE61135	ABE61135 Human HPG
C 408	17	60.7	1611	11	ADM56404	ADM56404 Human CDN	481	17	60.7	33231	14	ABE61135	ABE61135 Human HPG
C 409	17	60.7	1611	12	AD060276	AD060276 Human NOV	482	17	60.7	50272	4	ABL10156	ABL10156 Drosophi1
C 410	17	60.7	1612	12	AD119803	AD119803 Human NOV	483	17	60.7	53332	6	AAI48890	AAI48890 Human PFC
C 411	17	60.7	1748	10	ABQ83990	ABQ83990 Mouse ubi	484	17	60.7	54668	13	ADY87738	ADY87738 Streptococ
C 412	17	60.7	1748	12	ADY75854	ADY75854 Marker gen	485	17	60.7	54668	13	ADY78991	ADY78991 Streptococ
C 413	17	60.7	1813	12	AD008673	AD008673 Clona int	486	17	60.7	55906	13	ABD33337	ABD33337 Murine ca
C 414	17	60.7	1949	6	ABL14059	ABL14059 Arabidops	487	17	60.7	95001	12	AD079405	AD079405 CENPCL re
C 415	17	60.7	2000	6	AB215121	AB215121 Arabidops	488	17	60.7	95001	12	ADH56439	ADH56439 Human hyp
C 416	17	60.7	2006	10	AD585813	AD585813 Toxicity- r	489	17	60.7	96589	9	ADA02708	ADA02708 Human ZFH
C 417	17	60.7	2006	10	AD585813	AD585813 Toxicity- r	490	17	60.7	96589	9	ADB72446	ADB72446 Human ZFH
C 418	17	60.7	2006	13	ADY40982	ADY40982 Rat cardi	491	17	60.7	96589	10	AD595956	AD595956 Human ZFH
C 419	17	60.7	2006	13	ADY40982	ADY40982 Rat cardi	492	17	60.7	97415	13	ABD33254	ABD33254 Murine ca
C 420	17	60.7	2351	2	AAZ27259	AAZ27259 Human sec	493	17	60.7	110000	6	ABN71537	ABN71537 Streptococ
C 421	17	60.7	2351	8	ADA40378	ADA40378 Human sec	494	17	60.7	110000	10	AA053223_1	AA053223_1 Continuation (7 of
C 422	17	60.7	2351	8	ACC50751	ACC50751 Human sec	495	17	60.7	110000	10	AA053223_06	AA053223_06 Continuation (7 of
C 423	17	60.7	2351	8	ABZ71414	ABZ71414 Secretd	496	17	60.7	110000	13	ADY81204_00	ADY81204_00 Continuation (7 of
C 424	17	60.7	2351	9	ABZ71414	ABZ71414 Secretd	497	17	60.7	144392	15	ABP75162	ABP75162 Human pol
C 425	17	60.7	2351	10	ADC73861	ADC73861 Human sec	498	17	60.7	212231	11	ACN44598	ACN44598 Human gen
C 426	17	60.7	2351	10	ADA56544	ADA56544 Gene enco	499	17	60.7	242456	14	ABD76150	ABD76150 Mouse ca
C 427	17	60.7	2351	4	AAI60312	AAI60312 Human pol	500	17	60.7	312957	13	ADV15290	ADV15290 Human ca
C 428	17	60.7	2488	4	AAI58526	AAI58526 Human pol	501	17	60.7	312957	13	ABR32365	ABR32365 Human gen
C 429	17	60.7	2488	5	AD098743	AD098743 DNA encod	502	17	60.7	312972	13	ADV15293	ADV15293 Human oet
C 430	17	60.7	2486	8	ADBA48503	ADBA48503 Novel hum	503	17	60.7	312972	14	ABR32394	ABR32394 Human gen
C 431	17	60.7	2486	8	ADA39897	ADA39897 Human sec	504	17	60.7	313001	14	ADZ70075	ADZ70075 Human int
C 432	17	60.7	2486	8	ACC50487	ACC50487 Human sec	505	17	60.7	321019	13	ADS36450	ADS36450 Human int
C 433	17	60.7	2486	8	ABZ71269	ABZ71269 Human sec	506	17	60.7	325093	14	ABR25355	ABR25355 Human AR
C 434	17	60.7	2486	9	AD891175	AD891175 Human sec	507	17	60.7	325093	13	ABD32707	ABD32707 Human can
C 435	17	60.7	2486	10	ADC73550	ADC73550 Human sec	508	17	60.7	108	6	ABN88421	ABN88421 Mouse gen
C 436	17	60.7	2486	10	ADA56088	ADA56088 Gene enco	509	17	60.7	201	13	ADS38726	ADS38726 Human aut
C 437	17	60.7	2658	13	ADK54630	ADK54630 Plant ful	510	17	60.7	201	13	ADS38511	ADS38511 Human aut
C 438	17	60.7	2733	11	ADL22649	ADL22649 Human dis	511	17	60.7	201	13	ADK38724	ADK38724 Human imm
C 439	17	60.7	2913	14	AAH14622	AAH14622 Human CDN	512	17	60.7	669	5	AA591869	AA591869 DNA encod
C 440	17	60.7	2913	14	ADZ49660	ADZ49660 Insein s	513	17	60.7	802	5	ADJ38570	ADJ38570 Human ova
C 441	17	60.7	2981	4	ADDA6639	ADDA6639 Human gen	514	17	60.7	802	5	ADJ38570	ADJ38570 Human ova
C 442	17	60.7	3113	4	ABL18378	ABL18378 Drosophi1	515	17	60.7	802	5	ADJ38570	ADJ38570 Human ova
C 443	17	60.7	3732	4	ABL03714	ABL03714 Drosophi1	516	17	60.7	845	13	ADJ38570	ADJ38570 Human ova
C 444	17	60.7	3732	4	ABL20934	ABL20934 Drosophi1	517	17	60.7	845	13	ADJ38570	ADJ38570 Human ova
C 445	17	60.7	3737	8	AA056097	AA056097 Mouse Ccn	518	17	60.7	951	11	ACA37101	ACA37101 Mouse spe
C 446	17	60.7	3737	8	AA056097	AA056097 Mouse Ccn	519	17	60.7	1122	8	ACA37101	ACA37101 Rice abio
C 447	17	60.7	3737	10	ADH82198	ADH82198 Mouse Ccn	520	17	60.7	1248	13	ADT16096	ADT16096 Prokaryot
C 448	17	60.7	3737	10	ADH82198	ADH82198 Mouse Ccn	521	17	60.7	1356	10	ADG93171	ADG93171 E. faeciu
C 449	17	60.7	3751	10	ADH57823	ADH57823 Toxicity- r	522	17	60.7	1371	4	AA52516	AA52516 E. coli D
C 450	17	60.7	3751	10	ABT41704	ABT41704 Toxicity- r	523	17	60.7	1371	4	AA52516	AA52516 E. coli D
C 451	17	60.7	3751	11	ADW21750	ADW21750 Rat hepat	524	17	60.7	1530	8	ACA32583	ACA32583 Prokaryot
C 452	17	60.7	3751	12	AD009496	AD009496 Rat G1/8-	525	17	60.7	1574	6	ABK34944	ABK34944 Human CDN
C 453	17	60.7	3751	12	ADP72490	ADP72490 Renal tox	526	17	60.7	1516	6	ABO76427	ABO76427 S. cerevi
C 454	17	60.7	3751	12	ADP72490	ADP72490 Renal tox	527	17	60.7	1543	6	AA562515	AA562515 cDNA sequ
C 455	17	60.7	3751	13	ADV40791	ADV40791 Rat cardi	528	17	60.7	1786	14	ABD12000	ABD12000 Tobacco n
C 456	17	60.7	3751	14	ABE11825	ABE11825 Rat surro	529	17	60.7	1786	14	ABE06622	ABE06622 Tobacco n

C 530	16.8	60.0	1786	15	Aef97015	Tobacco n	603	16.6	59.3	47	3	AAZ65823	Aaz65823 Human map
531	16.8	60.0	1806	4	Aaf61036	P. putida	101	16.6	59.3	121	2	AAH85681	Aah85681 Human sin
532	16.8	60.0	1815	10	ADG28855	Perennial	C 604	16.6	59.3	121	12	ADK93903	Adk93903 Polynucle
533	16.8	60.0	1873	10	ADG28856	Tail feces	C 606	16.6	59.3	121	3	AAC23807	Aac23807 Human sec
534	16.8	60.0	1905	3	AAC79713	Human sec	607	16.6	59.3	121	12	ADP60308	Adp60308 Soybean c
535	16.8	60.0	2133	11	ADM01618	Human cdv	608	16.6	59.3	121	12	ADP59352	Adp59352 Soybean c
536	16.8	60.0	2133	14	AEC84548	Human cdv	609	16.6	59.3	265	12	ADP60307	Adp60307 Soybean c
537	16.8	60.0	2320	11	ADM03113	Human cdv	610	16.6	59.3	294	3	AAA43307	Aaa43307 Xenopus s
538	16.8	60.0	2320	14	AEC86043	Human cdv	C 611	16.6	59.3	385	5	ABV03093	Abv03093 Human pro
539	16.8	60.0	2341	10	ADB83479	Human cdv	C 612	16.6	59.3	408	5	ABV01262	Abv01262 Human pro
C 540	16.8	60.0	2464	6	ABQ70708	Listeria	C 613	16.6	59.3	446	5	ABV42330	Abv42330 Human pro
541	16.8	60.0	2647	11	ADM02143	Human cdv	C 614	16.6	59.3	446	5	ABV33407	Abv33407 Human pro
542	16.8	60.0	2647	14	AEC85073	Human cdv	C 615	16.6	59.3	459	6	ABN97022	Abn97022 Gene #352
543	16.8	60.0	2793	5	AA873600	DNA encod	C 616	16.6	59.3	461	13	ACR60858	Acf60858 Human SIR
544	16.8	60.0	3039	5	AA823385	DNA encod	C 617	16.6	59.3	552	13	ACR84219	Acf84219 Human SIR
C 545	16.8	60.0	3039	5	AA877331	DNA encod	C 618	16.6	59.3	644	13	ADX53382	Adx53382 Plant ful
546	16.8	60.0	3039	5	AA893075	DNA encod	C 619	16.6	59.3	684	8	ACA41274	Aca41274 Prokaryot
547	16.8	60.0	3333	5	AA889925	DNA encod	C 620	16.6	59.3	684	10	ABZ38326	Abz38326 N. gonorr
548	16.8	60.0	3344	10	ACA54668	Human NF-	C 621	16.6	59.3	784	14	AED14244	Aed14244 Human cum
549	16.8	60.0	3344	10	ADH83145	Human NF-	C 622	16.6	59.3	887	10	ADC24857	Adc24857 Human bre
550	16.8	60.0	3582	14	ABL17962	Human NF-	C 623	16.6	59.3	912	8	ADA29823	Ada29823 DNA encod
C 551	16.8	60.0	3684	11	ADM01821	Human cdv	C 624	16.6	59.3	914	8	ABZ51954	Abz51954 Aspergill
C 552	16.8	60.0	3684	14	AEC84751	Human cdv	C 625	16.6	59.3	1006	15	AEP11533	Aep11533 Rape meth
553	16.8	60.0	3910	5	AA879824	DNA encod	C 626	16.6	59.3	1044	6	ABZ13045	Abz13045 Arabidops
554	16.8	60.0	4092	14	AED81831	Hyperimmu	C 627	16.6	59.3	1125	4	AAH78265	Aah78265 Nucleotid
555	16.8	60.0	4109	3	AAAD00316	Human CAM	C 628	16.6	59.3	1439	12	ADP12796	Adp12796 Reference
556	16.8	60.0	4173	8	ABX71051	Novel hum	C 629	16.6	59.3	1544	3	AAC52745	Aac52745 Arabidops
557	16.8	60.0	4275	4	ABL09776	Drosophi	C 630	16.6	59.3	1750	2	AAT83352	Aat83352 B. c. alka
558	16.8	60.0	4275	4	ABL11776	Drosophi	C 631	16.6	59.3	1764	13	ADG46812	Adg46812 Bacteri
559	16.8	60.0	4845	12	ADQ23064	Human sof	C 632	16.6	59.3	1765	13	ADT05175	Adt05175 Haemophil
560	16.8	60.0	4845	12	ADQ25056	Human sof	C 633	16.6	59.3	2018	13	ADX54881	Adx54881 Plant ful
C 561	16.8	60.0	5008	8	ABK63351	Human sof	C 634	16.6	59.3	2188	2	AAQ79726	Aaq79726 Mouse L5/
C 562	16.8	60.0	6347	14	AED11994	Tobacco n	C 635	16.6	59.3	2188	2	AAT62441	Aat62441 Mouse gro
C 563	16.8	60.0	6347	14	AEE06617	Tobacco n	C 636	16.6	59.3	2213	12	AAV07384	Aav07384 DNA encod
C 564	16.8	60.0	6347	15	AEP97010	Tobacco n	C 637	16.6	59.3	2216	2	AAV72084	Aav72084 Mouse MSP
565	16.8	60.0	6675	12	ADQ97649	Mouse can	C 638	16.6	59.3	2324	4	ABL19952	Ab119952 Drosophi
566	16.8	60.0	11574	4	AA846244	DNA encod	C 639	16.6	59.3	2767	11	ADM64616	Adm64616 Mose (Phy
567	16.8	60.0	12832	9	ABK42692	Genomic s	C 640	16.6	59.3	2776	13	ADK60882	Adk60882 Plant ful
568	16.8	60.0	12832	9	ADB60848	Connectiv	C 641	16.6	59.3	3336	4	AA855220	Aae55220 StephiLoc
569	16.8	60.0	14226	6	ABL42494	Bacteriop	C 642	16.6	59.3	3389	10	ADE07125	Ade07125 Novel cod
570	16.8	60.0	17369	4	ABL02754	Drosophi	C 643	16.6	59.3	3389	14	ADU40282	Adu40282 Novel hum
C 571	16.8	60.0	29693	14	AEE04799	Cancer-as	C 644	16.6	59.3	3450	8	ACC62270	Acc62270 Human NOV
572	16.8	60.0	77367	14	AEB39164	Human cdn	C 645	16.6	59.3	3534	4	AAH78264	Aah78264 Nucleotid
C 573	16.8	60.0	80275	12	ADQ97310	Mouse can	C 646	16.6	59.3	3534	6	AAH74273	Aah74273 Human 441
574	16.8	60.0	80275	12	ADQ97310	Mouse can	C 647	16.6	59.3	3534	10	ADJ37494	Adj37494 Human tra
575	16.8	60.0	88607	12	ADQ97648	Mouse can	C 648	16.6	59.3	3534	12	ADJ27973	Adj27973 Human 441
C 576	16.8	60.0	105295	14	AEB35712	L. pneumo	C 649	16.6	59.3	3822	8	ABT14927	Abt14927 Pathogen
577	16.8	60.0	110000	4	AAI99682	41	C 650	16.6	59.3	3822	8	ACF72769	Acf72769 StephiLoc
578	16.8	60.0	110000	4	AAI99682	41	C 651	16.6	59.3	3825	8	ACA19783	Aca19783 Prokaryot
C 579	16.8	60.0	110000	6	ABA90521	14	C 652	16.6	59.3	3855	13	ADR44057	Adr44057 Pasteurel
580	16.8	60.0	110000	10	ABO84281	0	C 653	16.6	59.3	3858	13	ADR44058	Adr44058 Pasteurel
581	16.8	60.0	110000	11	ACN44932	2	C 654	16.6	59.3	4245	6	AAL44686	Aal44686 Human tra
582	16.8	60.0	110000	12	ADQ97050	4	C 655	16.6	59.3	4245	6	AAN91839	Aan91839 Pasteurel
583	16.8	60.0	110000	14	AEB39172	2	C 656	16.6	59.3	4380	15	AEE70376	Aee70376 Pasteurel
584	16.8	60.0	110000	14	AEB39175	30	C 657	16.6	59.3	4381	2	AAO10519	Aao10519 Pasteurel
585	16.8	60.0	110000	14	AEB39175	32	C 658	16.6	59.3	4417	9	AAL62510	Aal62510 Human tra
586	16.8	60.0	110000	14	AEB42401	28	C 659	16.6	59.3	4467	3	AAH73385	Aah73385 Heterosig
587	16.8	60.0	110000	14	AEB42401	30	C 660	16.6	59.3	4522	2	AAV74350	Aav74350 StephiLoc
588	16.8	60.0	110000	14	AEB42401	30	C 661	16.6	59.3	4522	2	AAV74350	Aav74350 StephiLoc
589	16.8	60.0	110000	14	AEB42736	15	C 662	16.6	59.3	6751	2	AAT62442	Aat62442 Mouse gro
590	16.8	60.0	149671	6	ABK84797	4	C 663	16.6	59.3	7204	10	ABR74178	Abt17478 Toxicity
591	16.8	60.0	149671	9	ADB70361	Human cdn	C 664	16.6	59.3	7204	12	ADP72599	Adp72599 Renal tox
592	16.8	60.0	149671	12	ADB70361	Human cdn	C 665	16.6	59.3	7204	13	ADR14992	Adr14992 Rat elect
593	16.8	60.0	165156	13	AD836459	Human mal	C 666	16.6	59.3	7221	6	ABQ74272	Abq74272 Human 441
C 594	16.8	60.0	175603	13	AD836459	Human mal	C 667	16.6	59.3	7221	6	ABQ74272	Abq74272 Human 441
595	16.8	60.0	229301	14	ADQ97554	Mouse can	C 668	16.6	59.3	7221	12	ADD337492	Add337492 Human tra
596	16.8	60.0	260027	11	AEB35719	L. pneumo	C 669	16.6	59.3	7221	12	ADJ27971	Adj27971 Human 441
C 597	16.8	60.0	349881	10	ADC86642	Human GPC	C 670	16.6	59.3	7232	4	AAK79332	Aak79332 Human imm
598	16.8	60.0	349881	10	ADC86642	Human GPC	C 671	16.6	59.3	7232	4	AAK79332	Aak79332 Human imm
C 599	16.8	60.0	349881	10	ADC86642	Human GPC	C 672	16.6	59.3	7232	4	AAH78265	Aah78265 Nucleotid
600	16.6	59.3	41	2	AAV50720	Brassica	C 673	16.6	59.3	7347	13	ADU97793	Adu97793 Protein E
601	16.6	59.3	41	2	AAV50729	Brassica	C 674	16.6	59.3	7347	13	ADU97793	Adu97793 Human ATP
602	16.6	59.3	41	2	AAV50726	Brassica	C 675	16.6	59.3	7683	8	ADR84477	Adr84477 Aspergill

C 676	16.6	59.3	7943	4	AAK85948	Aak85948 Human imm	C 749	16.4	58.6	1075	4	AAH32611	Aah32611 Human sec
C 677	16.6	59.3	7968	10	ADC19779	Adc19779 R. influe	C 750	16.4	58.6	1092	2	AAZ19223	Aaz19223 M. tuberc
C 678	16.6	59.3	8217	14	ADM94175	Adm94175 Staphyloc	C 751	16.4	58.6	1092	2	AAZ19435	Aaz19435 M. tuberc
C 679	16.6	59.3	10214	14	ADM94174	Adm94174 Staphyloc	C 752	16.4	58.6	1104	3	AAK47642	Aak47642 Arabidops
C 680	16.6	59.3	10630	4	ABL05498	Ab105498 Drosophill	C 753	16.4	58.6	1158	10	ACF70585	Acf70585 Photorhab
C 681	16.6	59.3	11244	4	AAK74606	Aak74606 Human imm	C 754	16.4	58.6	1167	13	ADT44282	Adt44282 Bacterial
C 682	16.6	59.3	15236	4	AAK74605	Aak74605 Human imm	C 755	16.4	58.6	1201	3	AAK49054	Aak49054 Arabidops
C 683	16.6	59.3	26811	2	AAK20253	Aak20253 Borrelia	C 756	16.4	58.6	1224	4	ABL21641	Ab121641 Drosophill
C 684	16.6	59.3	41540	11	ACN44338	Acn44338 Mouse gen	C 757	16.4	58.6	1229	2	AAQ46140	Aaq46140 NKX1. 3/2
C 685	16.6	59.3	95484	12	ADQ97298	Adq97298 Mouse can	C 758	16.4	58.6	1272	8	ACA53296	Aca53296 Prokaryot
C 686	16.6	59.3	110000	6	ABO69245_09	Continuaction (10 o	C 759	16.4	58.6	1281	11	ACM92123	AcM92123 Breast ca
C 687	16.6	59.3	110000	6	ABO67197_03	Continuaction (9 of	C 760	16.4	58.6	1291	12	ADL12859	Adl12859 Human sec
C 688	16.6	59.3	110000	14	ABE39175_03	Continuaction (4 of	C 761	16.4	58.6	1310	3	AAZ34554	Aaz34554 Human sec
C 689	16.6	59.3	110000	14	ABE342401_02	Continuaction (3 of	C 762	16.4	58.6	1311	10	ADR60103	Adr60103 Plant DNA
C 690	16.6	59.3	110000	14	ABE342401_03	Continuaction (4 of	C 763	16.4	58.6	1359	3	AAK48761	Aak48761 Arabidops
C 691	16.6	59.3	110000	14	ABE342737_13	Continuaction (14 o	C 764	16.4	58.6	1382	5	AAK74298	Aak74298 DNA encod
C 692	16.6	59.3	110000	14	ABE342736_05	Continuaction (6 of	C 765	16.4	58.6	1439	3	AAK40284	Aak40284 Arabidops
C 693	16.6	59.3	110000	15	ABE30206_08	Continuaction (9 of	C 766	16.4	58.6	1602	10	ADC30373	Adc30373 Human nov
C 694	16.6	59.3	110000	15	ABE60206_09	Continuaction (10 o	C 767	16.4	58.6	1649	2	AAK13356	Aak13356 Enterococ
C 695	16.6	59.3	118584	10	ADCE87623	Adce87623 Human GPC	C 768	16.4	58.6	1649	6	ABK39151	Abk39151 Enterococ
C 696	16.6	59.3	126932	15	AEF51725	Aef51725 Human rib	C 769	16.4	58.6	1724	4	AAH32609	Aah32609 Human sec
C 697	16.6	59.3	194588	14	ABE35717	AbE35717 L. pneumo	C 770	16.4	58.6	1761	4	AAK68428	Aak68428 Human imm
C 698	16.6	59.3	200000	12	AD047191	Ad047191 DNA seque	C 771	16.4	58.6	1761	4	AAK68427	Aak68427 Human imm
C 699	16.6	59.3	200622	14	ABE39167	AbE39167 L. pneumo	C 772	16.4	58.6	1799	13	ADK48649	Adk48649 Bacterial
C 700	16.6	59.3	207461	14	ABE39170	AbE39170 L. pneumo	C 773	16.4	58.6	1860	6	AAK57030	Aak57030 C. pneumo
C 701	16.6	59.3	349980	13	ADT05727	Adt05727 Haemophil	C 774	16.4	58.6	1860	10	ABL91273	Ab191273 Chlamydia
C 702	16.4	58.6	121	10	ADH92425	Adh92425 Human gen	C 775	16.4	58.6	1860	6	ADDA2824	AdDA2824 Chlamydia
C 703	16.4	58.6	184	2	AAO85523	AaQ85523 DNA probe	C 776	16.4	58.6	1875	8	ABV75001	Abv75001 C. pneumo
C 704	16.4	58.6	185	2	AAO85532	AaQ85532 DNA probe	C 777	16.4	58.6	2000	4	ABV72177	Abv72177 Rice gene
C 705	16.4	58.6	210	12	ACH82137	Ach82137 Human gen	C 778	16.4	58.6	2005	4	AAE81805	Aae81805 Human sec
C 706	16.4	58.6	216	8	ABX43084	Abx43084 Bovine ES	C 779	16.4	58.6	2060	6	AAH18753	Aah18753 Chlamydia
C 707	16.4	58.6	257	13	ADV39958	Adv39958 Rat card1	C 780	16.4	58.6	2097	13	ADT45518	AdT45518 Bacteriol
C 708	16.4	58.6	295	2	AAO61051	AaQ61051 Human bra	C 781	16.4	58.6	2147	14	ABE11429	Abe11429 Haematec C
C 709	16.4	58.6	300	6	AAO00946	AAO00946 Human cell	C 782	16.4	58.6	2157	6	ABZ66831	Abz66831 Arabidops
C 710	16.4	58.6	354	6	ABZ08713	Abz08713 Human leu	C 783	16.4	58.6	2157	6	ABZ66850	Abz66850 Arabidops
C 711	16.4	58.6	400	8	ABX37785	Abx37785 Bovine ES	C 784	16.4	58.6	2410	6	AB199458	Ab199458 Mouse 18c
C 712	16.4	58.6	414	8	ABX43970	Abx43970 Bovine ES	C 785	16.4	58.6	2417	4	AAH15011	Aah15011 Human CDN
C 713	16.4	58.6	430	8	ABX62051	Abx62051 Arabidops	C 786	16.4	58.6	2518	4	AAH46774	Aah46774 Human sec
C 714	16.4	58.6	504	11	ADT96410	Adt96410 Colon can	C 787	16.4	58.6	2522	6	ABA96879	AbA96879 Retinal b
C 715	16.4	58.6	504	11	ADK42892	Adk42892 Human CDN	C 788	16.4	58.6	2640	11	ACL27116	ACL27116 Rice abio
C 716	16.4	58.6	508	4	AAK57741	Aak57741 Human imm	C 789	16.4	58.6	2679	10	ADB63014	AdB63014 Human CDN
C 717	16.4	58.6	514	12	ACH68436	Ach68436 Human gen	C 790	16.4	58.6	2684	10	ACF58261	AcF58261 ENSIT0000
C 718	16.4	58.6	544	6	ABK45511	Abk45511 CDNA encod	C 791	16.4	58.6	2684	10	ADA53627	Ada53627 Human cod
C 719	16.4	58.6	581	13	ADRS9380	Adrs9380 Cotton CD	C 792	16.4	58.6	2684	12	ADNO6056	Adno6056 Antipsoxi
C 720	16.4	58.6	581	13	ACNS3030	Acns3030 Cotton an	C 793	16.4	58.6	2684	12	ADNO85844	AdNO85844 Colon can
C 721	16.4	58.6	582	13	ADR60447	Adr60447 Cotton CD	C 794	16.4	58.6	3007	9	ACF35894	AcF35894 Human ARP
C 722	16.4	58.6	601	13	ADV15466	Adv15466 Human oet	C 795	16.4	58.6	3007	12	ADQ74862	AdQ74862 Human and
C 723	16.4	58.6	601	13	ADV15465	Adv15465 Human oet	C 796	16.4	58.6	3015	6	ABZ66839	Abz66839 Arabidops
C 724	16.4	58.6	601	13	ADV15739	Adv15739 Human oet	C 797	16.4	58.6	3080	12	AD035586	Ad035586 Novel mou
C 725	16.4	58.6	601	13	ADV15740	Adv15740 Human oet	C 798	16.4	58.6	3110	3	AAA10672	Aaa10672 Human Bm
C 726	16.4	58.6	601	14	ABE32490	AbE32490 Human DNA	C 799	16.4	58.6	3110	12	ADP88598	Adp88598 Human POU
C 727	16.4	58.6	601	14	ABE33672	AbE33672 Human DNA	C 800	16.4	58.6	3110	14	ADZ49076	AdZ49076 Insulin s
C 728	16.4	58.6	601	14	ABE33672	AbE33672 Human DNA	C 801	16.4	58.6	3215	12	ADM16810	AdM16810 Hepatic tis
C 729	16.4	58.6	601	14	ABE33673	AbE33673 Human DNA	C 802	16.4	58.6	3351	13	ADT44214	AdT44214 Bacterial
C 730	16.4	58.6	612	10	ADC92687	Adc92687 E. faeciu	C 803	16.4	58.6	4788	4	ABL12772	Ab112772 Drosophill
C 731	16.4	58.6	615	13	ADQ79543	Adq79543 Novel can	C 804	16.4	58.6	4898	4	ABL19155	Ab119155 Drosophill
C 732	16.4	58.6	622	5	ABV52155	Abv52155 Human pro	C 805	16.4	58.6	4961	5	AAH45501	Aah45501 DNA encod
C 733	16.4	58.6	625	13	ADQ52294	Adq52294 Novel can	C 806	16.4	58.6	5033	8	ABZ74587	Abz74587 Secreted
C 734	16.4	58.6	628	13	ACNS3917	Acns3917 Cotton an	C 807	16.4	58.6	5033	10	ADC21005	Adc21005 Human sec
C 735	16.4	58.6	718	5	AAH77231	Aah77231 DNA encod	C 808	16.4	58.6	5033	10	ABZ68115	Abz68115 Human sec
C 736	16.4	58.6	718	5	AAH77476	Aah77476 DNA encod	C 809	16.4	58.6	5241	12	ADU40492	AdU40492 Arabidops
C 737	16.4	58.6	721	3	AAK38816	Aak38816 Arabidops	C 810	16.4	58.6	5259	4	ABL09917	AbL09917 Drosophill
C 738	16.4	58.6	753	10	ADC08043	Adc08043 Rice DNA	C 811	16.4	58.6	6236	4	AAK41724	Aak41724 Genomic s
C 739	16.4	58.6	753	11	ACL26296	ACL26296 Rice abio	C 812	16.4	58.6	6238	4	AAK41723	Aak41723 Genomic s
C 740	16.4	58.6	756	10	ADH83549	Adh83549 Enterococ	C 813	16.4	58.6	6374	4	ABL09964	AbL09964 Drosophill
C 741	16.4	58.6	759	10	ADH83549	Adh83549 Enterococ	C 814	16.4	58.6	6645	8	ABX34714	Abx34714 Human mdd
C 742	16.4	58.6	759	11	ACL30596	ACL30596 Rice abio	C 815	16.4	58.6	7966	4	ABL19154	Ab119154 Drosophill
C 743	16.4	58.6	769	11	ADMA5610	Adma5610 Insect re	C 816	16.4	58.6	8586	4	ABL07988	Ab107988 Drosophill
C 744	16.4	58.6	878	4	AAK67270	Aak67270 Human imm	C 817	16.4	58.6	8682	4	ABL10382	Ab110382 Drosophill
C 745	16.4	58.6	931	6	ABN98614	Abn98614 Arabidops	C 818	16.4	58.6	9031	10	ADG64990	AdG64990 Open read
C 746	16.4	58.6	999	13	ADT20083	Adt20083 Plant CDN	C 819	16.4	58.6	9835	4	ABL21524	Ab121524 Drosophill
C 747	16.4	58.6	1004	3	AAK51110	Aak51110 Arabidops	C 820	16.4	58.6	9903	4	ABL09916	Ab109916 Drosophill
C 748	16.4	58.6	1006	3	AAK34746	Aak34746 Arabidops	C 821	16.4	58.6	10478	2	AAV84691	Aav84691 Arabidops

822	16.4	58.6	12060	4	AAK80004	AAK80004 Human imm	895	16.2	57.9	41	2	AAV50725	AAV50725 Brassica
823	16.4	58.6	12687	2	AAQ98814	AAQ98814 EAV Gl. ge	896	16.2	57.9	41	2	AAV50727	AAV50727 Brassica
824	16.4	58.6	12687	2	AAQ70125	AAQ70125 Equine ar	897	16.2	57.9	57	2	AAV18144	AAV18144 Oligo use
825	16.4	58.6	12704	10	ADG64999	ADG64999 Equine ar	898	16.2	57.9	88	2	AAV73211	AAV73211 C. utilis
826	16.4	58.6	12827	2	AAV09036	AAV09036 Equine ar	899	16.2	57.9	124	2	AAQ13871	AAQ13871 Gp120 maj
827	16.4	58.6	13203	4	ABL30124	ABL30124 Drosophill	900	16.2	57.9	151	8	ACC79386	ACC79386 Mouse DST
828	16.4	58.6	15528	2	AAV09039	AAV09039 Equine ar	901	16.2	57.9	183	6	ABL61726	ABL61726 Colton ade
829	16.4	58.6	22659	14	ABE04761	ABE04761 Cancer-as	902	16.2	57.9	265	2	AAV73186	AAV73186 C. utilis
830	16.4	58.6	28180	4	AAK68939	AAK68939 Human imm	903	16.2	57.9	292	3	AAAC21393	AAAC21393 Human sec
831	16.4	58.6	28344	4	ABL21640	ABL21640 Drosophill	904	16.2	57.9	303	13	ACR83397	ACR83397 Human SIR
832	16.4	58.6	28564	10	ADD48832	ADD48832 Human gen	905	16.2	57.9	339	14	ACL65544	ACL65544 M. xanthu
833	16.4	58.6	32354	10	ADD47694	ADD47694 Human gen	906	16.2	57.9	363	10	ADH83831	ADH83831 Enterococ
834	16.4	58.6	32528	4	ABL09994	ABL09994 Drosophill	907	16.2	57.9	426	10	ADH89920	ADH89920 Bacterial
835	16.4	58.6	44234	11	AAK84724	AAK84724 Human imm	908	16.2	57.9	471	8	ACA45946	ACA45946 Prokaryot
836	16.4	58.6	42748	4	ACMA4064	ACMA4064 Mouse gen	909	16.2	57.9	509	12	ADPE6125	ADPE6125 Human CDN
837	16.4	58.6	48727	4	AAK67375	AAK67375 Human imm	910	16.2	57.9	534	10	ABT40874	ABT40874 Toxicity
838	16.4	58.6	55829	13	ABD33512	ABD33512 Human can	911	16.2	57.9	534	13	ADV39906	ADV39906 Rat card1
839	16.4	58.6	73544	8	ABBS56296	ABBS56296 Human tra	912	16.2	57.9	566	6	ABO46314	ABO46314 Oligonuc1
840	16.4	58.6	86149	12	ADQ97278	ADQ97278 Human can	913	16.2	57.9	566	6	ABO46315	ABO46315 Oligonuc1
841	16.4	58.6	88441	12	ADQ97097	ADQ97097 Mouse can	914	16.2	57.9	577	5	ABV55965	ABV55965 Human pro
842	16.4	58.6	89736	13	ABD22966_10	Continuation (11 o	915	16.2	57.9	582	3	AAAS8292	AAAS8292 DNA encod
843	16.4	58.6	96596	9	ADA02504	Ada02504 Human BAC	916	16.2	57.9	612	6	ABLS5999	ABLS5999 Human gro
844	16.4	58.6	96596	10	ADBR2242	ADBR2242 Human BAC	917	16.2	57.9	637	6	ABO18069	ABO18069 Oligonuc1
845	16.4	58.6	96596	10	ADBS5752	ADBS5752 Human BAC	918	16.2	57.9	637	6	ABO18068	ABO18068 Oligonuc1
846	16.4	58.6	99544	14	ADZ13273	ADZ13273 Human can	919	16.2	57.9	648	10	ADC90952	ADC90952 E. faeciu
847	16.4	58.6	99588	11	ACMA5034	ACMA5034 Human gen	920	16.2	57.9	692	13	ADX37150	ADX37150 Plant ful
848	16.4	58.6	110000	2	AAV28840_4	Continuation (5 of	921	16.2	57.9	694	13	ADX37150	ADX37150 Plant ful
849	16.4	58.6	110000	2	AAV21209_12	Continuation (13 o	922	16.2	57.9	788	14	ACL63584	ACL63584 M. xanthu
850	16.4	58.6	110000	2	AAV21209_12	Continuation (13 o	923	16.2	57.9	810	4	AAI96065	AAI96065 Human neu
851	16.4	58.6	110000	6	ABO69245_21	Continuation (12 o	924	16.2	57.9	816	6	ABO45906	ABO45906 Oligonuc1
852	16.4	58.6	110000	6	ABO69245_21	Continuation (22 o	925	16.2	57.9	816	6	ABO45907	ABO45907 Oligonuc1
853	16.4	58.6	110000	6	ABO69245_22	Continuation (23 o	926	16.2	57.9	845	13	ADX12504	ADX12504 Plant ful
854	16.4	58.6	110000	8	ABX15390_2	Continuation (23 o	927	16.2	57.9	866	13	ADX36971	ADX36971 Plant ful
855	16.4	58.6	110000	8	ABX15390_2	Continuation (3 of	928	16.2	57.9	927	2	AAV73179	AAV73179 C. utilis
856	16.4	58.6	110000	9	ADAI3411_0	ADAI3411 Human tra	929	16.2	57.9	975	15	AEF11545	AEF11545 Rape meth
857	16.4	58.6	110000	10	ACPF6385_5	Continuation (6 of	930	16.2	57.9	1000	14	AEBS8659	AEBS8659 Human pho
858	16.4	58.6	110000	10	ACPF67367_34	Continuation (35 o	931	16.2	57.9	1038	12	ADL03332	ADL03332 DNA encod
859	16.4	58.6	110000	10	ACPF67367_36	Continuation (37 o	932	16.2	57.9	1107	14	ABE67176	ABE67176 Rice geno
860	16.4	58.6	110000	10	ACPF65386_11	Continuation (12 o	933	16.2	57.9	1202	14	ABZ18474	ABZ18474 Group III
861	16.4	58.6	110000	11	ACMA5090_1	Continuation (2 of	934	16.2	57.9	1216	14	ADZ61286	ADZ61286 Murine 24
862	16.4	58.6	110000	12	ADQ59446_0	Adq59446 Human can	935	16.2	57.9	1425	5	AAAS84262	AAAS84262 DNA encod
863	16.4	58.6	110000	13	ABD32966_08	Continuation (9 of	936	16.2	57.9	1434	12	ADL42280	ADL42280 Plant tra
864	16.4	58.6	110000	14	ADZ13631_3	Continuation (4 of	937	16.2	57.9	1453	8	ADCO02738	ADCO02738 Soybean o
865	16.4	58.6	110000	14	ADZ13620_3	Continuation (4 of	938	16.2	57.9	1534	8	ACA33748	ACA33748 Prokaryot
866	16.4	58.6	110000	14	ADZ13757_0	Adz13757 Human can	939	16.2	57.9	1616	13	ADXS4113	ADXS4113 Plant ful
867	16.4	58.6	12767	13	ABD32657	ABD32657 Mouse can	940	16.2	57.9	2026	13	ADT16798	ADT16798 Plant CDN
868	16.4	58.6	137000	12	ADH77370	ADH77370 Human PTP	941	16.2	57.9	2156	4	AAH45046	AAH45046 TOL2 tran
869	16.4	58.6	137000	15	AEBS6219	AEBS6219 Human PTP	942	16.2	57.9	2156	9	ADBL17228	ADBL17228 Oryzias I
870	16.4	58.6	139308	8	ADBI2769	ADBI2769 Human PRX	943	16.2	57.9	2199	10	ADC08341	ADC08341 Rice DNA
871	16.4	58.6	153170	12	ADQ17382	Adq17382 Human sof	944	16.2	57.9	2251	3	AAAS0895	AAAS0895 Soybean p
872	16.4	58.6	160482	11	ACNA3914	ACNA3914 Human gen	945	16.2	57.9	2358	2	AAV45134	AAV45134 Mouse Fas
873	16.4	58.6	164991	10	ADL13635	ADL13635 Osteoarthe	946	16.2	57.9	2360	4	AAV72909	AAV72909 Mouse dax
874	16.4	58.6	168828	14	ADZ13592	Adz13592 Human can	947	16.2	57.9	2521	10	ADD68418	ADD68418 Human smo
875	16.4	58.6	171398	8	ADZ13359	Adz13359 Human can	948	16.2	57.9	2653	13	ADK49853	ADK49853 Plant ful
876	16.4	58.6	178870	10	ADL13512	Adl13512 Osteoarthe	949	16.2	57.9	2919	13	ADMS47919	ADMS47919 Bacterial
877	16.4	58.6	191584	13	ABD33586	ABD33586 Human can	950	16.2	57.9	2970	14	ADMO1698	ADMO1698 Human CDN
878	16.4	58.6	191584	13	ABD37026	ABD37026 Human can	951	16.2	57.9	2970	14	AECS4628	AECS4628 Human CDN
879	16.4	58.6	199994	14	AEAO7496	AEAO7496 Human can	952	16.2	57.9	2982	12	ACA24241	ACA24241 Prokaryot
880	16.4	58.6	200000	12	ADOA7496	Adoa7496 CTC-200D1	953	16.2	57.9	3324	8	ADCA24241	ADCA24241 4 syntes
881	16.4	58.6	213251	6	ABO67193	ABO67193 Listeria	954	16.2	57.9	3756	4	ABL16114	ABL16114 Drosophill
882	16.4	58.6	215974	12	ADQ97523	ADQ97523 Human can	955	16.2	57.9	3858	10	ADBE11731	ADBE11731 Human gen
883	16.4	58.6	309400	5	AAH68534	AAH68534 C glutami	956	16.2	57.9	4682	9	ADBE11735	ADBE11735 Human gen
884	16.4	58.6	312957	5	ADV15290	Adv15290 Human ost	957	16.2	57.9	4682	10	ADBI7230	ADBI7230 Oryzias I
885	16.4	58.6	312957	14	AEBS2365	AEBS2365 Human ost	958	16.2	57.9	5255	13	ADRO7897	ADRO7897 Full leng
886	16.4	58.6	312972	13	ADV15293	Adv15293 Human ost	959	16.2	57.9	5815	6	ABL33234	ABL33234 Human imm
887	16.4	58.6	312972	14	AEBS2394	AEBS2394 Human ost	960	16.2	57.9	6032	6	AAAS63310	AAAS63310 Chemical1
888	16.4	58.6	313001	14	ADZ70075	Adz70075 Human ins	961	16.2	57.9	6247	6	ABL32275	ABL32275 Human imm
889	16.4	58.6	313287	13	ABD33100	ABD33100 Human can	962	16.2	57.9	6283	6	ABK39991	ABK39991 Human che
890	16.4	58.6	321019	13	ADBS36450	ADBS36450 Human aut	963	16.2	57.9	6283	6	ABL32834	ABL32834 Human imm
891	16.4	58.6	325019	13	ABD32707	ABD32707 Human can	964	16.2	57.9	6858	15	AEBS5363	AEBS5363 Laminaria
892	16.4	58.6	345980	5	AAH68526	AAH68526 C glutami	965	16.2	57.9	6619	2	AAI31334	AAI31334 Enterococ
893	16.4	58.6	345980	5	AAH68533	AAH68533 C glutami	966	16.2	57.9	9619	6	ABSP98929	ABSP98929 Enterococ
894	16.4	58.6	345980	5	AAH68532	AAH68532 C glutami	967	16.2	57.9	22885	11	ACNA4576	ACNA4576 Mouse gen

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968 16.2 57.9 32872 4 ABL04072
969 16.2 57.9 107543 13 ABD33524
970 16.2 57.9 110000 6 ABX08336_03
971 16.2 57.9 110000 12 ADJ25965_03
972 16.2 57.9 110000 12 ADN97999_03
973 16.2 57.9 110000 12 ADOS0281_03
974 16.2 57.9 110000 14 AEB85185_03
975 16.2 57.9 168325 11 ACN44484
976 16.2 57.9 260160 12 ADQ20017
977 16.2 57.9 269223 4 AAF8554
978 16 57.1 70 2 AAT71528
979 16 57.1 149 6 ABL86945
980 16 57.1 149 14 ACL62395
981 16 57.1 149 14 ACL54642
982 16 57.1 171 4 AAL24284
983 16 57.1 243 12 ADP28157
984 16 57.1 272 4 AAS58298
985 16 57.1 285 4 AAS5455
986 16 57.1 285 13 ADK44507
987 16 57.1 293 6 ABK31067
988 16 57.1 351 12 ADL02689
989 16 57.1 379 4 AAI82699
990 16 57.1 389 13 ADOS2446
991 16 57.1 405 4 AAF59800
992 16 57.1 442 12 ADQ17797
993 16 57.1 448 9 AAC74671
994 16 57.1 488 9 ACH32021
995 16 57.1 503 9 ACH37381
996 16 57.1 508 6 ABQ44663
997 16 57.1 508 6 ABQ44662
998 16 57.1 509 6 ACN87951
999 16 57.1 519 13 ADR63921
1000 16 57.1 519 13 ACN59775

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ALIGNMENTS

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RESULT 1
ID AAT03309 standard; DNA; 28 BP.
XX
AC AAT03309;
XX
DT 27-AUG-2003 (revised)
DT 11-APR-1996 (first entry)
XX
DE HPV E6 gene contg. plasmid restriction fragment hybridisation probe.
XX
KM Enzyme inhibition suppressor; polymerase; detergent; SDS; LLS; probe;
KM sodium dodecyl sulphate; lithium lauryl sulphate; detection;
KM polymerase chain reaction; ss.
XX
OS Human papillomavirus.
XX
PN BP671473-A1.
XX
PD 13-SEP-1995.
XX
PF 10-MAR-1995; 95EP-00103520.
XX
PR 10-MAR-1994; 94US-00212131.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Kacian DL, Mcallister DL;
XX
DR WPI; 1995-312773/41.
XX
PT Use of nonionic detergent to suppress enzyme inhibition by ionic
PT detergent - partic. to enhance activity of e.g. DNA or RNA polymerase in
PT nucleic acid amplification(s).
XX

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PS Example 4; Page 9; 20pp; English.
XX
XX AAT03307-08 and T3309 are a pair of primers and a probe respectively, for
CC the amplification and detection of a human papilloma virus E6 gene
CC restriction fragment. They are used to exemplify a new method for
CC conducting nucleic acid amplification reactions in the presence of an
CC ionic detergent such as SDS or LLS. The method can be used for enhancing
CC the activity of enzymes such as DNA-directed DNA polymerase, RNA-directed
CC DNA polymerase, DNA-directed RNA polymerase, RNA-hydrolysing enzyme,
CC restriction endonucleases or proteases. (Updated on 27-AUG-2003 to
CC correct OS field.)
XX
SQ Sequence 28 BP; 11 A; 6 C; 6 G; 5 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 28; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 GAAACGCAATACAAACAAACCGTTGTGTG 28
Db 1 GAACAGCAATACAAACAAACCGTTGTGTG 28

```

```

RESULT 2
ID AAT72300 standard; DNA; 28 BP.
XX
AC AAT72300;
XX
DT 09-FEB-1998 (first entry)
XX
DE Human Papillomavirus Type 16 target region.
XX
KM Human Papillomavirus; probe; target region; genital cancer; HPV;
KM cervical smear; ss.
XX
OS Human papillomavirus.
XX
PN BP74518-A2.
XX
PD 21-MAY-1997.
XX
PF 15-NOV-1996; 96EP-00308264.
XX
PR 15-NOV-1995; 95US-0006854P.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Gordon P, Brentano ST, Carter NM, Hammond PW;
XX
DR WPI; 1997-274349/25.
XX
PT Probes for detection of Human Papillomavirus Type 16 and Type 18 - can
PT distinguish between Type 16 and 18, associated with genital cancers.
XX
PS Claim 1; Page 34; 70pp; English.
XX
XX Novel hybridisation assay probes have been developed comprising an
CC oligonucleotide which will hybridise under selected conditions to Human
CC Papillomavirus (HPV) Type 16 and/or 18 (but not Types 6, 11, 31, 33, 35,
CC 39, 45, 51, 52, or 58) target nucleic acids to form detectable target;
CC probe duplex. The present sequence represents a specifically claimed
CC target region. Oligonucleotides are useful to detect HPV Type 16 and/or
CC 18 in samples e.g. cervical smears, body fluid, and distinguish these
CC from other HPV variants. Papillomaviruses are small DNA viruses and HPV
CC Types 16 and 18 are associated with genital cancers. HPV PCR primers can
CC amplify HPV Type 16 and/or 18 nucleic acid in a sample. HPV Type 16
CC and/or 18 can be detected by adding a probe and detecting probe:target
CC duplex formation; target nucleic acid is optionally amplified. Type 16 or
CC 18 can be specifically detected by amplifying nucleic acids with at least
CC one specifically claimed PCR primer. For Type 18 detection, a helper
CC probe may be used. Oligonucleotides can distinguish target sequences from
CC phylogenetically close HPV Types 16 and 18 whilst available detection

```

CC sera react with antigens of all papillomaviruses
 XX Sequence 28 BP; 5 A; 6 C; 6 G; 11 T; 0 U; 0 Other;
 SQ

Query Match 100.0%; Score 28; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.025;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACAGCAATACAAACCGTGTGTG 28
 DB 28 GAACAGCAATACAAACCGTGTGTG 1

RESULT 3
 AAT72335/C
 ID AAT72335 standard; RNA; 28 BP.
 XX
 AC AAT72335;
 XX
 DT 09-FEB-1998 (first entry)
 XX
 DE Human Papillomavirus Type 16 target region.
 XX
 KM Human Papillomavirus; probe; target region; genital cancer; HPV;
 KM cervical smear; ss.
 XX
 OS Human papillomavirus.
 XX
 PN EP774518-A2.
 XX
 PD 21-MAY-1997.
 XX
 PF 15-NOV-1996; 96EP-00308264.
 XX
 PR 15-NOV-1995; 95US-0006854P.
 XX
 PA (GENP-) GEN-PROBE INC.
 XX
 PI Gordon P, Brentano ST, Carter NM, Hammond PW;
 XX
 DR WPI; 1997-274349/25.
 XX
 PT Probes for detection of Human Papillomavirus Type 16 and Type 18 - can
 PT distinguish between Type 16 and 18, associated with genital cancers.
 XX
 PS Claim 1; Page 34; 70pp; English.
 XX
 CC Novel hybridisation assay probes have been developed comprising an
 CC oligonucleotide which will hybridise under selected conditions to Human
 CC Papillomavirus (HPV) Type 16 and/or 18 (but not Types 6, 11, 31, 33, 35,
 CC 39, 45, 51, 52, or 58) target nucleic acids to form detectable target;
 CC probe duplex. The present sequence represents a specifically claimed
 CC target region. Oligonucleotides are useful to detect HPV Type 16 and/or
 CC 18 in samples e.g. cervical smears, body fluid, and distinguish these
 CC from other HPV variants. Papillomaviruses are small DNA viruses and HPV
 CC Types 16 and 18 are associated with genital cancers. HPV PCR primers can
 CC amplify HPV Type 16 and/or 18 nucleic acid in a sample. HPV Type 16
 CC and/or 18 can be detected by adding a probe and detecting probe:target
 CC duplex formation; target nucleic acid is optionally amplified. Type 16 or
 CC 18 can be specifically detected by amplifying nucleic acids with at least
 CC one specifically claimed PCR primer. For Type 18 detection, a helper
 CC probe may be used. Oligonucleotides can distinguish target sequences from
 CC phylogenetically close HPV Types 16 and 18 whilst available detection
 CC sera react with antigens of all papillomaviruses
 CC
 XX
 SQ Sequence 28 BP; 5 A; 6 C; 6 G; 0 T; 11 U; 0 Other;
 XX

Query Match 100.0%; Score 28; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.025;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACAGCAATACAAACCGTGTGTG 28
 DB 28 GAACAGCAATACAAACCGTGTGTG 1

DB 28 GAACAGCAATACAAACCGTGTGTG 1

RESULT 4
 AAT72299
 ID AAT72299 standard; DNA; 28 BP.
 XX
 AC AAT72299;
 XX
 DT 09-FEB-1998 (first entry)
 XX
 DE Human Papillomavirus Type 16 target region.
 XX
 KM Human Papillomavirus; probe; target region; genital cancer; HPV;
 KM cervical smear; ss.
 XX
 OS Human papillomavirus.
 XX
 PN EP774518-A2.
 XX
 PD 21-MAY-1997.
 XX
 PF 15-NOV-1996; 96EP-00308264.
 XX
 PR 15-NOV-1995; 95US-0006854P.
 XX
 PA (GENP-) GEN-PROBE INC.
 XX
 PI Gordon P, Brentano ST, Carter NM, Hammond PW;
 XX
 DR WPI; 1997-274349/25.
 XX
 PT Probes for detection of Human Papillomavirus Type 16 and Type 18 - can
 PT distinguish between Type 16 and 18, associated with genital cancers.
 XX
 PS Claim 1; Page 34; 70pp; English.
 XX
 CC Novel hybridisation assay probes have been developed comprising an
 CC oligonucleotide which will hybridise under selected conditions to Human
 CC Papillomavirus (HPV) Type 16 and/or 18 (but not Types 6, 11, 31, 33, 35,
 CC 39, 45, 51, 52, or 58) target nucleic acids to form detectable target;
 CC probe duplex. The present sequence represents a specifically claimed
 CC target region. Oligonucleotides are useful to detect HPV Type 16 and/or
 CC 18 in samples e.g. cervical smears, body fluid, and distinguish these
 CC from other HPV variants. Papillomaviruses are small DNA viruses and HPV
 CC Types 16 and 18 are associated with genital cancers. HPV PCR primers can
 CC amplify HPV Type 16 and/or 18 nucleic acid in a sample. HPV Type 16
 CC and/or 18 can be detected by adding a probe and detecting probe:target
 CC duplex formation; target nucleic acid is optionally amplified. Type 16 or
 CC 18 can be specifically detected by amplifying nucleic acids with at least
 CC one specifically claimed PCR primer. For Type 18 detection, a helper
 CC probe may be used. Oligonucleotides can distinguish target sequences from
 CC phylogenetically close HPV Types 16 and 18 whilst available detection
 CC sera react with antigens of all papillomaviruses
 CC
 XX
 SQ Sequence 28 BP; 11 A; 6 C; 6 G; 5 T; 0 U; 0 Other;
 XX

Query Match 100.0%; Score 28; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.025;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACAGCAATACAAACCGTGTGTG 28
 DB 28 GAACAGCAATACAAACCGTGTGTG 1

RESULT 5
 AAT72334
 ID AAT72334 standard; RNA; 28 BP.
 XX
 AC AAT72334;
 XX
 DT 09-FEB-1998 (first entry)
 XX

XX DE Human Papillomavirus Type 16 target region.
 XX XX Human Papillomavirus; probe; target region; genital cancer; HPV;
 XX KM cervical smear; ss.
 XX OS Human papillomavirus.
 XX PN EP774518-A2.
 XX PD 21-MAY-1997.
 XX PF 15-NOV-1996; 96EP-00308264.
 XX PR 15-NOV-1995; 95US-0006854P.
 XX PA (GENP-) GEN-PROBE INC.
 XX PI Gordon P, Brentano ST, Carter NM, Hammond PW,
 XX DR WPI; 1997-274349/25.
 XX PT Probes for detection of Human Papillomavirus Type 16 and Type 18 - can
 PT distinguish between Type 16 and 18, associated with genital cancers.
 XX PS Claim 1; Page 34; 70pp; English.
 XX CC Novel hybridization assay probes have been developed comprising an
 CC oligonucleotide which will hybridise under selected conditions to Human
 CC Papillomavirus (HPV) Type 16 and/or 18 (but not Types 6, 11, 31, 33, 35,
 CC 39, 45, 51, 52, or 58) target nucleic acids to form detectable target;
 CC probe duplex. The present sequence represents a specifically claimed
 CC target region. Oligonucleotides are useful to detect HPV Type 16 and/or
 CC 18 in samples e.g. cervical smears, body fluid, and distinguish these
 CC from other HPV variants. Papillomaviruses are small DNA viruses and HPV
 CC Types 16 and 18 are associated with genital cancers. HPV PCR primers can
 CC amplify HPV Type 16 and/or 18 nucleic acid in a sample. HPV Type 16
 CC and/or 18 can be detected by adding a probe and detecting probe:target
 CC duplex formation; target nucleic acid is optionally amplified. Type 16 or
 CC 18 can be specifically detected by amplifying nucleic acids with at least
 CC one specifically claimed PCR primer. For Type 18 detection, a helper
 CC probe may be used. Oligonucleotides can distinguish target sequences from
 CC phylogenetically close HPV Types 16 and 18 whilst available detection
 CC sera react with antigens of all papillomaviruses
 XX SO Sequence 28 BP; 11 A; 6 C; 6 G; 0 T; 5 U; 0 Other;
 Query Match 100.0%; Score 28; DB 2; Length 28;
 Best Local Similarity 82.14; Pred. No. 0.025;
 Matches 23; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GAACAGCAATACAAACCGTTGTG 28
 Db 1 GAACAGCAATACAAACCGTTGTG 28
 RESULT 6
 ADX26909
 ID ADX26909 standard; DNA; 452 BP.
 AC ADX26909;
 XX 05-MAY-2005 (first entry)
 XX DE Human papillomavirus type 16 B6 delta151 mutant DNA.
 XX KM cell culture; immortalization; Gynecology and obstetrics; Andrology;
 XX KW cancer; neoplasm; mutant; ds.
 XX OS Human papillomavirus type 16.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers

FT misc_difference 3..4
 FT /*tag= a
 FT /note= "Wild-type bases 4-25 have been removed"
 FT misc_difference 449..450
 FT /*tag= b
 FT /note= "Wild-type bases 472-474 have been removed"
 XX JP2005046117-A.
 XX PN 24-FEB-2005.
 XX PD 31-JUL-2003; 2003JP-00283911.
 XX PF 31-JUL-2003; 2003JP-00283911.
 XX PR 31-JUL-2003; 2003JP-00283911.
 XX PA (UYKA-) UNITV KANAZAWA TLO YG.
 XX PA (KOKU-) KOKURITSU GAN CENT SOCHO.
 XX DR WPI; 2005-175815/19.
 XX PT Immortalized endometrial glandular epithelial cell strain containing
 PT exogenous immortalizing gene and maintains properties of non-cancer cell
 PT and typical glandular epithelial cells, useful in field of research of
 PT reproduction.
 XX PS Claim 5; SEQ ID NO 4; 22pp; Japanese.
 XX CC The invention relates to a novel immortalized endometrial glandular
 CC epithelial cell strain in which an exogenous immortalizing gene is
 CC introduced and the properties of the cell line as non-cancer typical
 CC glandular epithelial cells, are maintained. The cell line of the
 CC invention may be useful for research of reproduction, particularly for
 CC analyzing the adhesion of the fertilized egg during implantation,
 CC analyzing the effect of steroid hormones, analyzing the mechanism of
 CC multistep canceration of the inner glandular epithelial membrane by
 CC genetic engineering of the cell line which is otherwise non-cancerous,
 CC and analyzing the effect of carcinogenic substances on the cell line. The
 CC cell line maintains the properties of normal somatic cells and the
 CC properties of endometrial glandular epithelial cells. The current
 CC sequence is that of the Human Papillomavirus type 16 B6 delta151 mutant
 CC DNA of the invention.
 XX SO Sequence 452 BP; 156 A; 70 C; 98 G; 128 T; 0 U; 0 Other;
 Query Match 100.0%; Score 28; DB 14; Length 452;
 Best Local Similarity 100.0%; Pred. No. 0.034;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GAACAGCAATACAAACCGTTGTG 28
 Db 264 GAACAGCAATACAAACCGTTGTG 291
 RESULT 7
 ABQ76223
 ID ABQ76223 standard; DNA; 456 BP.
 AC ABQ76223;
 XX 21-OCT-2002 (first entry)
 XX DE Human papillomavirus B6 tumour antigen derived DNA.
 XX KM Tumour antigen; human; vaccine; cellular immune response; immunogen; B6;
 XX KW cancer; tumour; ds.
 XX OS Human papillomavirus.
 XX OS US6287569-B1.
 XX PN 11-SEP-2001.
 XX PD 06-APR-1998; 98US-00056105.
 XX PF

XX Jackson A, Ooi CE, Lewin DA, Cuthill S;
PI WPI; 2003-689668/65.
XX P-PsDB; ADP09515.
DR
XX New purified complex comprising a first polypeptide and a second
PT polypeptide, useful for identifying agents for treating/preventing a
PT condition involving altered level of the complex e.g. human papilloma
PT virus infection, or cancer.
XX
PS Example 3; SEQ ID NO 108; 156pp; English.
XX The invention relates to a novel purified complex comprising a first
CC polypeptide and a second polypeptide, where the polypeptides comprise
CC defined amino acid sequences listed in the specification, and where the
CC first polypeptide binds to the second polypeptide. A complex of the
CC invention has virucide and cytostatic activity, and may have a use as a
CC vaccine. The complex is useful for identifying agents for treating or
CC preventing a conditions involving altered level of the complex, e.g.
CC human papilloma virus (HPV) infection, or cancer. The compositions,
CC antibodies, vectors and methods are useful for treating such diseases.
CC The sequences shown in ADP09584-ADP09697 represent CDNA's of the
CC invention.
XX
SQ Sequence 477 BP; 167 A; 76 C; 103 G; 131 T; 0 U; 0 Other;
Query Match 100.0%; Score 28; DB 10; Length 477;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAACAGCAATACAAACCGTTGTGTG 28
Db 286 GAACAGCAATACAAACCGTTGTGTG 313
RESULT 10
AAL54430
ID AAL54430 standard; DNA; 477 BP.
XX
AC AAL54430;
XX
DT 03-APR-2003 (first entry)
XX
DE B6 siRNA sequence.
XX
KM Virucide; cytostatic; anti-HIV; dermatological; small interfering RNA;
KM selective post-translational silencing; siRNA; oncogene; genital wart;
KM human papilloma virus; HPV gene; cancer; human cervical cancer; HIV;
KM smallpox; flu; common cold; cervical cancer; penile cancer;
KM malignant squamous cell carcinoma; verruca vulgaris; gene therapy; de.
XX
OS Human papilloma virus.
XX
PN WO2003008573-A2.
XX
PD 30-JAN-2003.
XX
PF 17-JUL-2002; 2002WO-GB003300.
XX
PR 17-JUL-2001; 2001GB-00017358.
PR 14-JAN-2002; 2002GB-00000688.
PR 17-JUN-2002; 2002GB-00013855.
XX
PA (MILN/) MILNER A J.
XX
PI Milner AJ;
XX
DR WPI; 2003-221850/21.
XX
PT Selective post-transcriptional silencing of an exogenous viral gene (e.g.
PT human papilloma virus (HPV) B6), for treating e.g. cancer, comprises
PT using a small interfering RNA (siRNA) construct homologous to an mRNA of

PT the gene.
XX
PS Disclosure; Fig 1A; 44pp; English.
XX
XX The invention relates to a novel method for selective post-translational
CC silencing in a mammalian cell of the expression of an exogenous gene of
CC viral origin. The method comprises introducing into the cell a small
CC interfering RNA (siRNA) construct that is homologous to a part of the
CC mRNA sequence of the gene. The method is useful for the selective post-
CC transcriptional silencing of an exogenous gene of viral origin (e.g. an
CC oncogene or human papilloma virus (HPV) gene) in a mammalian cell. The
CC method or the siRNA is particularly useful for treating cancer, human
CC cervical cancer, human immunodeficiency virus (HIV), smallpox, flu,
CC common cold, or a disease caused by a HPV (e.g. genital warts, cervical
CC cancer, penile cancer, malignant squamous cell carcinomas or verruca
CC vulgaris). An siRNA construct or vector is useful for use as a medicament
CC for the diseases mentioned. The polynucleotide sequence of the invention
CC can be used to treat disorders by gene therapy. This polynucleotide
CC sequence represents the DNA of the B6 siRNA sequence of the invention
XX
SQ Sequence 477 BP; 167 A; 76 C; 103 G; 131 T; 0 U; 0 Other;
Query Match 100.0%; Score 28; DB 10; Length 477;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAACAGCAATACAAACCGTTGTGTG 28
Db 286 GAACAGCAATACAAACCGTTGTGTG 313
RESULT 11
AAL54445
ID AAL54445 standard; DNA; 477 BP.
XX
AC AAL54445;
XX
DT 03-APR-2003 (first entry)
XX
DE HPV16 B6 siRNA derived DNA sequence.
XX
KM Virucide; cytostatic; anti-HIV; dermatological; small interfering RNA;
KM selective post-translational silencing; siRNA; oncogene; genital wart;
KM human papilloma virus; HPV gene; cancer; human cervical cancer; HIV;
KM smallpox; flu; common cold; cervical cancer; penile cancer;
KM malignant squamous cell carcinoma; verruca vulgaris; gene therapy; de.
XX
OS Human papilloma virus.
XX
PN WO2003008573-A2.
XX
PD 30-JAN-2003.
XX
PF 17-JUL-2002; 2002WO-GB003300.
XX
PR 17-JUL-2001; 2001GB-00017358.
PR 14-JAN-2002; 2002GB-00000688.
PR 17-JUN-2002; 2002GB-00013855.
XX
PA (MILN/) MILNER A J.
XX
PI Milner AJ;
XX
DR WPI; 2003-221850/21.
XX
PT Selective post-transcriptional silencing of an exogenous viral gene (e.g.
PT human papilloma virus (HPV) B6), for treating e.g. cancer, comprises
PT using a small interfering RNA (siRNA) construct homologous to an mRNA of
PT the gene.
XX
PS Claim 11; Fig 11; 44pp; English.
XX
CC The invention relates to a novel method for selective post-translational

CC silencing in a mammalian cell of the expression of an exogenous gene of
 CC viral origin. The method comprises introducing into the cell a small
 CC interfering RNA (siRNA) construct that is homologous to a part of the
 CC mRNA sequence of the gene. The method is useful for the selective post-
 CC transcriptional silencing of an exogenous gene of viral origin (e.g. an
 CC oncogene or human papilloma virus (HPV) gene) in a mammalian cell. The
 CC method or the siRNA is particularly useful for treating cancer, human
 CC cervical cancer, human immunodeficiency virus (HIV), smallpox, flu,
 CC common cold, or a disease caused by a HPV (e.g. genital warts, cervical
 CC cancer, penile cancer, malignant squamous cell carcinomas or verruca
 CC vulgaris). An siRNA construct or vector is useful for use as a medicament
 CC for the diseases mentioned. The polynucleotide sequence of the invention
 CC can be used to treat disorder by gene therapy. This polynucleotide
 CC sequence represents the DNA of a HPV siRNA sequence of the invention
 XX

SQ Sequence 477 BP; 167 A; 75 C; 104 G; 131 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 10; Length 477;
 Best Local Similarity 100.0%; Pred. No. 0.034;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACAGCAATACAAACCGTTGTG 28
 ||||||||||||||||||||||||||||
 Db 286 GAACAGCAATACAAACCGTTGTG 313

RESULT 12

ADXX26908
 ID ADX26908 standard; DNA; 477 BP.

XX AC ADX26908;
 XX

DT 05-MAY-2005 (first entry)

XX Human papillomavirus type 16 E6 wild-type gene.
 DE
 XX
 XX cell culture; immortalization; gynecology and obstetrics; Andrology;
 KM cancer; neoplasms; ds.
 KM
 XX Human papillomavirus type 16.
 OS
 XX JP2005046117-A.
 PN
 XX 24-FEB-2005.
 PD
 XX 31-JUL-2003; 2003JP-00283911.
 PF
 XX 31-JUL-2003; 2003JP-00283911.
 PR
 XX (UYKA-) UNIV KANAZAMA TLO YG.
 PA (KOKU-) KOKURITSU GAN CENT SOCHO.
 PA
 XX WPI; 2005-175815/19.
 DR
 XX

PT Immortalized endometrial glandular epithelial cell strain containing
 PT exogenous immortalizing gene and maintains properties of non-cancer cell
 PT and typical glandular epithelial cells, useful in field of research of
 PT reproduction.
 PT
 XX Claim 4; SEQ ID NO 3; 22pp; Japanese.
 PS
 XX

CC The invention relates to a novel immortalized endometrial glandular
 CC epithelial cell strain in which an exogenous immortalizing gene is
 CC introduced and the properties of the cell line as non-cancer typical
 CC glandular epithelial cells, are maintained. The cell line of the
 CC invention may be useful for research of reproduction, particularly for
 CC analyzing the adhesion of the fertilized egg during implantation,
 CC analyzing the effect of steroid hormones, analyzing the mechanism of
 CC multistep canceration of the inner glandular epithelial membrane by
 CC genetic engineering of the cell line which is otherwise non-cancerous,
 CC and analyzing the effect of carcinogenic substances on the cell line. The
 CC cell line maintains the properties of normal somatic cells and the
 CC properties of endometrial glandular epithelial cells. The current

CC sequence is that of the Human papillomavirus type 16 E6 wild-type gene of
 CC the invention.
 CC

SQ Sequence 477 BP; 167 A; 76 C; 103 G; 131 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 14; Length 477;
 Best Local Similarity 100.0%; Pred. No. 0.034;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACAGCAATACAAACCGTTGTG 28
 ||||||||||||||||||||||||||||
 Db 286 GAACAGCAATACAAACCGTTGTG 313

RESULT 13

AEAS1113
 ID AEAS1113 standard; DNA; 477 BP.

XX AC AEAS1113;
 XX

DT 11-AUG-2005 (first entry)

XX Human papillomavirus type 16 E6/E7 gene fragment, SEQ ID NO: 17.
 DE
 XX
 XX Delivery mechanism; gene therapy; cytostatic; vulnery; virocidic;
 KM injury; infection; cancer; gastrointestinal disease;
 KM gynecology and obstetrics; tumor; colorectal tumor;
 KM uterine cervix tumor; squamous cell carcinoma; neoplasms; E7 gene; ds,
 KM E6 gene.
 KM
 XX Human papillomavirus.
 OS
 XX WO2005051431-A1.
 PN
 XX 09-JUN-2005.
 PD
 XX 25-NOV-2004; 2004WO-GB004979.
 PE
 XX 25-NOV-2003; 2003GB-00027409.
 PR
 XX 05-MAR-2004; 2004US-0549919P.
 XX
 XX (MILN/) MILNER A J.
 PA
 XX Milner AJ;
 PI
 XX WPI; 2005-405310/41.
 DR
 XX

PT Composition useful for delivering an agent into a cell comprises the
 PT agent, a transfer agent and a solid or colloidal carrier medium.
 PT
 XX Disclosure; SEQ ID NO 17; 56pp; English.
 PS
 XX

CC The present invention relates to a method and composition comprising a
 CC transfer agent and a solid or colloidal carrier medium for delivering
 CC biological agents into cells. The invention is useful for the treatment
 CC of cancer, tumor, carcinoma of cutaneous, squamous or cervical epithelia
 CC and colorectal carcinoma, wounds, burns and scars. The invention is also
 CC useful in gene therapy. The present sequence is the human papillomavirus
 CC type 16 E6/E7 gene fragment. This sequence is useful in a method for
 CC treating carcinomas.
 CC

SQ Sequence 477 BP; 167 A; 75 C; 104 G; 131 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 14; Length 477;
 Best Local Similarity 100.0%; Pred. No. 0.034;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACAGCAATACAAACCGTTGTG 28
 ||||||||||||||||||||||||||||
 Db 286 GAACAGCAATACAAACCGTTGTG 313

RESULT 14

AAT31834
 ID AAT31834 standard; DNA; 519 BP.
 XX
 AC AAT31834;
 XX
 DT 27-AUG-2003 (revised)
 DT 11-JAN-1997 (first entry)
 XX
 DE Human papilloma virus E6/E7 protein variant.
 XX
 KM Human papilloma virus; E6, E7; deletion mutant; HPV; immune response;
 KM humoral immune response; cellular immune response; vaccine; ss.
 XX
 OS Human papillomavirus.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..519
 FT /*tag= a
 FT /product= "E6/E7 fusion protein (deletion mutant)."
 FT 109..111
 FT /*tag= b
 FT /transl_except= TAC encodes Ile
 FT 115..117
 FT /*tag= c
 FT /transl_except= AAA encodes Cys
 FT 118..120
 FT /*tag= d
 FT /transl_except= CCG encodes Gln
 FT 121..123
 FT /*tag= e
 FT /transl_except= TTG encodes Lys
 FT 124..126
 FT /*tag= f
 FT /transl_except= TGT encodes Pro
 FT 127..129
 FT /*tag= g
 FT /transl_except= GAT encodes Tyr
 FT 130..132
 FT /*tag= h
 FT /transl_except= TTG encodes Aen
 FT 133..135
 FT /*tag= i
 FT /transl_except= TTA encodes Lys
 FT 136..138
 FT /*tag= j
 FT /transl_except= ATT encodes Pro
 FT 139..141
 FT /*tag= k
 FT /transl_except= AGG encodes Leu
 FT 142..144
 FT /*tag= l
 FT /transl_except= TGT encodes Cys
 FT 145..147
 FT /*tag= m
 FT /transl_except= ATT encodes Asp
 FT 148..150
 FT /*tag= n
 FT /transl_except= AAC encodes Leu
 FT 151..153
 FT /*tag= o
 FT /transl_except= TGT encodes Leu
 FT 154..156
 FT /*tag= p
 FT /transl_except= CAA encodes Ile
 FT 157..159
 FT /*tag= q
 FT /transl_except= AAG encodes Arg
 FT 160..162
 FT /*tag= r
 FT /transl_except= CCA encodes Cys
 XX
 PN WO9619496-A1.
 XX

PD 27-JUN-1996.
 XX
 PF 20-DEC-1995; 95MO-AU000868.
 XX
 PR 20-DEC-1994; 94AU-00000157.
 XX
 PA (CSLC-) CSL LTD.
 PA (UYOU) UNIV QUEBENS LAND.
 XX
 PI Edwards SJ, Cox J, Webb EA, Frazer I;
 XX
 DR WPI, 1996-309518/31.
 DR P-PSDB; AAR97562.
 XX
 PT Vaccine variants of human papilloma virus antigens - contain variants of
 PT E6 and/or E7 protein, pref. deletion mutants, and are used to treat or
 PT prevent HPV infection.
 XX
 PS Example 3; Page 17; 37pp; English.
 XX
 CC A variant of the human papilloma virus (HPV) E6 or E7 protein which
 CC elicits a humoral and/or cellular immune response against HPV can be used
 CC in vaccines against HPV or to treat HPV infection. The variant is
 CC preferably a deletion mutant comprising at least half, and preferably two
 CC thirds of full length E6 or E7 protein starting from the N- or C-
 CC terminal, or is a full length E6 moiety fused to a full length E7 moiety.
 CC The variant optionally has a linkage moiety and a foreign protein or
 CC peptide which facilitates the purification of, and enhances the
 CC immunogenicity of, the fusion protein. This sequence encodes a fusion
 CC between the C-terminal end of E6 and the N-terminal end of E7. The
 CC protein is also a deletion mutant generated from the sequence described
 CC in AAT31833. (Updated on 27-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 519 BP; 175 A; 92 C; 113 G; 139 T; 0 U; 0 Other;
 XX
 QY 1 GAACAGCAATACAAACCGTTGTGG 28
 Db 100 GAACAGCAATACAAACCGTTGTGG 127
 XX
 RESULT 15
 ID ADF31984 standard; DNA; 543 BP.
 XX
 AC ADF31984;
 XX
 DT 12-FEB-2004 (first entry)
 DT
 XX
 DE Human papillomavirus fusion gene encoding sequence.
 XX
 KM human papillomavirus; cervix cancer; ds.
 KM
 OS Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT CDS 1..543
 FT /*tag= a
 XX
 PN CN1381583-A.
 XX
 PD 27-NOV-2002.
 XX
 PF 24-APR-2002; 2002CN-00117143.
 XX
 PR 24-APR-2002; 2002CN-00117143.
 XX
 PA (ONCO-) INST ONCOLOGY TUMOR HOSPITAL CHINESE ACA.
 PA
 XX
 PI Zhao Q;
 XX

XX WPI: 2003-258260/26.
 DR P-PSDB; ADF31985.
 XX
 XX Human papillomavirus E6/E7 fusion gene and its efficient expression
 PT carrier and fusion protein vaccine.
 XX
 PS Claim 3; SEQ ID NO 1; 16pp; Chinese.
 CC The present invention relates to human papillomavirus E6/E7 fusion gene,
 CC its preparing process, the process for configuring the efficient
 CC expression carrier containing the gene and resultant expression carrier,
 CC the fusion protein prepared from the gene, and the application of the
 CC fusion gene and expression protein to medical science and medicine to
 CC treat cervix cancer are disclosed. The present sequence represents the
 CC human papillomavirus fusion gene encoding sequence.
 CC
 SQ Sequence 543 BP; 185 A; 89 C; 118 G; 151 T; 0 U; 0 Other;
 Query Match 100.0%; Score 28; DB 10; Length 543;
 Best Local Similarity 100.0%; Pred. No. 0.035;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GAACAGCAATACACAAACCGTTGTG 28
 DB 286 GAACAGCAATACACAAACCGTTGTG 313
 RESULT 16
 AAQ75470
 ID AAQ75470 standard; DNA; 570 BP.
 AC AAQ75470;
 XX
 DT 16-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 28-JUN-1995 (first entry)
 XX
 DE HPV16 E6/E7 encoding region.
 XX
 KM HPV; HPV16; E6 protein; E7 protein; diagnosis; cervical dysplasia;
 KM cervix cancer; ds.
 XX
 OS Human papillomavirus; strain 16.
 XX
 FH Key Location/Qualifiers
 FT CDS 2..478
 FT /*tag= a
 FT /label= B6_encoding_region
 FT 481..570
 FT /*tag= b
 FT /label= E7_encoding_region
 XX
 PN WO9426934-A2.
 XX
 PD 24-NOV-1994.
 XX
 PF 06-MAY-1994; 94MO-US005085.
 XX
 PR 06-MAY-1993; 93US-00058920.
 XX
 PA (BAXT) BAXTER DIAGNOSTICS INC.
 PI Brown UT;
 XX
 DR WPI: 1995-006821/01.
 DR P-PSDB; AAR63865.
 XX
 PT Human papilloma virus detection assay - by amplification using self
 PT sustained sequence replication and hybridisation with a detector probe.
 XX
 PS Disclosure; Page 24-26; 79pp; English.
 XX

CC The sequences of the E6 and E7 polypeptide-encoding regions of human
 CC papillomavirus (HPV) 16 and 18 are given in AAQ75470-71 and the encoded
 CC proteins in AAR63865-66, respectively. Probes and primers based on these
 CC sequences were used for HPV infection diagnosis; expression of E6 and E7
 CC is diagnostic for cervical cancer or pre-malignant states. (Updated on
 CC 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-2003 to standardise
 CC OS field)
 CC
 SQ Sequence 570 BP; 199 A; 93 C; 119 G; 159 T; 0 U; 0 Other;
 Query Match 100.0%; Score 28; DB 2; Length 570;
 Best Local Similarity 100.0%; Pred. No. 0.035;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GAACAGCAATACACAAACCGTTGTG 28
 DB 287 GAACAGCAATACACAAACCGTTGTG 314
 RESULT 17
 AAN91600
 ID AAN91600 standard; DNA; 712 BP.
 AC AAN91600;
 XX
 DT 27-AUG-2003 (revised)
 DT 17-JUL-1990 (first entry)
 XX
 DE Partial nucleotide sequence (5' end) of human papilloma virus (HPV) type
 DE 16 (HPV-16).
 XX
 KM Human papilloma virus; type 16; in situ hybridisation assay;
 KM cellular smear; benign cervical wart; cervical cancer.
 XX
 OS Human papillomavirus.
 XX
 PN WO8902934-A.
 XX
 PD 06-APR-1989.
 XX
 PF 30-SEP-1988; 88MO-US003367.
 XX
 PR 02-OCT-1987; 87US-00103979.
 XX
 PA (MICR-) MICROPROBE CORP.
 PI Schwartz DE; Adams TH;
 XX
 DR WPI: 1989-114406/15.
 XX
 PT Hybridisation test for human papilloma virus in cell smears - by reaction
 PT with long labelled probe specific for particular virus types, esp. for
 PT examining cervical smears.
 XX
 PS Disclosure; Page 7; 39pp; English.
 XX
 CC The patent is for a rapid in situ hybridisation assay for detecting and
 CC typing human papilloma virus (HPV) in non-frozen cellular smears fixed to
 CC a support in absence of aldehyde-based crosslinking reagents. The assay
 CC comprises: (1) combining nucleic acid in the sample with at least one
 CC detectable probe able to hybridise with 1 or more HPV types; and (2)
 CC detecting presence or absence of hybrid complex. Opt. several probes
 CC are used, eg one for HPV types 6 and 11, associated with benign warts,
 CC and one for types 16, 18, 31, 33 and 35, associated with cervical cancer.
 CC The assay can differentiate between HPV types. It is esp. used as a
 CC secondary test. The probes can be synthesised or cloned. (Updated on 27-
 CC AUG-2003 to correct OS field.)
 CC
 SQ Sequence 712 BP; 253 A; 120 C; 155 G; 184 T; 0 U; 0 Other;
 Query Match 100.0%; Score 28; DB 1; Length 712;
 Best Local Similarity 100.0%; Pred. No. 0.036;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACAGCAATACAAACCGTTGTG 28
DB 368 GAACAGCAATACAAACCGTTGTG 395

RESULT 18

ID ADO44067 standard; DNA; 747 BP.

AC ADO44067;

DT 15-JUL-2004 (first entry)

DE Nucleotide sequence of an E7E6 fusion protein.

XX E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer;
KM cervical cancer; immune response; lower gastrointestinal tract cancer;
KM anal cancer; reproductive system cancer; penile cancer; vulvar cancer;
KM gene; ss.

XX Human papillomavirus type 16.

OS Synthetic.

FH Key Location/Qualifiers

FT CDS 1..747

FT /product= "E7E6 fusion protein"

PN MO2004030636-A2.

PD 15-APR-2004.

PF 02-OCT-2003; 2003MO-US031726.

PR 03-OCT-2002; 2002US-0415929P.

PA (AMHP) WYETH HOLDINGS CORP.

PI Smith L, Cassetti MC;

DR WPI; 2004-316328/29.

DR P-PSDB; ADO44066.

XX New polypeptide comprising human papillomavirus E6 and E7 polypeptides,
PT useful for treating or preventing human papillomavirus (HPV)-associated
PT cancers, e.g. cervical cancer.

XX Example 1; Page 73; 101pp; English.

XX The present sequence encodes an E7E6 fusion protein, comprising wild type
CC E7 and E6 polypeptides from human papillomavirus type 16 (HPV16). The
CC specification describes human papillomavirus E6 and E7 polypeptides,
CC where the E7 polypeptide has mutations at any one or more of the amino
CC acids corresponding to amino acids 24, 26 or 91 of the sequence given in
CC ADO44073 and the E6 polypeptide has no mutations or has mutations at any
CC one or more of the amino acids corresponding to amino acids 63 or 106 of
CC the sequence given in ADO44072. The polypeptides of the invention are
CC useful for treating or preventing human papillomavirus (HPV)-associated
CC cancers, such as cervical cancer. The fusion proteins and nucleic acids
CC encoding the fusion proteins are useful for generating immune responses
CC against HPV. They are also useful for treating lower gastrointestinal
CC tract cancers, e.g. anal cancer, and other cancers of the reproductive
CC system, including penile and vulvar cancer.

XX Sequence 747 BP; 247 A; 132 C; 166 G; 202 T; 0 U; 0 Other;

QY Query Match 100.0%; Score 28; DB 12; Length 747;

Best Local Similarity 100.0%; Pred. No. 0.036;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACAGCAATACAAACCGTTGTG 28

DB 556 GAACAGCAATACAAACCGTTGTG 583

RESULT 19

ID ADO44065 standard; DNA; 747 BP.

AC ADO44065;

DT 15-JUL-2004 (first entry)

DE Nucleotide sequence of a fusion protein designated E6E7PentM.

XX E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer;
KM cervical cancer; immune response; lower gastrointestinal tract cancer;
KM anal cancer; reproductive system cancer; penile cancer; vulvar cancer;
KM gene; ss.

XX Human papillomavirus type 16.

OS Synthetic.

FH Key Location/Qualifiers

FT CDS 1..747

FT /product= "E6E7PentM fusion protein"

PN MO2004030636-A2.

PD 15-APR-2004.

PF 02-OCT-2003; 2003MO-US031726.

PR 03-OCT-2002; 2002US-0415929P.

PA (AMHP) WYETH HOLDINGS CORP.

PI Smith L, Cassetti MC;

DR WPI; 2004-316328/29.

DR P-PSDB; ADO44064.

XX New polypeptide comprising human papillomavirus E6 and E7 polypeptides,
PT useful for treating or preventing human papillomavirus (HPV)-associated
PT cancers, e.g. cervical cancer.

XX Claim 24; Page 71; 101pp; English.

XX The present sequence encodes a fusion protein, comprising E6 and E7
CC polypeptides from human papillomavirus type 16 (HPV16). The fusion
CC protein is designated E6E7PentM, and comprises an E6 amino terminus
CC (where residues 63 and 106 have been replaced with glycine) and an E7
CC carboxy terminus (where residues 24, 26 and 91 have been replaced with
CC glycine). E6E7PentM is representative of fusion proteins of the
CC invention. The specification describes human papillomavirus E6 and E7
CC polypeptides, where the E7 polypeptide has mutations at any one or more
CC of the amino acids corresponding to amino acids 24, 26 or 91 of the
CC sequence given in ADO44073 and the E6 polypeptide has no mutations or has
CC mutations at any one or more of the amino acids corresponding to amino
CC acids 63 or 106 of the sequence given in ADO44072. The polypeptides of
CC the invention are useful for treating or preventing human papillomavirus
CC (HPV)-associated cancers, such as cervical cancer. The fusion proteins
CC and nucleic acids encoding the fusion proteins are useful for generating
CC immune responses against HPV. They are also useful for treating lower
CC gastrointestinal tract cancers, e.g. anal cancer, and other cancers of
CC the reproductive system, including penile and vulvar cancer.

XX Sequence 747 BP; 246 A; 132 C; 171 G; 198 T; 0 U; 0 Other;

QY Query Match 100.0%; Score 28; DB 12; Length 747;

Best Local Similarity 100.0%; Pred. No. 0.036;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACAGCAATACAAACCGTTGTG 28

Db 265 GAACAGCAATATCAACAACCGTTGTGTG 292

RESULT 20

ADO44061 ID ADO44061 standard; DNA; 747 BP.

AC ADO44061;

DT 15-JUL-2004 (first entry)

DE Nucleotide sequence of an E6E7 fusion protein.

XX B6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer;
KM cervical cancer; immune response; lower gastrointestinal tract cancer;
KM anal cancer; reproductive system cancer; penile cancer; vulvar cancer;
KW gene; ss.

XX Human papillomavirus type 16.
OS Synthetic.

XX Key Location/Qualifiers
FH 1..747
FT /*tag= a
CDS /product= "E6E7 fusion protein"

XX WO2004030636-A2.

XX 15-APR-2004.

XX 02-OCT-2003; 2003WC-US031726.

XX 03-OCT-2002; 2002US-0415929P.

XX (AMHP) WYETH HOLDINGS CORP.

XX Smith L, Cassetti MC;

XX WPI; 2004-316328/29.

XX P-PSDB; ADO44060.

XX New polypeptide comprising human papillomavirus E6 and E7 polypeptides,
PT useful for treating or preventing human papillomavirus (HPV)-associated
PT cancers, e.g. cervical cancer.

XX Example 1; Page 68; 101pp; English.

XX The present sequence encodes an E6E7 fusion protein, comprising wild type
CC E6 and E7 polypeptides from human papillomavirus type 16 (HPV16). The
CC specification describes human papillomavirus E6 and E7 polypeptides,
CC where the E7 polypeptide has mutations at any one or more of the amino
CC acids corresponding to amino acids 24, 26 or 91 of the sequence given in
CC ADO44073 and the E6 polypeptide has no mutations or has mutations at any
CC one or more of the amino acids corresponding to amino acids 63 or 106 of
CC the sequence given in ADO44072. The polypeptides of the invention are
CC useful for treating or preventing human papillomavirus (HPV)-associated
CC cancers, such as cervical cancer. The fusion proteins and nucleic acids
CC encoding the fusion proteins are useful for generating immune responses
CC against HPV. They are also useful for treating lower gastrointestinal
CC tract cancer, e.g. anal cancer, and other cancers of the reproductive
CC system, including penile and vulvar cancer.

XX Sequence 747 BP; 247 A; 132 C; 166 G; 202 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 28; DB 12; Length 747;

XX Best Local Similarity 100.0%; Pred. No. 0.036;

XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 GAACAGCAATATCAACAACCGTTGTGTG 28

Db 265 GAACAGCAATATCAACAACCGTTGTGTG 292

RESULT 21

ADO44063 ID ADO44063 standard; DNA; 747 BP.

AC ADO44063;

DT 15-JUL-2004 (first entry)

DE Nucleotide sequence of a fusion protein designated E6E7recM.

XX B6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer;
KM cervical cancer; immune response; lower gastrointestinal tract cancer;
KM anal cancer; reproductive system cancer; penile cancer; vulvar cancer;
KW gene; ss.

XX Human papillomavirus type 16.
OS Synthetic.

XX Key Location/Qualifiers
FH 1..747
FT /*tag= a
CDS /product= "E6E7recM fusion protein"

XX WO2004030636-A2.

XX 15-APR-2004.

XX 02-OCT-2003; 2003WC-US031726.

XX 03-OCT-2002; 2002US-0415929P.

XX (AMHP) WYETH HOLDINGS CORP.

XX Smith L, Cassetti MC;

XX WPI; 2004-316328/29.

XX P-PSDB; ADO44062.

XX New polypeptide comprising human papillomavirus E6 and E7 polypeptides,
PT useful for treating or preventing human papillomavirus (HPV)-associated
PT cancers, e.g. cervical cancer.

XX Claim 24; Page 70; 101pp; English.

XX The present sequence encodes a fusion protein, comprising E6 and E7
CC polypeptides from human papillomavirus type 16 (HPV16). The fusion
CC protein is designated E6E7recM, and comprises an E6 amino terminus (where
CC residues 63 and 106 have been replaced with glycine) and an E7 carboxy
CC terminus (where residues 24 and 26 have been replaced with glycine).
CC E6E7recM is representative of fusion proteins of the invention. The
CC specification describes human papillomavirus E6 and E7 polypeptides,
CC where the E7 polypeptide has mutations at any one or more of the amino
CC acids corresponding to amino acids 24, 26 or 91 of the sequence given in
CC ADO44073 and the E6 polypeptide has no mutations or has mutations at any
CC one or more of the amino acids corresponding to amino acids 63 or 106 of
CC the sequence given in ADO44072. The polypeptides of the invention are
CC useful for treating or preventing human papillomavirus (HPV)-associated
CC cancers, such as cervical cancer. The fusion proteins and nucleic acids
CC encoding the fusion proteins are useful for generating immune responses
CC against HPV. They are also useful for treating lower gastrointestinal
CC tract cancer, e.g. anal cancer, and other cancers of the reproductive
CC system, including penile and vulvar cancer.

XX Sequence 747 BP; 246 A; 132 C; 170 G; 199 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 28; DB 12; Length 747;

XX Best Local Similarity 100.0%; Pred. No. 0.036;

XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 GAACAGCAATATCAACAACCGTTGTGTG 28

Db 265 GAACAGCAATATCAACAACCGTTGTGTG 292

RESULT 22
ADO44069
ID ADO44069 standard; DNA; 747 BP.
AC ADO44069;
XX
DT 15-JUL-2004 (first entry)
XX
DE Nucleotide sequence of a fusion protein designated E7E6rectm.
XX
KW E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer;
KM cervical cancer; immune response; lower gastrointestinal tract cancer;
KM anal cancer; reproductive system cancer; penile cancer; vulvar cancer;
KM gene; ss.
XX
OS Human papillomavirus type 16.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1..747
FT /tag= a
FT /product= "E7E6rectm fusion protein"
XX
XX MO2004030636-A2.
XX
PD 15-APR-2004.
XX
PF 02-OCT-2003; 2003MO-US031726.
XX
PR 03-OCT-2002; 2002US-0415929P.
XX
PA (AMHP) WYETH HOLDINGS CORP.
XX
PI Smith L, Cassetti MC;
XX
PI WPI; 2004-316328/29.
DR P-PSDB; ADO44068.
XX
XX New polypeptide comprising human papillomavirus E6 and E7 polypeptides,
PT useful for treating or preventing human papillomavirus (HPV)-associated
PT cancers, e.g. cervical cancer.
XX
XX Claim 24; Page 74-75; 101pp; English.
XX
PS The present sequence encodes a fusion protein, comprising E7 and E6
CC polypeptides from human papillomavirus type 16 (HPV16). The fusion
CC protein is designated E7E6rectm, and comprises an E7 amino terminus (where
CC residues 24 and 26 have been replaced with glycine) and an E6 carboxy
CC terminus (where residues 63 and 106 have been replaced with glycine).
CC E7E6rectm is representative of fusion proteins of the invention. The
CC specification describes human papillomavirus E6 and E7 polypeptides,
CC where the E7 polypeptide has mutations at any one or more of the amino
CC acids corresponding to amino acids 24, 26 or 91 of the sequence given in
CC ADO44073 and the E6 polypeptide has no mutations or has mutations at any
CC one or more of the amino acids corresponding to amino acids 63 or 106 of
CC the sequence given in ADO44072. The polypeptides of the invention are
CC useful for treating or preventing human papillomavirus (HPV)-associated
CC cancers, such as cervical cancer. The fusion proteins and nucleic acids
CC encoding the fusion proteins are useful for generating immune responses
CC against HPV. They are also useful for treating lower gastrointestinal
CC tract cancers, e.g. anal cancer, and other cancers of the reproductive
CC system, including penile and vulvar cancer.
XX
XX Sequence 747 BP; 246 A; 132 C; 170 G; 199 T; 0 U; 0 Other;
SQ

Query Match 100.0%; Score 28; DB 12; Length 747;
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 GAACGCAATACAAACCGTTGTGTG 28
|||||

DB 556 GAACGCAATACAAACCGTTGTGTG 583
RESULT 23
ADO44071
ID ADO44071 standard; DNA; 747 BP.
AC ADO44071;
XX
DT 15-JUL-2004 (first entry)
XX
DE Nucleotide sequence of a fusion protein designated E7E6Pentm.
XX
KW E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer;
KM cervical cancer; immune response; lower gastrointestinal tract cancer;
KM anal cancer; reproductive system cancer; penile cancer; vulvar cancer;
KM gene; ss.
XX
OS Human papillomavirus type 16.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1..747
FT /tag= a
FT /product= "E7E6Pentm fusion protein"
XX
XX MO2004030636-A2.
XX
PD 15-APR-2004.
XX
PF 02-OCT-2003; 2003MO-US031726.
XX
PR 03-OCT-2002; 2002US-0415929P.
XX
PA (AMHP) WYETH HOLDINGS CORP.
XX
PI Smith L, Cassetti MC;
XX
PI WPI; 2004-316328/29.
DR P-PSDB; ADO44070.
XX
XX New polypeptide comprising human papillomavirus E6 and E7 polypeptides,
PT useful for treating or preventing human papillomavirus (HPV)-associated
PT cancers, e.g. cervical cancer.
XX
XX Claim 24; Page 76; 101pp; English.
XX
PS The present sequence encodes a fusion protein, comprising E7 and E6
CC polypeptides from human papillomavirus type 16 (HPV16). The fusion
CC protein is designated E7E6Pentm, and comprises an E7 amino terminus
CC (where residues 24, 26 and 91 have been replaced with glycine) and an E6
CC carboxy terminus (where residues 63 and 106 have been replaced with
CC glycine). E7E6Pentm is representative of fusion proteins of the
CC invention. The specification describes human papillomavirus E6 and E7
CC polypeptides, where the E7 polypeptide has mutations at any one or more
CC of the amino acids corresponding to amino acids 24, 26 or 91 of the
CC sequence given in ADO44073 and the E6 polypeptide has no mutations or has
CC mutations at any one or more of the amino acids corresponding to amino
CC acids 63 or 106 of the sequence given in ADO44072. The polypeptides of
CC the invention are useful for treating or preventing human papillomavirus
CC (HPV)-associated cancers, such as cervical cancer. The fusion proteins
CC and nucleic acids encoding the fusion proteins are useful for generating
CC immune responses against HPV. They are also useful for treating lower
CC gastrointestinal tract cancers, e.g. anal cancer, and other cancers of
CC the reproductive system, including penile and vulvar cancer.
XX
XX Sequence 747 BP; 246 A; 132 C; 171 G; 198 T; 0 U; 0 Other;
SQ

Query Match 100.0%; Score 28; DB 12; Length 747;
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 GAACGCAATACAAACCGTTGTGTG 28
|||||

Db 556 GAACAGCAATPACAAACCGTTGTG 583

RESULT 24
ADRA7004

ID ADRA7004 standard; DNA; 768 BP.

AC ADRA7004;

DT 18-NOV-2004 (first entry)

DE Human papillomavirus type 16 E7 gene for Dengue virus vaccine.

XX da; gene; cytostatic; virucide; dengue virus; recombinant replicon;
XX deletion; prem protein; C protein; NSI protein signal; vaccine;
KM cervical cancer; viral disease; antigen; dendritic cell; immune response;
KM human papillomavirus.

XX Human papillomavirus type 16.

XX Key Location/Qualifiers

FT 1..768

FT /*tag= a

FT /product= "HPV-16 E7 protein"

XX WO2004072274-A1.

XX 26-AUG-2004.

XX 30-JAN-2004; 2004WO-CN000088.

XX 30-JAN-2003; 2003CN-00115272.

XX 30-JAN-2003; 2003CN-00115273.

XX (SHAN-) SHANGHAI TENGGEN BIOMEDICAL CO LTD.

XX (TENG-) TENGGEN BIOMEDICAL CO.

XX (BEIJ-) BEIJING ORIENTAL TENGGEN TECHNOLOGY DEV C.

XX Pang X;

XX WPI; 2004-625870/60.

XX P-PSDB; ADRA7005.

XX GENBANK; AF486352.

XX virus-like particle vaccines containing dengue virus recombinant replicon

XX as core for carrier, applicable in preventives or/and remedies for tumors

XX like cervical cancer and viral diseases.

XX Example 2; SEQ ID NO 1; 38pp; Chinese.

XX A dengue virus recombinant replicon has a deletion of the complete coding

XX sequence for prem protein of dengue virus and also includes elements of

XX e.g. the non-coding region in the whole of the 5'-end, the coding region

XX of the front 20 amino acids in the C protein, and the coding region of

XX NSI protein signal; coding regions of all non-structural proteins. The

XX obtained vaccines are useful in producing preventives or/and remedies for

XX cancer like cervical cancer and viral diseases. Such vaccines can

XX efficiently express antigen in infected cells, which is because dengue

XX virus can infect dendritic cells, and can effectively present antigen to

XX provide immunity effect. Different types of dengue virus can be used to

XX repeatedly produce efficient immune response thereby strengthening the

XX body's immune system against the pathogen that contains such antigen.

XX Human papillomavirus (HPV) vaccines were prepared by using a gene-

Best Local Similarity 100.0%; Pred. No. 0.036;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACAGCAATPACAAACCGTTGTG 28

Db 580 GAACAGCAATPACAAACCGTTGTG 607

RESULT 25

AEF40156

ID AEF40156 standard; DNA; 768 BP.

AC AEF40156;

DT 23-MAR-2006 (first entry)

DE Human papillomavirus 16 (HPV-16) E7-E6 oncogene.

XX Vaccine; virus-like particle; replicon; therapeutic; cancer; cytostatic;

XX neoplasm; viral infection; virucide; infection; oncogene;

XX coding sequence; db.

XX Human papillomavirus type 16.

XX Key Location/Qualifiers

FT 1..768

FT /*tag= a

FT /partial

FT /product= "Human papillomavirus 16 (HPV-16) E7-E6

FT oncoprotein"

FT /note= "No stop codon"

XX US2006018928-A1.

XX 26-JAN-2006.

XX 29-JUL-2005; 2005US-00192923.

XX 30-JAN-2003; 2003CN-00115272.

XX 30-JAN-2003; 2003CN-00115273.

XX 30-JAN-2004; 2004WO-00072274.

XX (PANG/) PANG X.

XX Pang X;

XX WPI; 2006-109169/11.

XX P-PSDB; AEF40157.

XX GENBANK; AF486352, AF469197, AF472508.

XX New recombinant DEN replicons with a deletion of prem, useful for

XX producing a drug for the prophylaxis and treatment of cancer or viral

XX infection.

XX Example 2; SEQ ID NO 1; 24pp; English.

XX The present invention provides a virus-like particle (VLP) vaccine which

XX contains dengue virus (DEN) recombinant replicon as its core. The DEN

XX replicon contains exogenous nucleotide sequences such as human

XX papillomavirus (HPV) antigen proteins, immune regulators or combination

XX of HPV antigen and immune regulators. The invention is useful for

XX producing a drug for the prophylaxis and treatment of cancer or viral

XX infection. The present sequence is a human papillomavirus oncogene.

XX Sequence 768 BP; 255 A; 139 C; 172 G; 202 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 28; DB 15; Length 768;

XX Best Local Similarity 100.0%; Pred. No. 0.036;

XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACAGCAATPACAAACCGTTGTG 28

Db 580 GAACAGCAATPACAAACCGTTGTG 607

RESULT 26	AA114663	standard; DNA; 776 BP.
XX	AA114663;	
XX	27-AUG-2003 (revised)	
DT	25-MAR-2003 (revised)	
DT	10-OCT-1996 (first entry)	
XX	E6/E7 region of Human Papilloma Virus 16 (HPV 16).	
XX	Human papilloma virus; HPV; detection; cervical cancer; amplification;	
KM	hybridisation; diagnosis; transformed cell; E6; E7; ss.	
XX	Human papillomavirus type 16.	
OS	Key	Location/Qualifiers
XX	primer_bind	1..24
FT	primer_bind	/tag= a
FT	primer_bind	/note= "Primer BB113 binding site."
FT	primer_bind	30..55
FT	primer_bind	/tag= b
FT	primer_bind	/note= "Primer H16-58 binding site."
FT	primer_bind	37..57
FT	primer_bind	/tag= c
FT	primer_bind	/note= "Primer BB4 binding site."
FT	primer_bind	454..474
FT	primer_bind	/tag= d
FT	primer_bind	/note= "Primer BB114 binding site."
FT	primer_bind	480..503
FT	primer_bind	/tag= e
FT	primer_bind	/note= "Primer BB111 binding site."
FT	primer_bind	591..621
FT	primer_bind	/tag= f
FT	primer_bind	/note= "Primer BB109 binding site."
FT	primer_bind	658..681
FT	primer_bind	/tag= g
FT	primer_bind	/note= "Primer H16-686 binding site."
FT	primer_bind	660..683
FT	primer_bind	/tag= h
FT	primer_bind	/note= "Primer BB112 binding site."
FT	primer_bind	715..738
FT	primer_bind	/tag= i
FT	primer_bind	/note= "Primer H16-743 binding site."
FT	primer_bind	745..768
FT	primer_bind	/tag= j
FT	primer_bind	/note= "Primer H16-773 binding site."
XX	US5506105-A.	
XX	09-APR-1996.	
XX	22-MAR-1994; 94US-00216233.	
XX	10-DEC-1991; 91US-00808456.	
XX	(DADE-) DADE INT INC.	
XX	Haydock PV;	
XX	WPI; 1996-200273/20.	
XX	Detection of low copy number intracellular markers - by 3SR amplification	
XX	of target RNA in fixed cells then hybridisation with labelled probe, for	
XX	detecting human papilloma virus in cervical cells.	
XX	Example 2; Fig 3; 21pp; English.	
XX	An in situ hybridisation assay for detecting an intracellular marker of	
XX	low copy number in cells comprises fixing the cells to a support using	

CC	paraformaldehyde; treating the cells with a protease to permeabilise them
CC	without altering morphology; adding amplification reagents; incubating
CC	the cells at below fifty degrees celcius to perform amplification by self
CC	-sustained sequence replication; adding a labelled probe complementary to
CC	the region between the primers; washing cells to remove unhybridised
CC	probe and then detecting the labelled probe. The B6/E7 region of human
CC	papilloma virus (HPV) 16 is used especially to detect mRNA being
CC	transcribed from this region which becomes active in transformed cells.
CC	The method can be used for the early diagnosis of cervical cancer.
CC	primers used to amplify fragments of the B6/E7 region are described in
CC	AAT14664-114674. (Updated on 25-MAR-2003 to correct PF field.) (Updated
CC	on 27-AUG-2003 to correct OS field.)
XX	
SQ	Sequence 776 BP; 260 A; 139 C; 169 G; 208 T; 0 U; 0 Other;
Query Match	100.0%; Score 28; Length 776;
Best Local Similarity	100.0%; Pred. NO. 0.036;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	1 GAACGCAATTCACAACAACCCTGTGTG 28 DB 286 GAACGCAATTCACAACAACCCTGTGTG 313
RESULT 27	
ID	AAx89756 standard; DNA; 779 BP.
XX	
AC	AAx89756;
XX	
DT	27-AUG-2003 (revised)
DT	12-OCT-1999 (first entry)
XX	
DE	Probe sequence for HPV 16 E6/E7.
XX	
KW	human papilloma virus; infection; gene expression; probe; detection;
KW	assay; cancer; virus; HPV; ss.
KX	
XX	Synthetic.
OS	Human papillomavirus.
PX	
PN	MO9929890-A2.
XX	
PD	17-JUN-1999.
PF	
PF	11-DEC-1998; 98WO-US026447.
XX	
PR	12-DEC-1997; 97US-0069426P.
PR	05-JAN-1998; 98US-0070486P.
PR	17-APR-1998; 98US-0082167P.
XX	
PA	(DIGE-) DIGENE CORP.
PI	
PI	Lorincz AT;
XX	
DR	WP1; 1999-443850/37.
XX	
PT	New method for assessing Human Papilloma Virus (HPV) infection by
PT	comparison of gene expression levels.
XX	
PS	Disclosure; Fig 5; 35pp; English.
XX	
CC	This nucleotide probe is specific for the HPV16 Human Papilloma Virus
CC	(HPV) gene. The degree of HPV infection can be assessed, by measuring the
CC	levels of expression of genes involved in the diseased state, and
CC	comparing the expression to each other or to reference genes. (Updated on
CC	27-AUG-2003 to correct OS field.)
XX	
SQ	Sequence 779 BP; 259 A; 139 C; 170 G; 211 T; 0 U; 0 Other;
Query Match	100.0%; Score 28; DB 2; Length 779;
Best Local Similarity	100.0%; Pred. NO. 0.036;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	


```

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 GAACAGCAATACAAACCGTTGTG 28
      |||
      286 GAACAGCAATACAAACCGTTGTG 313

RESULT 30
AAK78792
ID      AAK78792 standard; DNA; 822 BP.
XX
AC      AAK78792;
XX
DT      06-SEP-1999 (first entry)
XX
DE      HPV fusion protein D1/3-B6-His/HPV16 DNA.
XX
KM      Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour;
KM      immunological fusion partner; CpG oligonucleotide; immune response;
KM      HPV antigen; prevention; treatment; ss.
XX
OS      Synthetic.
OS      Human papillomavirus.
XX
PN      WO933868-A2.
XX
PD      08-JUL-1999.
XX
PF      18-DEC-1998; 98WO-EP008563.
XX
PR      24-DEC-1997; 97GB-00027262.
XX
PA      (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI      Delemans WLJ, Gerard CMG;
XX
DR      WPI; 1999-405485/34.
XX
DR      P-PSDB; AAY25376.
XX
PT      Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to
PT      induce immune response to HPV.
XX
PS      Example II, Page 48; 62pp; English.
XX
CC      AAK78791-X78801 represent nucleic acid sequences which encode novel
CC      constructs comprising an E6 or E7 protein or E6/E7 fusion protein from
CC      HPV (represented in AAY25375-Y25386). These constructs are optionally
CC      linked to an immunological fusion partner and an immunomodulatory CpG
CC      oligonucleotide. The products of the invention can be used to induce an
CC      immune response in a patient to an HPV antigen. They can also be used for
CC      preventing or treating HPV induced tumours
XX
SQ      Sequence 822 BP; 277 A; 147 C; 168 G; 230 T; 0 U; 0 Other;
Query Match 100.0%; Score 28; DB 2; Length 822;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 GAACAGCAATACAAACCGTTGTG 28
      |||
      604 GAACAGCAATACAAACCGTTGTG 631

RESULT 31
AAK29781
ID      AAK29781 standard; DNA; 822 BP.
XX
AC      AAK29781;
XX
DT      17-OCT-2003 (revised)
DT      22-JUN-1999 (first entry)
XX
DE      Prot. D1/3-B6-His/HPV16 coding sequence.

```

```

XX      KM      Chimeric; E6; E7; fusion protein; protein D; vaccine; immunotherapy;
XX      KM      tumour; lesion; benign; malignant; virus; infection; ss.
XX
OS      Human papillomavirus.
OS      Haemophilus influenzae.
OS      Chimeric.
XX
PN      WO910375-A2.
XX
PD      04-MAR-1999.
XX
PF      17-AUG-1998; 98WO-EP005285.
XX
PR      22-AUG-1997; 97GB-00017953.
XX
PA      (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI      Bruck C, Cabazon Silva T, Delisse ABF, Gerard CMG;
PI      Lombardo-Bencheikh A;
XX
DR      WPI; 1999-190587/16.
XX
PT      Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for
PT      treatment or prophylaxis of HPV induced lesions.
XX
PS      Disclosure; Fig 3; 95pp; English.
XX
CC      This sequence represents the coding region for a chimeric E6 or E7
CC      protein or E6/E7 fusion protein from Human papillomavirus (HPV) linked to
CC      an immunological fusion partner. In this case, a fragment of the
CC      Haemophilus influenzae B protein D. The sequence also contains a
CC      histidine tag at the C-terminus of the encoded protein. The protein can
CC      be used in a vaccine, for immuno-therapeutically treating HPV induced
CC      tumour lesions (benign or malignant) and preventing HPV viral infection.
CC      (updated on 17-OCT-2003 to standardise OS field)
XX
SQ      Sequence 822 BP; 277 A; 147 C; 168 G; 230 T; 0 U; 0 Other;
Query Match 100.0%; Score 28; DB 2; Length 822;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 GAACAGCAATACAAACCGTTGTG 28
      |||
      604 GAACAGCAATACAAACCGTTGTG 631

RESULT 32
AED52633
ID      AED52633 standard; DNA; 822 BP.
XX
AC      AED52633;
XX
DT      29-DEC-2005 (first entry)
XX
DE      Fusion protein D1/3-B6-His/HPV16, DNA.
XX
KM      Fusion protein; vaccine; papilloma; cytotoxic; papillomavirus infection;
KM      virucide; uterine cervix tumor; E6; del gene; D protein.
XX
OS      Haemophilus influenzae; strain 772.
OS      Human papillomavirus type 16.
OS      Synthetic.
OS      Chimeric.
XX
FH      Key Location/Qualifiers
FT      CDS 1..822 /*tag= a
FT      /product= "Fusion protein D1/3-B6-His/HPV16"
XX
PN      IN9801903-14.

```

PD 04-MAR-2005.
 XX
 XX 24-AUG-1998; 98IN-CH001903.
 PF
 XX 22-AUG-1997; 97EP-00179535.
 PR
 XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 PA
 XX Tyrell AMR;
 PI
 XX WPI; 2005-557648/57.
 DR
 XX P-PSDB; AED52634.
 DR
 XX
 XX Vaccine.
 PT
 PS Example 4; Fig 3; 96pp; English.
 XX
 CC The invention relates to human Papilloma virus (HPV) fusion proteins,
 CC linked to an immunological fusion partner that provides T helper epitopes
 CC to the HPV antigen. Vaccine formulations comprising the fusion proteins
 CC are useful in the treatment or prophylaxis of HPV induced lesions
 CC (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7
 CC proteins (singly, as an E6-E7 fusion or mutated) were fused to either
 CC Haemophilus influenzae D protein (20-127), the C-terminus of
 CC Streptococcus pneumoniae Lyta protein (CLYTA) or thiorodoxin. The present
 CC sequence encodes an HPV-H. influenzae D protein, fusion protein of the
 CC invention.
 CC
 XX Sequence 822 BP; 277 A; 147 C; 168 G; 230 T; 0 U; 0 Other;
 SQ
 XX
 XX Query Match 100.0%; Score 28; DB 14; Length 822;
 Best Local Similarity 100.0%; Pred. No. 0.0377;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GAACAGCAATACAAACACCGTTGTGTG 28
 Db 604 GAACAGCAATACAAACACCGTTGTGTG 631
 Db
 XX
 XX RESULT 33
 AAX78795
 ID AAX78795 standard; DNA; 879 BP.
 XX
 AC AAX78795;
 XX
 DT 06-SEP-1999 (first entry)
 XX
 DE HPV fusion protein CLYTA-E6-His/HPV16 DNA.
 XX
 KW Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour;
 KW immunological fusion partner; Cpg oligonucleotide; immune response;
 KW HIV antigen; prevention; treatment; ss.
 XX
 XX Synthetic.
 OS Human papillomavirus.
 OS
 PN WO9933868-A2.
 PN
 PD 08-JUL-1999.
 PD
 PF 18-DEC-1998; 98NO-EP008563.
 PF
 XX 24-DEC-1997; 97GB-00027262.
 XX
 XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 PA
 PI Dalemans WLJ, Gerard CMG;
 PI
 XX WPI; 1999-405485/34.
 DR
 XX P-PSDB; AAY25379.
 DR
 PT Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to
 PT induce immune response to HPV.

XX
 PS Example VI; Page 52; 62pp; English.
 XX
 CC AAX78791-X78801 represent nucleic acid sequences which encode novel
 CC constructs comprising an E6 or E7 protein or E6/E7 fusion protein from
 CC HPV (represented in AAY25375-Y25386). These constructs are optionally
 CC linked to an immunological fusion partner and an immunomodulatory Cpg
 CC oligonucleotide. The products of the invention can be used to induce an
 CC immune response in a patient to an HPV antigen. They can also be used for
 CC preventing or treating HPV induced tumours
 CC
 XX Sequence 879 BP; 289 A; 168 C; 209 G; 213 T; 0 U; 0 Other;
 SQ
 XX
 XX Query Match 100.0%; Score 28; DB 2; Length 879;
 Best Local Similarity 100.0%; Pred. No. 0.0377;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GAACAGCAATACAAACACCGTTGTGTG 28
 Db 661 GAACAGCAATACAAACACCGTTGTGTG 688
 Db
 XX
 XX RESULT 34
 AAX29784
 ID AAX29784 standard; DNA; 879 BP.
 XX
 AC AAX29784;
 XX
 DT 17-OCT-2003 (revised)
 DT 22-JUN-1999 (first entry)
 XX
 DE CLYTA-E6-His coding sequence.
 XX
 KW Chimeric; E6; E7; fusion protein; CLYTA; vaccine; immunotherapy; tumour;
 KW lesion; benign; malignant; virus; infection; ss.
 XX
 XX Human papillomavirus.
 OS Streptococcus pneumoniae.
 OS Chimeric.
 OS
 PN WO9910375-A2.
 PN
 PD 04-MAR-1999.
 PD
 PF 17-AUG-1998; 98NO-EP005285.
 PF
 XX 22-AUG-1997; 97GB-00017953.
 XX
 XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 PA
 PI Bruck C, Cabezon Silva T, Delisse ABF, Gerard CMG;
 PI Lombardo-Bencheikh A;
 PI
 XX WPI; 1999-190587/16.
 DR
 XX P-PSDB; AAY02635.
 DR
 XX Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for
 PT treatment or prophylaxis of HPV induced lesions.
 PT
 PS Disclosure; Fig 10; 95pp; English.
 XX
 CC This sequence represents the coding region for a chimeric E6 or E7
 CC protein or E6/E7 fusion protein from Human papillomavirus (HPV) linked to
 CC an immunological fusion partner, in this case, a fragment of the
 CC Streptococcus pneumoniae CLYTA protein. The sequence also contains a
 CC histidine tag at the C-terminus of the encoded protein. The protein can
 CC be used in a vaccine, for immuno-therapeutically treating HPV induced
 CC tumour lesions (benign or malignant) and preventing HPV viral infection.
 CC (Updated on 17-OCT-2003 to standardise OS field)
 CC
 XX Sequence 879 BP; 289 A; 168 C; 209 G; 213 T; 0 U; 0 Other;
 SQ
 XX
 XX Query Match 100.0%; Score 28; DB 2; Length 879;
 Best Local Similarity 100.0%; Pred. No. 0.0377;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAACAGCAATACAAACCGTTGTGTG 28
DB 661 GAACAGCAATACAAACCGTTGTGTG 688

RESULT 35
AED52641

ID AED52641 standard; DNA; 879 BP.

AC AED52641;

DT 29-DEC-2005 (first entry)

DE Fusion protein clytA-B6-His/HPV16, DNA.

KW Fusion protein; vaccine; papilloma; cytostatic; papillomavirus infection;

KM virucide; uterine cervix tumor; B6; ds; gene; lytA.

OS Streptococcus pneumoniae.

OS Human papillomavirus type 16.

OS Synthetic.

OS Chimeric.

Key Location/Qualifiers
FT CDS 1..879
FT /tag= a
FT /product= "Fusion protein clytA-B6-His/HPV16"

IN9801903-14.

PD 04-MAR-2005.

PF 24-AUG-1998; 981N-CH001903.

PR 22-AUG-1997; 97BP-00179535.

PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

PI Tytrell AMR;

DR MPI; 2005-557648/57.

DR P-PSDB; AED52642.

XX Vaccine.

PS Example 10; Fig 10; 96pp; English.

CC The invention relates to human Papilloma virus (HPV) fusion proteins,
CC linked to an immunological fusion partner that provides T helper epitopes
CC to the HPV antigen. Vaccine formulations comprising the fusion proteins
CC are useful in the treatment or prophylaxis of HPV induced lesions
CC (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) B6 and E7
CC proteins (singly, as an B6-E7 fusion or mutated) were fused to either
CC Haemophilus influenzae p protein (20-127), the C-terminus of
CC Streptococcus pneumoniae lytA protein (clytA) or thiorodoxin. The present
CC sequence encodes an HPV-lytA, fusion protein of the invention.

XX Sequence 879 BP; 289 A; 168 C; 209 G; 213 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 14; Length 879;

Best Local Similarity 100.0%; Pred. No. 0.037;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAACAGCAATACAAACCGTTGTGTG 28
DB 661 GAACAGCAATACAAACCGTTGTGTG 688

RESULT 36
AAA09477

ID AAA09477 standard; DNA; 921 BP.

AC AAA09477;

DT 29-AUG-2000 (first entry)

DE Human papillomavirus type 16 B6 and E7 open reading frames.

KW hINV; involucrin; regulatory region; tissue-specific; promoter; oncogene;

KM suprabasal; stratified; squamous; epithelial tissue; animal model;

KW neoplasia; papillomavirus 16; B6; E7; blistering; proliferative;

KM ichthyosis; cancer; se.

OS Human papillomavirus type 16.

OS Human papillomavirus type 16.

OS Human papillomavirus type 16.

FT mat_peptide
FT /tag= a
FT /label= B6
FT 628..921
FT /tag= b
FT /label= E7

PN WO200026343-A2.

PD 11-MAY-2000.

PF 29-OCT-1999; 99WO-US025516.

PR 30-OCT-1998; 98US-0106495P.

PR 29-OCT-1999; 99US-00430201.

PA (UYCA-) UNIV CASE WESTERN RESERVE.

PI Eckert RL, Crish JF;

DR MPI; 2000-365596/31.

PT Transgenic animals that express oncogenes in epithelial tissue, useful as
PT disease models for neoplastic conditions such as psoriasis and melanomas.

PS Disclosure; Fig 13; 86pp; English.

CC The invention concerns transgenic non-human animals that express
CC oncogenes of interest in their epithelial cells, and materials and
CC methods for their production. Expression of the oncogenes is controlled
CC by a sequence from the human involucrin upstream regulatory region (see
CC AA09476) which targets expression to desired tissues and cells (i.e.
CC suprabasal stratified squamous epithelial tissue). The transgenic animals
CC are useful as animal models for studying neoplastic diseases that affect
CC epithelial tissues, such as those caused by the papillomavirus 16
CC oncogene B6 or E7 nucleic acid sequences and including blistering
CC diseases (e.g. epidermolytic hyperkeratosis, Dowling-Meara disease),
CC proliferative diseases (e.g. psoriasis, epidermal dysplasia and Bullous
CC pemphig), ichthyosis disease (e.g. Ichthyosis bullosa Simons and
CC recessive X-linked ichthyosis) and cancers of the skin, breast, lung,
CC colon, cervix and liver. The animal models may also be used to screen
CC candidate agents for the ability to prevent or treat these diseases
CC (claimed)

XX Sequence 921 BP; 308 A; 167 C; 197 G; 249 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 3; Length 921;

Best Local Similarity 100.0%; Pred. No. 0.037;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAACAGCAATACAAACCGTTGTGTG 28
DB 434 GAACAGCAATACAAACCGTTGTGTG 461

RESULT 37
AAD5101

```
ID AAD35101 standard; DNA; 939 BP.
XX
AC AAD35101;
XX
XX 25-JUL-2002 (first entry)
XX
XX Human papillomavirus enhE6,7 construct DNA.
XX
XX Alphavirus vector system; human papilloma virus; HPV, cervical cancer;
XX therapy; vaccine; virucide; cytostatic; ds.
XX
XX Human papillomavirus.
XX
XX EP195438-A1.
XX
XX 10-APR-2002.
XX
XX 06-OCT-2000; 2000BP-00203472.
XX
XX 06-OCT-2000; 2000BP-00203472.
XX
XX (UYGR-) RIJXSUNITV GRONINGEN.
XX
XX Regts DG, Wilschut JC, Holtrop M, Daemen CAH;
XX
XX WPI; 2002-354156/39.
XX
XX New alphavirus system, useful for genetic immunization against cervical
XX cancer, comprises papilloma virus nucleic acid.
XX
XX Example 2; Fig 19; 45pp; English.
XX
XX The present invention relates to an alphavirus vector system comprising
XX nucleic acid derived from a human papilloma virus (HPV). The invention or
XX cells containing it, are used in treatment and prevention of cervical
XX cancer, particularly as a vaccine. By selecting the nucleic acid that
XX encode E6/E7 proteins without ability to bind to pRb and p53, the risk
XX that cells infected with the alphavirus vector system may become
XX oncogenic is avoided (contrast use of other viral vectors). The present
XX sequence is Human papillomavirus enhE6,7 construct DNA
XX
XX Sequence 939 BP; 284 A; 197 C; 217 G; 241 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 28; DB 6; Length 939;
XX Best Local Similarity 100.0%; Pred. No. 0.037;
XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GAACAGCATATCAACAACCGTTGTG 28
XX 450 GAACAGCATATCAACAACCGTTGTG 477
XX
XX Db
XX
XX RESULT 38
XX AAQ08627
XX ID AAQ08627 standard; DNA; 1000 BP.
XX
XX AAQ08627;
XX
XX 24-OCT-2003 (revised)
XX 21-APR-1994 (first entry)
XX
XX HPV-16 fragment.
XX
XX HPV-18, HPV-16, amplification; primer; polymerase chain reaction; PCR;
XX ss.
XX
XX Human papillomavirus type 16.
XX
XX Key Location/Qualifiers
XX misc_binding 198..207
XX /tag= a
XX /note= "primer (AAQ08628) binding site"
XX
XX misc_binding 601..620
```

```
FT /*tag= b
FT /note= "primer (AAQ08629) binding site"
FT misc_binding 658..677
FT /tag= c
FT /note= "primer (AAQ08630) binding site"
XX
XX DE3838269-A.
XX
XX 17-MAY-1990.
XX
XX 11-NOV-1988; 88DE-03838269.
XX
XX 11-NOV-1988; 88DE-03838269.
XX
XX (BEHW ) BEHRINGER AG.
XX
XX Cerutti P, Whitcomb J, Zijlstra J, Devilliers EM;
XX
XX WPI; 1990-156905/21.
XX
XX Detection of human papilloma virus - by DNA amplification and analysis.
XX
XX Example 4b; Page 4; 11pp; German.
XX
XX Example 4b describes the results of the amplification of HPV-16 DNA by
XX PCR using primers. (Updated on 24-OCT-2003 to standardise OS field)
XX
XX Sequence 1000 BP; 340 A; 171 C; 230 G; 259 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 28; DB 2; Length 1000;
XX Best Local Similarity 100.0%; Pred. No. 0.037;
XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GAACAGCATATCAACAACCGTTGTG 28
XX 368 GAACAGCATATCAACAACCGTTGTG 395
XX
XX Db
XX
XX RESULT 39
XX AAN91784
XX ID AAN91784 standard; DNA; 1005 BP.
XX
XX AAN91784;
XX
XX 27-AUG-2003 (revised)
XX 25-MAR-2003 (revised)
XX 16-MAR-1990 (first entry)
XX
XX DNA probe complementary to human papilloma virus type 16.
XX
XX Cervical cancer.
XX
XX Human papillomavirus type 16.
XX
XX WO8909940-A.
XX
XX 19-OCT-1989.
XX
XX 04-APR-1989; 89WO-US001318.
XX
XX 04-APR-1988; 88US-00177404.
XX 31-MAR-1989; 89US-00330381.
XX
XX (ONCO-) ONCOR INC.
XX
XX George AL, Groff DE;
XX
XX WPI; 1989-324314/44.
XX
XX Rapid detection of specific human papilloma virus genotypes - by
XX hybridisation of DNA digest with new labelled nucleic acid probes.
XX
XX Claim 40; Page 46; 81pp; English.
XX
XX PS
```

XX Obtd. by cutting HPV16 with BamHI and PvuII. The patent describes probes
CC (DNA or RNA) and their complements capable of detecting one or a
CC combination of HPV types 6, 11, 16, 18, 31, 33 and 35. (Updated on 25-MAR
CC -2003 to correct PR field.) (Updated on 27-AUG-2003 to correct OS field.)
XX

SQ Sequence 1005 BP; 325 A; 182 C; 190 G; 308 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 1; Length 1005;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACAGCAATACAAACCGTTGTGTG 28
Db 820 GAACAGCAATACAAACCGTTGTGTG 847

RESULT 40
AAx78793
ID AAX78793 standard; DNA; 1116 BP.

XX AAX78793;
XX
XX 06-SEP-1999 (first entry)

XX HPV fusion protein D1/3-B6-E7-His/HPV16 DNA.

XX Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour;
XX immunological fusion partner; CpG oligonucleotide; immune response;
XX HPV antigen; prevention; treatment; ss.

XX Synthetic.
XX Human papillomavirus.

XX WO933868-A2.

XX 08-JUL-1999.

XX 18-DEC-1998; 98WO-EP008563.

XX 24-DEC-1997; 97GB-00027262.

XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

XX Dalemans WLD, Gerard CMG;

XX WPI; 1999-405485/34.

XX P-PADB; AAY25377.

XX Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to
XX induce immune response to HPV.

XX Example III; Page 49; 62pp; English.

XX AAX78791-X78801 represent nucleic acid sequences which encode novel
CC constructs comprising an E6 or E7 protein or E6/E7 fusion protein from
CC HPV (represented in AAY25375-Y25386). These constructs are optionally
CC linked to an immunological fusion partner and an immunomodulatory CpG
CC oligonucleotide. The products of the invention can be used to induce an
CC immune response in a patient to an HPV antigen. They can also be used for
CC preventing or treating HPV induced tumours

XX Sequence 1116 BP; 368 A; 208 C; 235 G; 305 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 2; Length 1116;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACAGCAATACAAACCGTTGTGTG 28
Db 604 GAACAGCAATACAAACCGTTGTGTG 631

RESULT 41
AAX29782
ID AAX29782 standard; DNA; 1116 BP.

XX AAX29782;

XX 17-OCT-2003 (revised)

XX 22-JUN-1999 (first entry)

XX Prot.D1/3-B6-E7-His/HPV16 coding sequence.

XX Chimeric; E6; E7; fusion protein; protein D; vaccine; immunotherapy;
XX tumour; lesion; benign; malignant; virus; infection; ss.

XX Human papillomavirus.

XX Haemophilus influenzae.

XX Chimeric.

XX WO9910375-A2.

XX 04-MAR-1999.

XX 17-AUG-1998; 98WO-EP005285.

XX 22-AUG-1997; 97GB-00017953.

XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

XX Bruck C, Cabezon Silva T, Delisse ABF, Gerard CMG;
XX Lombardo-Bencheikh A;

XX WPI; 1999-190587/16.

XX P-PADB; AAY02633.

XX Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for
XX treatment or prophylaxis of HPV induced lesions.

XX Disclosure; Fig 6; 95pp; English.

XX This sequence represents the coding region for a chimeric E6 or E7
CC protein or E6/E7 fusion protein from Human papillomavirus (HPV) linked to
CC an immunological fusion partner. In this case, a fragment of the
CC Haemophilus influenzae B protein D. The sequence also contains a
CC histidine tag at the C-terminus of the encoded protein. The protein can
CC be used in a vaccine, for immuno-therapeutically treating HPV induced
CC tumour lesions (benign or malignant) and preventing HPV viral infection.
CC (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 1116 BP; 368 A; 208 C; 235 G; 305 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 2; Length 1116;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACAGCAATACAAACCGTTGTGTG 28
Db 604 GAACAGCAATACAAACCGTTGTGTG 631

RESULT 42
AED52637
ID AED52637 standard; DNA; 1116 BP.

XX AED52637;

XX 29-DEC-2005 (first entry)

XX Fusion protein D1/3-B6-E7-His/HPV16, DNA.

XX Fusion protein; vaccine; papilloma; cytostatic; papillomavirus infection;
XX virucide; uterine cervix tumor; E7; E6; gene; D protein.

XX Haemophilus influenzae; strain 772.

OS	Human Papillomavirus type 16.
OS	Synthetic.
OS	Chimeric.
XX	
XX	Key
XX	Location/Qualifiers
XX	1..1116
XX	/*tag= a
XX	/product= "Fusion protein DI/3-B-E6-E7-His/HPV16"
XX	
XX	IN9801903-14.
XX	
XX	04-MAR-2005.
XX	
XX	24-AUG-1998; 98IN-CH001903.
XX	
XX	22-AUG-1997; 97EP-00179535.
XX	
XX	(SMIK) SMITHGLINE BEECHAM BIOLOGICALS.
XX	
XX	Tyrell AMR;
XX	
XX	WPI; 2005-557648/57.
XX	P-PSDB; AED52638.
XX	
XX	Vaccine.
XX	
XX	Example 6, Fig 6, 96pp; English.
XX	
XX	The invention relates to human Papilloma virus (HPV) fusion proteins,
XX	linked to an immunological fusion partner that provides T helper epitopes
XX	to the HPV antigen. Vaccine formulations comprising the fusion proteins
XX	are useful in the treatment or prophylaxis of HPV induced lesions
XX	(papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7
XX	proteins (singly, as an E6-E7 fusion or mutated) were fused to either
XX	Haemophilus influenzae D protein (20-127), the C-terminus of
XX	Streptococcus pneumoniae lyta protein (clyta) or chloretoxin. The present
XX	invention encodes an HPV-H. Influenzae D protein, fusion protein of the
XX	invention.
XX	
XX	Sequence 1116 BP; 368 A; 208 C; 235 G; 305 T; 0 U; 0 Other;
XX	
XX	Query Match 100.0%; Score 28; DB 14; Length 1116;
XX	Best Local Similarity 100.0%; Pred. No. 0.038;
XX	Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 GAACGACATACCAACAAACCGTGTGTG 28
DB	
DB	604 GAACGACATACCAACAAACCGTGTGTG 631
XX	
XX	RESULT 43
XX	AAK78797
XX	ID AAK78797 standard; DNA; 1173 BP.
XX	
XX	AAK78797;
XX	
XX	06-SEP-1999 (first entry)
XX	
XX	HPV fusion protein C1YTA-BE67-His/HPV16 DNA.
XX	
XX	Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour;
XX	immunological fusion partner; Cpg oligonucleotide; immune response;
XX	HPV antigen; prevention; treatment; ss.
XX	
XX	Synthetic.
XX	Human papillomavirus.
XX	
XX	WO9933868-A2.
XX	
XX	08-JUL-1999.
XX	
XX	18-DEC-1998; 98MO-EP008563.
XX	

```

PR 24-DEC-1997; 97GB-00027262.
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
PI Dalemans WJ, Gerard CMG;
XX
XX WPI; 1999-405485/34.
DR P-PSDB; AAY25381.
XX
XX Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to
PT induce immune response to HPV.
XX
XX Example VIII; Page 54-55; 62pp; English.
XX
XX AAY78791-X78801 represent nucleic acid sequences which encode novel
CC constructs comprising an B6 or E7 protein or B6/E7 fusion protein from
CC HPV (represented in AAY25375-Y25386). These constructs are optionally
CC linked to an immunological fusion partner and an immunomodulatory CpG
CC oligonucleotide. The products of the invention can be used to induce an
CC immune response in a patient to an HPV antigen. They can also be used for
CC preventing or treating HPV induced tumours
XX
XX Sequence 1173 BP; 380 A; 229 C; 276 G; 288 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 28; DB 2; Length 1173;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 GAACGCAATCAACAAACCGTGTGNG 28
DB 661 GAACGCAATCAACAAACCGTGTGNG 668
RESULT 44
AAX29786
ID AAX29786 standard; DNA; 1173 BP.
XX
XX AAX29786;
AC 17-OCT-2003 (revised)
XX
XX 22-JUN-1999 (first entry)
DT
DE CLYTA-B6E7-His coding sequence.
XX
XX Chimeric; E6; E7; fusion protein; CLYTA; vaccine; immunotherapy; tumour;
KW lesion; benign; malignant; virus; infection; ss.
XX
XX Human papillomavirus.
OS Streptococcus pneumoniae.
XX
XX Chimeric.
OS
XX
XX WO9910375-A2.
PN
XX
XX 04-MAR-1999.
PD
XX
XX 17-AUG-1998; 98WO-EP005285.
PF
XX
XX 22-AUG-1997; 97GB-00017953.
PR
XX
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
PA
XX
XX Bruck C, Cabezon Silva T, Deliese AEF, Gerard CMG;
PI Lombardo-Bencheikh A;
XX
XX WPI; 1999-190587/16.
DR
XX
XX P-PSDB; AAY02637.
PT
XX
XX Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for
XX treatment or prophylaxis of HPV induced lesions.
XX
XX Disclosure; Fig 14; 95pp; English.
XX
XX This sequence represents the coding region for a chimeric B6 or E7

```

CC protein or E6/E7 fusion protein from Human papillomavirus (HPV) linked to
CC an immunological fusion partner, in this case, a fragment of the
CC Streptococcus pneumoniae CLYTA protein. The sequence also contains a
CC histidine tag at the C-terminus of the encoded protein. The protein can
CC be used in a vaccine, for immuno-therapeutically treating HPV induced
CC tumour lesions (benign or malignant) and preventing HPV viral infection.
CC (Updated on 17-Oct-2003 to standardise OS field)

XX
SQ Sequence 1173 BP; 380 A; 229 C; 276 G; 288 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 2; Length 1173;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACAGCAATACAAACCGTTGTGTG 28
|||||
Db 661 GAACAGCAATACAAACCGTTGTGTG 688

RESULT 45
AED52645
ID AED52645 standard; DNA; 1173 BP.

XX AED52645;

XX 29-DEC-2005 (first entry)

XX Fusion protein cLYTA-B6-E7-His/HPV16, DNA.

XX Fusion protein; vaccine; papilloma; cytosolic; papillomavirus infection;
XX virulence; uterine cervix tumor; E7; E6; de; gene; LyTA.

XX Streptococcus pneumoniae.

XX Human papillomavirus type 16.

XX Synthetic.

XX Chimeric.

XX Key Location/Qualifiers
FT 1..1173
FT /tag= a
FT /product= "Fusion protein cLYTA-B6-E7-His/HPV16"

XX IN9801903-14.

XX 04-MAR-2005.

XX 24-AUG-1998; 98IN-CH001903.

XX 22-AUG-1997; 97EP-00179535.

XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

XX Tytrell AMR;

XX WPI; 2005-557648/57.

XX P-PSDB; AED52646.

XX Vaccine.

XX Example 12; Fig 14; 96pp; English.

XX The invention relates to human Papilloma virus (HPV) fusion proteins,
XX linked to an immunological fusion partner that provides T helper epitopes
XX to the HPV antigen. Vaccine formulations comprising the fusion proteins
XX are useful in the treatment or prophylaxis of HPV induced lesions
XX (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7
XX proteins (singly, as an E6-E7 fusion or mutated) were fused to either
XX Haemophilus influenzae D protein (20-127), the C-terminus of
XX Streptococcus pneumoniae LyTA protein (cLYTA) or thiorodoxin. The present
XX sequence encodes an HPV-LyTA, fusion protein of the invention.

XX Sequence 1173 BP; 380 A; 229 C; 276 G; 288 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 14; Length 1173;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACAGCAATACAAACCGTTGTGTG 28
|||||
Db 661 GAACAGCAATACAAACCGTTGTGTG 688

RESULT 46

AAFS5127
ID AAF55127 standard; DNA; 7840 BP.

XX AAF55127;

XX 29-MAY-2001 (first entry)

XX Nucleotide sequence of the vector pRetroFF-E6E7.

XX Stem cell; gene therapy; cell therapy; stem cell disorder; ss.

XX Synthetic.

XX Key Location/Qualifiers

XX misc_feature

XX /tag= d
XX /note= "this base is given as N because it was illegible
XX in the figure"

XX /tag= e
XX /note= "this base is given as N because it was illegible
XX in the figure"

XX /tag= f
XX /note= "this base is given as N because it was illegible
XX in the figure"

XX /tag= g
XX /note= "this base is given as N because it was illegible
XX in the figure"

XX /tag= h
XX /note= "this base is given as N because it was illegible
XX in the figure"

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XX in the figure"

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XX in the figure"

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XX in the figure"

XX /tag= b
XX /note= "this base is given as N because it was illegible
XX in the figure"

XX /tag= k
XX /note= "this base is given as N because it was illegible
XX in the figure"

XX /tag= c
XX /note= "this base is given as N because it was illegible
XX in the figure"

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XX in the figure"

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XX in the figure"

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XX /note= "this base is given as N because it was illegible
XX in the figure"

XX /tag= 1
XX /note= "this base is given as N because it was illegible
XX in the figure"

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FT	/note= "this base is given as N because it was illegible	
PT	in the figure"	
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PT	in the figure"	
PT	6150	
misc_feature	/+tag= o	
PT	/note= "this base is given as N because it was illegible	
PT	in the figure"	
PT	6200	
misc_feature	/+tag= p	
PT	/note= "this base is given as N because it was illegible	
PT	in the figure"	
PT	6250	
misc_feature	/+tag= q	
PT	/note= "this base is given as N because it was illegible	
PT	in the figure"	
PT	6300	
misc_feature	/+tag= r	
PT	/note= "this base is given as N because it was illegible	
PT	in the figure"	
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PT	/note= "this base is given as N because it was illegible	
PT	in the figure"	
PT	6400	
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PT	in the figure"	
PT	6450	
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misc_feature	/+tag= v	
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misc_feature	/+tag= x	
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PT	in the figure"	
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PT	in the figure"	
PT	6900	
misc_feature	/+tag= ac	
PT	/note= "this base is given as N because it was illegible	
PT	in the figure"	
PT	6950	
misc_feature	/+tag= ad	
PT	/note= "this base is given as N because it was illegible	
PT	in the figure"	
PT	7000	
misc_feature	/+tag= ae	

DB	QY	Query Match	Best Local Similarity	100.0%; Score 28; DB 5; Length 7840;	Pred. No. 0.047;	Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
FT	FT	/note= "this base is given as N because it was illegible in the figure"				
FT	FT	7050				
FT	FT	/*tag= ah				
FT	FT	/note= "this base is given as N because it was illegible in the figure"				
FT	FT	7100				
FT	FT	/*tag= al				
FT	FT	/note= "this base is given as N because it was illegible in the figure"				
FT	FT	7150				
FT	FT	/*tag= aj				
FT	FT	/note= "this base is given as N because it was illegible in the figure"				
FT	FT	7200				
FT	FT	/*tag= ak				
FT	FT	/note= "this base is given as N because it was illegible in the figure"				
FT	FT	7250				
FT	FT	/*tag= al				
FT	FT	/note= "this base is given as N because it was illegible in the figure"				
FT	FT	7300				
FT	FT	/*tag= am				
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FT	FT	7400				
FT	FT	/*tag= ao				
FT	FT	/note= "this base is given as N because it was illegible in the figure"				
FT	FT	7450				
FT	FT	/*tag= ap				
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FT	FT	7500				
FT	FT	/*tag= aq				
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FT	FT	7550				
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FT	FT	7600				
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FT	FT	7650				
FT	FT	/*tag= at				
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FT	FT	7700				
FT	FT	/*tag= au				
FT	FT	/note= "this base is given as N because it was illegible in the figure"				
FT	FT	7750				
FT	FT	/*tag= av				
FT	FT	/note= "this base is given as N because it was illegible in the figure"				
FT	FT	7800				
FT	FT	/*tag= ax				
FT	FT	/note= "this base is given as N because it was illegible in the figure"				

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RESULT 47
AAT09847
ID AAT09847 standard; DNA; 7902 BP.
XX
AC AAT09847;
XX
DT 27-AUG-2003 (revised)
DT 02-JAN-1997 (first entry)
XX
DE Human papilloma virus 16 genomic DNA.
XX
KM Human papilloma virus; HPV; ribozyme; cleavage; E6; E7; keratinocyte;
KW infection; genital warts; neoplasia; cervical cancer; warts; ds.
XX
OS Human papillomavirus type 16.
PN MO95J1552-A2.
XX
PD 23-NOV-1995.
XX
PF 15-MAY-1995; 95MO-US006016.
XX
PR 13-MAY-1994; 94US-00242665.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (UYNF-) UNIV NORTHERN ILLINOIS.
XX
PI Hampel A, DiPaolo J, Siwkowski A,
XX
DR WPI; 1996-010937/01.
XX
PT Synthetic ribozyme(s) for human papilloma virus (HPV) - useful in
PT treatment of cervical cancer and in detection of HPV.
XX
PS disclosure; Page 25-29; 60pp; English.
XX
CC Synthetic ribozymes directed against human papilloma virus (HPV) 16 may
CC be used to cleave HPV or to detect HPV in human tissue. The ribozymes
CC cleave HPV to lower the production of the E6 and E7 proteins which play a
CC key role in keratinocyte transformation. They can be used for the
CC treatment of HPV infections which are associated with genital warts and
CC genital neoplasms. In particular they can be used for the treatment of
CC cervical cancer optionally with other agents such as cisplatin. Ribozymes
CC are described in AAT40306-T40315. (Updated on 27-AUG-2003 to correct OS
CC field.)
XX
SQ Sequence 7902 BP; 2601 A; 1376 C; 1507 G; 2418 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 28; DB 2; Length 7902;
Best local Similarity 100.0%; Pred. No. 0.047;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAACAGCAATACAAACACCGTTGTG 28
Db 368 GAACAGCAATACAAACACCGTTGTG 395

```

```

OS Human papillomavirus type 16.
XX
FH Key Location/Qualifiers
FT 17..23
FT TATA_signal
FT /tag= a
FT 65..71
FT TATA_signal
FT /tag= b
FT 83..559
FT CDS
FT /product= "E6 transforming protein"
FT /note= "E6 ORF from 65 to 559; putative"
FT 350
FT mutation
FT /tag= d
FT /note= "Mutated from the normal T in the reference
FT sequence (AAT94723)"
FT 562..858
FT CDS
FT /tag= e
FT /product= "E7 transforming protein"
FT /note= "E7 ORF 544 to 858; putative"
FT 865..2813
FT CDS
FT /tag= f
FT /product= "E1 replication protein"
FT /note= "E1 interrupted ORF from 859 to 2813; putative"
FT 2755..3852
FT CDS
FT /tag= g
FT /product= "E2 regulatory protein"
FT /note= "E2 ORF from 2725 to 3852; putative"
FT 3332..3619
FT CDS
FT /tag= h
FT /product= "E4"
FT /note= "E4 ORF from 3332 to 3619; putative"
FT 3863..4099
FT CDS
FT /tag= i
FT /product= "E5"
FT /note= "E5 ORF from 3863 to 4099; putative"
FT 4213..4218
FT polyA_signal
FT /tag= j
FT /note= "Putative"
FT 4235..5656
FT CDS
FT /tag= k
FT /product= "L2 minor capsid protein"
FT /note= "L2 ORF from 4133 to 5656; putative"
FT 4289..4295
FT TATA_signal
FT /tag= l
FT 5559..7154
FT CDS
FT /tag= m
FT /product= "L1 major capsid protein"
FT /note= "L1 ORF from 5526 to 7154; putative"
FT 7260..7265
FT polyA_signal
FT /tag= n
XX
XX US5679509-A.
XX
XX 21-OCT-1997.
XX
XX 30-SEP-1994; 94US-00316239.
XX
XX 28-SEP-1993; 93US-00127906.
XX
XX (UYNF-) UNIV NEW MEXICO STATE.
XX
XX Wheeler CM, Parmenter CA;
XX
XX WPI; 1997-525714/48.
XX
XX P-PsDB; AAM35742.
XX
XX Evaluating risk of cervical dysplasia or cervical cancer - by detecting
XX variant form of human papilloma virus 16.
XX
XX Claim 1; Col 15-24; 33pp; English.
XX
XX Methods have been developed for distinguishing a subset of human
XX papilloma virus (HPV) that is associated with an increased risk of
CC

```

CC developing cervical dysplasia or cervical cancer. The methods involve:
 CC (1) preparing a cervical sample to expose any HPV-16 E6 gene in the
 CC sample and determining if the base at position 350 of the E6 gene (see
 CC AAT94723 and AAT94724 for comparison) is T or G, where the presence of G
 CC at position 350 is associated with an increased risk of developing
 CC cervical dysplasia or cervical cancer; and (2) preparing a cervical
 CC sample to expose any HPV-16 E6 protein in the sample and determining if
 CC the amino acid at position 83 of the protein (see position 90 in AAW35741
 CC and AAW35742 for comparison) is Val or Leu, where the presence of Val at
 CC position 83 that is associated with an increased risk of developing
 CC cervical dysplasia or cervical cancer. The present sequence represents
 CC the variant nucleotide sequence for HPV-16 E6. The 350G variant
 CC correlates well with Pap scores: 350T:350G ratios among 45 HPV16 samples
 CC were 10:4 for negative Pap scores; 4:2 for CIN I, 1:6 for CIN II; 2:9 for
 CC CIN III; 0:3 for cancer. (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 7904 BP; 2601 A; 1377 C; 1510 G; 2416 T; 0 U; 0 Other;
 Query Match 100.0%; Score 28; DB 2; Length 7904;
 Best Local Similarity 100.0%; Pred. No. 0.047;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GAACAGCAATACAAACCGTTGTGTG 28
 Db 368 GAACAGCAATACAAACCGTTGTGTG 395
 RESULT 49
 AAT94723
 ID AAT94723 standard; DNA; 7904 BP.
 XX AAT94723;
 AC
 XX 25-MAR-2003 (revised)
 DT 16-FEB-1998 (first entry)
 XX
 DE Human papillomavirus type 16 B6 complete genome.
 XX
 XX Complete genome; circular; human papillomavirus type 16; HPV16 E6;
 KM cervical dysplasia; cervical cancer; cervical smear; ds.
 XX
 OS Human papillomavirus type 16.
 XX
 FH Key Location/Qualifiers
 FT TATA_signal 17..23
 FT TATA_signal /*tag= a
 FT 65..71
 FT /*tag= b
 FT 83..559
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 XX USS679509-A.
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 XX 21-OCT-1997.
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 XX 30-SEP-1994; 94US-00316239.
 PF
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 XX 28-SEP-1993; 93US-00127906.
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 XX (UNNE-) UNIV NEW MEXICO STATE.
 PA
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 XX Wheeler CM, Parmenter CA;
 PI
 XX
 XX WPI; 1997-525714/48.
 DR
 XX
 XX P-PSDB; AAW35741.
 DR
 XX
 XX Evaluating risk of cervical dysplasia or cervical cancer - by detecting
 PT variant form of human papilloma virus 16.
 PT
 XX
 XX
 PS Claim 1; Col 9-16; 33pp; English.
 XX
 XX Methods have been developed for distinguishing a subset of human
 CC papilloma virus (HPV) that is associated with an increased risk of
 CC developing cervical dysplasia or cervical cancer. The methods involve:
 CC (1) preparing a cervical sample to expose any HPV-16 E6 gene in the
 CC sample and determining if the base at position 350 of the E6 gene (see
 CC AAT94723 and AAT94724 for comparison) is T or G, where the presence of G
 CC at position 350 is associated with an increased risk of developing
 CC cervical dysplasia or cervical cancer; and (2) preparing a cervical
 CC sample to expose any HPV-16 E6 protein in the sample and determining if
 CC the amino acid at position 83 of the protein (see position 90 in AAW35741
 CC and AAW35742 for comparison) is Val or Leu, where the presence of Val at
 CC position 83 that is associated with an increased risk of developing
 CC cervical dysplasia or cervical cancer. The present sequence represents
 CC the reference nucleotide sequence for HPV-16 E6. The 350G variant
 CC correlates well with Pap scores: 350T:350G ratios among 45 HPV16 samples
 CC were 10:4 for negative Pap scores; 4:2 for CIN I, 1:6 for CIN II; 2:9 for
 CC CIN III; 0:3 for cancer. (Updated on 25-MAR-2003 to correct PF field.)
 CC
 XX
 XX Sequence 7904 BP; 2601 A; 1377 C; 1509 G; 2417 T; 0 U; 0 Other;
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 Query Match 100.0%; Score 28; DB 2; Length 7904;
 Best Local Similarity 100.0%; Pred. No. 0.047;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GAACAGCAATACAAACCGTTGTGTG 28
 Db 368 GAACAGCAATACAAACCGTTGTGTG 395
 RESULT 50
 AAX33881
 ID AAX33881 standard; DNA; 7904 BP.
 XX
 XX AAX33881;
 AC

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XX 17-OCT-2003 (revised)
DT 25-JUN-1999 (first entry)
XX
XX HPV-16 genomic sequence.
DE
XX HPV-16; inhibitor; antisense oligonucleotide; E6/E7 gene; human;
KM keratinocyte; cervical cell; cervical tumour; PCR primer; beta-actin; ss.
XX
OS Human papillomavirus type 16.
XX
PN W09913071-A1.
XX
PD 18-MAR-1999.
XX
PF 03-SEP-1998; 98WO-US018320.
XX
PR 05-SEP-1997; 97US-00929140.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI DiPaolo J, Alvarez-Salas L;
XX
DR WPI, 1999-243727/20.
XX
XX New antisense oligonucleotide analogs for inhibiting growth of cervical
PT tumors.
XX
PS Disclosure; Page 28-32; 40pp; English.
XX
XX This sequence represents a sequence from the HPV-16 genome. This
CC invention relates to antisense oligonucleotide analogs (ONs) that have a
CC sequence complementary to a sequence of nucleotides 415-445 of human
CC papilloma virus-16 (HPV-16). The antisense ONs can be used to inhibit
CC expression of HPV gene E6/E7 in living cells, preferably human
CC keratinocytes or human cervical cells. They bind to E6/E7 mRNA in the
CC cell, prevent mRNA translation and promote mRNA degradation by
CC intracellular RNase H. They can be used for preventing transformation of
CC living cells by HPV. The antisense ONs are used particularly for
CC inhibiting the growth of cervical tumours. (Updated on 17-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 7904 BP; 2601 A; 1377 C; 1509 G; 2417 T; 0 U; 0 Other;

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Query Match 100.0%; Score 28; DB 2; Length 7904;
 Best Local Similarity 100.0%; Pred. No. 0.047;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GAACAGCAATACACAAACCGTTGTGTG 28
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DB 368 GAACAGCAATACACAAACCGTTGTGTG 395

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Search completed: May 24, 2006, 05:56:28
 Job time : 335.037 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 24, 2006, 05:47:01 ; Search time 1932.77 Seconds
(without alignments)
810.102 Million cell updates/sec

Title: US-10-601-913-5
Perfect score: 28
Sequence: 1 GAACAGCAATACAAACAACGGTGTGTG 28

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1000 summaries

Database :

EST:
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_hic:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gsa1:*
12: gb_gsa2:*
13: gb_gsa3:*
14: gb_gsa4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	20.6	73.6	532	11	AZ412297
7	20.6	73.6	600	11	BZ314774
8	20.6	73.6	1058	11	CC274364
9	20	71.4	207	11	AQ075030
10	20	71.4	593	11	AQ265336
11	20	71.4	675	11	AQ505344
12	20	71.4	762	11	DR982710
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C 102	19	67.9	731	8	CV559307	CV559307	un-M-H2O-	C 175	18.6	66.4	705	11	AZ340332	AZ340332	AZ340332	AZ340332
C 103	19	67.9	746	14	CT454665	CT454665	Sus_gcrof	C 176	18.6	66.4	724	3	BM932548	BM932548	BM932548	BM932548
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C 106	19	67.9	766	7	BE034698	BE034698	ML03B11.M	C 179	18.6	66.4	762	3	BU247293	BU247293	BU247293	BU247293
C 107	19	67.9	778	12	CG857991	CG857991	ZMMBB026	C 180	18.6	66.4	770	12	CG397581	CG397581	CG397581	CG397581
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C 109	19	67.9	796	10	DV624608	DV624608	94175.1.C	C 182	18.6	66.4	780	14	BM137533	BM137533	BM137533	BM137533
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C 114	19	67.9	836	9	DA572060	DA572060	DA572060	C 187	18.6	66.4	794	12	CC140238	CC140238	CC140238	CC140238
C 115	19	67.9	845	11	BH086823	BH086823	RPC1-24.3	C 188	18.6	66.4	795	13	CZ773607	CZ773607	CZ773607	CZ773607
C 116	19	67.9	848	13	CZ540043	CZ540043	SRAA_aad2	C 189	18.6	66.4	801	13	DU241667	DU241667	DU241667	DU241667
C 117	19	67.9	861	10	DR690125	DR690125	SR108021	C 190	18.6	66.4	810	12	CC389170	CC389170	CC389170	CC389170
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C 124	19	67.9	999	12	CL037952	CL037952	CH216-44H	C 197	18.6	66.4	840	10	DY334673	DY334673	DY334673	DY334673
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C 137	18.8	67.1	1649	7	BF129403	BF129403	601811403	C 210	18.4	65.7	272	12	CE614632	CE614632	CE614632	CE614632
C 138	18.8	67.1	41	11	BZ289694	BZ289694	SALK_0230	C 211	18.4	65.7	365	5	CD190374	CD190374	CD190374	CD190374
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C 141	18.6	66.4	276	8	CO050928	CO050928	Le_mxo_21	C 214	18.4	65.7	386	1	AL039060	AL039060	AL039060	AL039060
142	18.6	66.4	342	13	CN575705	CN575705	rc57E07.x	C 215	18.4	65.7	393	11	AQ796835	AQ796835	AQ796835	AQ796835
143	18.6	66.4	342	13	CZ813758	CZ813758	OC_Ba018	C 216	18.4	65.7	398	9	DN830567	DN830567	DN830567	DN830567
C 144	18.6	66.4	366	8	CN576354	CN576354	rc63B01.x	C 217	18.4	65.7	411	11	AQ979872	AQ979872	AQ979872	AQ979872
C 145	18.6	66.4	389	3	BM952303	BM952303	rc57E07.Y	C 218	18.4	65.7	432	4	CD091062	CD091062	CD091062	CD091062
C 146	18.6	66.4	401	3	BQ563145	BQ563145	at05-d01	C 219	18.4	65.7	447	4	BM52737	BM52737	BM52737	BM52737
C 147	18.6	66.4	425	11	BI4896	BI4896	343F13.TP.C	C 220	18.4	65.7	448	4	BM533326	BM533326	BM533326	BM533326
148	18.6	66.4	448	11	AQ009738	AQ009738	CIT-HSP-2	C 221	18.4	65.7	454	8	CX280527	CX280527	CX280527	CX280527
149	18.6	66.4	474	11	AZ125886	AZ125886	OSUNB009	C 222	18.4	65.7	458	4	BM594086	BM594086	BM594086	BM594086
C 150	18.6	66.4	477	1	AA232260	AA232260	rx23c07.r	C 223	18.4	65.7	461	7	AM296554	AM296554	AM296554	AM296554
C 151	18.6	66.4	480	4	BM739507	BM739507	EX739507	C 224	18.4	65.7	470	2	BG993187	BG993187	BG993187	BG993187
152	18.6	66.4	485	1	AI230487	AI230487	EST227182	C 225	18.4	65.7	477	4	BM564260	BM564260	BM564260	BM564260
153	18.6	66.4	497	1	AI231705	AI231705	CR967916	C 226	18.4	65.7	481	8	CX257213	CX257213	CX257213	CX257213
C 154	18.6	66.4	510	14	AG877966	AG877966	mtch4-35D2	C 227	18.4	65.7	483	10	DR791285	DR791285	DR791285	DR791285
C 155	18.6	66.4	516	11	AO877366	AO877366	HS_2145.B	C 228	18.4	65.7	483	10	DM554073	DM554073	DM554073	DM554073
C 156	18.6	66.4	517	9	DR077652	DR077652	Lr_Cd2CF	C 229	18.4	65.7	484	2	BJ665518	BJ665518	BJ665518	BJ665518
157	18.6	66.4	527	11	BS9650	BS9650	CIT-HSP-3f3	C 230	18.4	65.7	490	4	BM590610	BM590610	BM590610	BM590610
C 158	18.6	66.4	529	11	BH004287	BH004287	EMBA007L1	C 231	18.4	65.7	497	4	BM577382	BM577382	BM577382	BM577382
C 159	18.6	66.4	571	1	AJ640761	AJ640761	BP354296	C 232	18.4	65.7	502	2	BI349732	BI349732	BI349732	BI349732
C 160	18.6	66.4	581	3	BP354296	BP354296	OC_Ba022	C 233	18.4	65.7	517	4	BM704401	BM704401	BM704401	BM704401
161	18.6	66.4	596	13	CZ841049	CZ841049	CC_Ba012	C 234	18.4	65.7	521	10	DR584434	DR584434	DR584434	DR584434
162	18.6	66.4	609	14	DUE21116	DUE21116	OC_Ba012	C 235	18.4	65.7	521	10	DR584434	DR584434	DR584434	DR584434
163	18.6	66.4	617	12	CC785539	CC785539	ZMMBB015	C 236	18.4	65.7	521	10	DR584434	DR584434	DR584434	DR584434
164	18.6	66.4	621	13	CZ708874	CZ708874	OC_Ba002	C 237	18.4	65.7	521	10	DR584434	DR584434	DR584434	DR584434
C 165	18.6	66.4	625	1												

239	18.4	65.7	528	4	BW534781	BW534781	BM534781	C 312	18.4	65.7	937	13	CZ521096	CZ521096	GMW2-86L2
240	18.4	65.7	537	7	AW519969	AW519969	660058A04	C 313	18.4	65.7	941	12	CG265046	CG265046	OC3D052TH
241	18.4	65.7	537	12	CG706619	CG706619	BARC_BFGL	C 314	18.4	65.7	946	10	DV0060903	DV0060903	CMB243-FO
242	18.4	65.7	543	8	CV904193	CV904193	PD04A411	C 315	18.4	65.7	955	12	CG394452	CG394452	ZMMBBC000
243	18.4	65.7	547	9	DA623668	DA623668	DA623668	C 316	18.4	65.7	975	13	CL069002	CL069002	CH216-115
244	18.4	65.7	561	3	BW776568	BW776568	fy42f08.x	C 317	18.4	65.7	980	13	CL286073	CL286073	ZMMBBC063
245	18.4	65.7	565	11	AZ027838	AZ027838	RPCI-23-3	C 318	18.4	65.7	998	12	CG265055	CG265055	OC3DQ52TV
246	18.4	65.7	567	11	DB036175	DB036175	DB036175	C 319	18.4	65.7	1103	5	CD498334	CD498334	CD433-A08
247	18.4	65.7	580	8	CX269212	CX269212	38RDBRM_U	C 320	18.4	65.7	1145	3	BU412541	BU412541	603154519
248	18.4	65.7	584	9	DA126049	DA126049	DA126049	C 321	18.4	65.7	1197	4	AG186993	AG186993	Pan-rt091
249	18.4	65.7	586	1	AI981187	AI981187	pac_pk004	C 322	18.4	65.7	1204	5	CD509495	CD509495	CDA96-F04
250	18.4	65.7	590	2	B1649228	B1649228	603277446	C 323	18.4	65.7	1290	3	BU368834	BU368834	603595844
251	18.4	65.7	594	5	CF010859	CF010859	QB4f02.p	C 324	18.2	65.0	147	4	CA188229	CA188229	SCCCAM1C0
252	18.4	65.7	602	4	BX079501	BX079501	BX079501	C 325	18.2	65.0	204	4	CA074169	CA074169	SCCBOM104
253	18.4	65.7	604	14	DE012579	DE012579	Branch105	C 326	18.2	65.0	229	10	R61674	R61674	yh09h08_r1
254	18.4	65.7	605	10	DV535042	DV535042	ZM_BEP022	C 327	18.2	65.0	288	10	DM421348	DM421348	HRABE0210
255	18.4	65.7	611	4	BX079500	BX079500	BX079500	C 328	18.2	65.0	303	7	BE004518	BE004518	CM2-BN010
256	18.4	65.7	614	10	DV952385	DV952385	SH03022B2	C 329	18.2	65.0	308	10	DM416756	DM416756	HAAGE0174
257	18.4	65.7	617	11	AQ326024	AQ326024	nbdx0022P	C 330	18.2	65.0	338	7	BP001045	BP001045	7146a02.x
258	18.4	65.7	619	8	CV904964	CV904964	PDpcd_038	C 331	18.2	65.0	344	2	B1043599	B1043599	PMO-OT021
259	18.4	65.7	625	11	AZ026979	AZ026979	RPCI-23-3	C 332	18.2	65.0	349	10	Z43070	Z43070	HSC12G011_n
260	18.4	65.7	629	14	CA055536	CA055536	sba1r3a51	C 333	18.2	65.0	355	1	AV556319	AV556319	AV556319
261	18.4	65.7	636	9	CX888379	CX888379	JGI_CAM2	C 334	18.2	65.0	360	7	AM608740	AM608740	QV2-PT001
262	18.4	65.7	638	9	AA603112	AA603112	np37c01.s	C 335	18.2	65.0	372	7	BF431728	BF431728	nab49e02.s
263	18.4	65.7	646	1	BF166748	BF166748	601776264	C 336	18.2	65.0	396	1	AA654845	AA654845	nc77b08.s
264	18.4	65.7	646	5	CF428288	CF428288	PHI_14_E0	C 337	18.2	65.0	399	5	CF137006	CF137006	UI-HF-BN0
265	18.4	65.7	649	5	CM303239	CM303239	104_787_1	C 338	18.2	65.0	404	13	DU381977	DU381977	109831304
266	18.4	65.7	654	13	BX242869	BX242869	Dan10_rer	C 339	18.2	65.0	405	7	AV813536	AV813536	AV813536
267	18.4	65.7	656	14	EX085074	EX085074	LM_GLS_00	C 340	18.2	65.0	410	3	BP603580	BP603580	BP603580
268	18.4	65.7	657	8	CO837876	CO837876	imageqc_5	C 341	18.2	65.0	417	1	AA620667	AA620667	attf1727_st
269	18.4	65.7	667	8	CV938264	CV938264	PMPcm0_00	C 342	18.2	65.0	417	14	AY403684	AY403684	AY403684
270	18.4	65.7	679	2	B1523121	B1523121	603175832	C 343	18.2	65.0	417	14	AY403684	AY403684	AY403684
271	18.4	65.7	700	8	CM090920	CM090920	EC2BBA34B	C 344	18.2	65.0	418	7	AV820481	AV820481	AV820481
272	18.4	65.7	703	8	BM171666	BM171666	imageqc_5	C 345	18.2	65.0	419	1	AA808883	AA808883	nt68h11.s
273	18.4	65.7	711	4	BX085075	BX085075	BX085075	C 346	18.2	65.0	422	3	BP781429	BP781429	BP781429
274	18.4	65.7	712	4	BX082117	BX082117	BX082117	C 347	18.2	65.0	446	7	BF592278	BF592278	7153e09.x
275	18.4	65.7	718	2	BG427101	BG427101	602493827	C 348	18.2	65.0	446	3	BP593514	BP593514	BP593514
276	18.4	65.7	721	8	CV908041	CV908041	PDtpcd_30	C 349	18.2	65.0	456	14	DE027250	DE027250	DE027250
277	18.4	65.7	722	14	AG359874	AG359874	Mus_muscu	C 350	18.2	65.0	460	3	BP616531	BP616531	BP616531
278	18.4	65.7	731	14	CV937877	CV937877	PMPcm0_00	C 351	18.2	65.0	463	2	BI094462	BI094462	602850036
279	18.4	65.7	740	14	AG359827	AG359827	Mus_muscu	C 352	18.2	65.0	472	2	BJ455317	BJ455317	BJ455317
280	18.4	65.7	744	10	DR816190	DR816190	ZM_BFP004	C 353	18.2	65.0	473	1	AA859708	AA859708	UI-R-B0-b
281	18.4	65.7	746	12	CG932511	CG932511	MBEK433TR	C 354	18.2	65.0	483	2	BJ447566	BJ447566	BJ447566
282	18.4	65.7	749	8	CR538443	CR538443	DKFZP459B	C 355	18.2	65.0	484	1	AA129646	AA129646	2112f11_r
283	18.4	65.7	752	14	AG313882	AG313882	Mus_muscu	C 356	18.2	65.0	487	4	CA268829	CA268829	SCURRT306
284	18.4	65.7	767	9	CX806004	CX806004	JGI_CAJJ1	C 357	18.2	65.0	491	4	CB066954	CB066954	1q33h09.x
285	18.4	65.7	767	9	CF222548	CF222548	AGENCOURT	C 358	18.2	65.0	494	1	AA899200	AA899200	UI-R-B0-b
286	18.4	65.7	773	14	BX174233	BX174233	Dan10_rer	C 359	18.2	65.0	494	1	AA900526	AA900526	UI-R-B0-d
287	18.4	65.7	777	9	CX799941	CX799941	JGI_CAJJ1	C 360	18.2	65.0	495	4	CB142360	CB142360	K-BST0196
288	18.4	65.7	783	12	CG273503	CG273503	OCMUR61TV	C 361	18.2	65.0	495	14	DX282918	DX282918	OR_ABA018
289	18.4	65.7	783	14	AG543969	AG543969	Mus_muscu	C 362	18.2	65.0	503	9	DN196565	DN196565	USDA-FP_1
290	18.4	65.7	786	6	AY111141	AY111141	Zea_mays	C 363	18.2	65.0	506	7	BE166435	BE166435	QVO-HT049
291	18.4	65.7	794	6	B1904852	B1904852	603168844	C 364	18.2	65.0	512	1	AL120965	AL120965	DKFZP762G
292	18.4	65.7	795	7	BF120786	BF120786	601758180	C 365	18.2	65.0	522	14	AY403683	AY403683	Homo_sapi
293	18.4	65.7	796	14	CT089231	CT089231	Sus_scrof	C 366	18.2	65.0	525	9	DB010538	DB010538	DB010538
294	18.4	65.7	800	7	BF167927	BF167927	601775662	C 367	18.2	65.0	528	8	CV919403	CV919403	PH021810
295	18.4	65.7	801	4	BX073902	BX073902	BX073902	C 368	18.2	65.0	535	8	CR929777	CR929777	CR929777
296	18.4	65.7	804	11	B2388120	B2388120	EINAQ42TR	C 369	18.2	65.0	537	1	AA651004	AA651004	31118_Lam
297	18.4	65.7	809	9	DNS32841	DNS32841	1360924_M	C 370	18.2	65.0	538	9	DA212267	DA212267	DA212267
298	18.4	65.7	811	9	CX803274	CX803274	JGI_CAJJ1	C 371	18.2	65.0	539	9	DB272081	DB272081	DB272081
299	18.4	65.7	822	9	DNS31444	DNS31444	1355388_M	C 372	18.2	65.0	541	4	CA233257	CA233257	SCRFLP306
300	18.4	65.7	822	12	CG365086	CG365086	OG1C144TV	C 373	18.2	65.0	548	9	DB062794	DB062794	DB062794
301	18.4	65.7	847	9	DN044805	DN044805	JGI_CABAB	C 374	18.2	65.0	550	3	BP225226	BP225226	BP225226
302	18.4	65.7	854	9	DN044805	DN044805	JGI_CABAB	C 375	18.2	65.0	551	9	DB055760	DB055760	DB055760
303	18.4	65.7	854	13	DUI143834	DUI143834	OG_Aba004	C 376	18.2	65.0	552	3	BP220670	BP220670	BP220670
304	18.4	65.7	856	10	DT507970	DT507970	W602419_B	C 377	18.2	65.0	556	9	DA811400	DA811400	DA811400
305	18.4	65.7	866	9	DN046363	DN046363	JGI_CABAB	C 378	18.2	65.0	559	9	DB182319	DB182319	DB182319
306	18.4	65.7	866	12	CG058723	CG058723	PUELO36TB	C 379	18.2	65.0	561	9	DA563674	DA563674	DA563674
307	18.4	65.7	875	14	DUI49064	DUI49064	109841557	C 380	18.2	65.0	561	9	DA582329	DA582329	DA582329
308	18.4	65.7	880	13	DN111495	DN111495	1110623_M	C 381	18.2	65.0	565	9	DA406339	DA406339	DA406339
309	18.4	65.7	880	13	CZ771074	CZ771074	OC_Ba012	C 382	18.2	65.0	566	9	DA430322	DA430322	DA430322
310	18.4	65.7	888	12	CG058726	CG058726	PUELO36TD	C 383	18.2	65.0	568	9	DB222940	DB222940	DB222940
311	18.4	65.7	932	2	BI411242	BI411242	602964584	C 384	18.2	65.0	573	9	DA326772	DA326772	DA326772

C 385	18.2	65.0	573	9	DA645571	DA645571	C 458	18.2	65.0	923	3	BO439332	BO439332
C 386	18.2	65.0	577	13	CM439888	CM439888	C 459	18.2	65.0	931	5	CF272246	CF272246
C 387	18.2	65.0	580	9	DA805032	DA805032	C 460	18.2	65.0	935	8	CO744483	CO744483
C 388	18.2	65.0	580	9	DB235482	DB235482	C 461	18.2	65.0	939	12	BZ796528	BZ796528
C 389	18.2	65.0	583	3	BP219199	BP219199	C 462	18.2	65.0	943	4	CA272360	CA272360
C 390	18.2	65.0	587	13	CM173235	CM173235	C 463	18.2	65.0	966	2	BG177968	BG177968
C 391	18.2	65.0	590	3	BU952508	BU952508	C 464	18.2	65.0	977	1	AL538186	AL538186
C 392	18.2	65.0	590	4	CA140756	CA140756	C 465	18.2	65.0	978	13	CZ818147	CZ818147
C 393	18.2	65.0	591	9	DA235634	DA235634	C 466	18.2	65.0	1002	4	BX328168	BX328168
C 394	18.2	65.0	594	10	DR376669	DR376669	C 467	18.2	65.0	1003	14	CNS0707CB	CNS0707CB
C 395	18.2	65.0	599	2	BG522609	BG522609	C 468	18.2	65.0	1043	12	CL117657	CL117657
C 396	18.2	65.0	608	1	AU005947	AU005947	C 469	18.2	65.0	1045	14	CNS010BE	CNS010BE
C 397	18.2	65.0	608	8	CO961294	CO961294	C 470	18.2	65.0	1054	3	BM800749	BM800749
C 398	18.2	65.0	616	3	BM341304	BM341304	C 471	18.2	65.0	1135	9	DT738343	DT738343
C 399	18.2	65.0	618	5	CD464626	CD464626	C 472	18.2	65.0	1139	5	CD498135	CD498135
C 400	18.2	65.0	632	7	BE835265	BE835265	C 473	18.2	65.0	1145	9	DN683027	DN683027
C 401	18.2	65.0	635	14	DE021735	DE021735	C 474	18.2	65.0	1208	3	BU962144	BU962144
C 402	18.2	65.0	638	9	CX528852	CX528852	C 475	18.2	65.0	1228	3	BU274693	BU274693
C 403	18.2	65.0	640	3	BP004973	BP004973	C 476	18.2	65.0	1283	10	DT958400	DT958400
C 404	18.2	65.0	640	4	BX508802	BX508802	C 477	18.2	65.0	1633	6	CNS0ACU7	CNS0ACU7
C 405	18.2	65.0	640	4	CA195268	CA195268	C 478	18.2	65.0	1665	6	CNS0AD8U	CNS0AD8U
C 406	18.2	65.0	643	10	DR373358	DR373358	C 479	18.2	65.0	2033	7	BE964846	BE964846
C 407	18.2	65.0	652	3	BU635676	BU635676	C 480	18.2	65.0	2300	6	CR602427	CR602427
C 408	18.2	65.0	654	10	DV083520	DV083520	C 481	18.2	65.0	3487	6	CR860117	CR860117
C 409	18.2	65.0	658	2	BI092246	BI092246	C 482	18.2	65.0	4781	6	CR749458	CR749458
C 410	18.2	65.0	666	8	CR771758	CR771758	C 483	18.2	65.0	4781	6	CR749458	CR749458
C 411	18.2	65.0	671	5	CK591123	CK591123	C 484	18.2	65.0	1333	6	AK201353	AK201353
C 412	18.2	65.0	672	8	CD641207	CD641207	C 485	18.2	65.0	165	8	CR738298	CR738298
C 413	18.2	65.0	676	8	CO961265	CO961265	C 486	18.2	65.0	181	13	CL272036	CL272036
C 414	18.2	65.0	676	14	DX271221	DX271221	C 487	18.2	65.0	205	1	AV309083	AV309083
C 415	18.2	65.0	683	3	BM478345	BM478345	C 488	18.2	65.0	208	14	CT021072	CT021072
C 416	18.2	65.0	690	8	CM423284	CM423284	C 489	18.2	65.0	218	11	BH178047	BH178047
C 417	18.2	65.0	694	10	DT134404	DT134404	C 490	18.2	65.0	225	7	CNS0707CA	CNS0707CA
C 418	18.2	65.0	700	2	BI255430	BI255430	C 491	18.2	65.0	225	7	BO48018	BO48018
C 419	18.2	65.0	710	10	DM282542	DM282542	C 492	18.2	65.0	230	1	AV369045	AV369045
C 420	18.2	65.0	711	10	DM271030	DM271030	C 493	18.2	65.0	239	1	AV364657	AV364657
C 421	18.2	65.0	713	13	CZ774847	CZ774847	C 494	18.2	65.0	259	12	CG422372	CG422372
C 422	18.2	65.0	720	1	DM267359	DM267359	C 495	18.2	65.0	276	7	BB117256	BB117256
C 423	18.2	65.0	723	3	BG565570	BG565570	C 496	18.2	65.0	280	7	BB089624	BB089624
C 424	18.2	65.0	727	2	BM031052	BM031052	C 497	18.2	65.0	283	1	AV138118	AV138118
C 425	18.2	65.0	733	5	CD520101	CD520101	C 498	18.2	65.0	283	1	AV165915	AV165915
C 426	18.2	65.0	741	5	CG252571	CG252571	C 499	18.2	65.0	283	7	BB423881	BB423881
C 427	18.2	65.0	761	12	BG252589	BG252589	C 500	18.2	65.0	286	11	AQ096554	AQ096554
C 428	18.2	65.0	767	4	CA139649	CA139649	C 501	18.2	65.0	289	1	AV133243	AV133243
C 429	18.2	65.0	768	4	CA139649	CA139649	C 502	18.2	65.0	290	7	BB113403	BB113403
C 430	18.2	65.0	779	12	CG428568	CG428568	C 503	18.2	65.0	294	1	AA752403	AA752403
C 431	18.2	65.0	780	5	CD522765	CD522765	C 504	18.2	65.0	294	10	DM100231	DM100231
C 432	18.2	65.0	785	3	BU942395	BU942395	C 505	18.2	65.0	295	1	AV139986	AV139986
C 433	18.2	65.0	795	2	BF796991	BF796991	C 506	18.2	65.0	301	1	AV305877	AV305877
C 434	18.2	65.0	796	12	BZ738253	BZ738253	C 507	18.2	65.0	301	7	BB463309	BB463309
C 435	18.2	65.0	820	14	CNS03HOP	AL244536	C 508	18.2	65.0	303	1	AV145461	AV145461
C 436	18.2	65.0	825	14	DU981676	DU981676	C 509	18.2	65.0	310	7	BB101150	BB101150
C 437	18.2	65.0	831	10	DT191750	DT191750	C 510	18.2	65.0	312	10	DM590603	DM590603
C 438	18.2	65.0	832	10	DT581174	DT581174	C 511	18.2	65.0	314	7	BB459285	BB459285
C 439	18.2	65.0	833	13	DU235681	DU235681	C 512	18.2	65.0	315	4	BY518836	BY518836
C 440	18.2	65.0	834	13	DR761505	DR761505	C 513	18.2	65.0	319	7	BB138243	BB138243
C 441	18.2	65.0	836	13	DU427808	DU427808	C 514	18.2	65.0	319	7	BB462386	BB462386
C 442	18.2	65.0	842	3	BU208078	BU208078	C 515	18.2	65.0	326	4	BY518900	BY518900
C 443	18.2	65.0	848	1	AU118142	AU118142	C 516	18.2	65.0	326	4	CA130357	CA130357
C 444	18.2	65.0	851	4	CA268870	CA268870	C 517	18.2	65.0	336	1	DM172543	DM172543
C 445	18.2	65.0	854	4	BQ431402	BQ431402	C 518	18.2	65.0	341	1	AI555397	AI555397
C 446	18.2	65.0	866	14	CR186150	CR186150	C 519	18.2	65.0	342	1	AA963352	AA963352
C 447	18.2	65.0	866	14	CG252903	CG252903	C 520	18.2	65.0	346	4	BM779292	BM779292
C 448	18.2	65.0	882	10	BG282937	BG282937	C 521	18.2	65.0	347	9	DN798724	DN798724
C 449	18.2	65.0	886	10	DM146986	DM146986	C 522	18.2	65.0	348	10	T065780	T065780
C 450	18.2	65.0	906	14	AG891226	AG891226	C 523	18.2	65.0	350	9	CX625815	CX625815
C 451	18.2	65.0	907	3	BQ425943	BQ425943	C 524	18.2	65.0	359	1	AM083571	AM083571
C 452	18.2	65.0	907	14	CNS03NCV	AL251886	C 525	18.2	65.0	364	1	AL890379	AL890379
C 453	18.2	65.0	915	2	BG460620	BG460620	C 526	18.2	65.0	365	3	BU394530	BU394530
C 454	18.2	65.0	915	7	BR880238	BR880238	C 527	18.2	65.0	368	12	CE378300	CE378300
C 455	18.2	65.0	917	2	AL556802	AL556802	C 528	18.2	65.0	381	12	BM779578	BM779578
C 456	18.2	65.0	917	2	BM457887	BM457887	C 529	18.2	65.0	381	14	DU618221	DU618221
C 457	18.2	65.0	921	5	CF272506	CF272506	C 530	18.2	65.0	381	14	DU618221	DU618221

C 531	18	64.3	389	4	BY670564	BY670564	BY670564	604	18	64.3	587	8	CN947941	CN947941 020805AVB
C 532	18	64.3	393	4	BY420719	BY420719	BY420719	605	18	64.3	590	3	BU776576	BU776576 SUBCOD09
C 533	18	64.3	398	7	BB677135	BB677135	BB677135	606	18	64.3	593	2	BM177412	BM177412 aa18a109.
C 534	18	64.3	398	7	BB766435	BB766435	BB766435	607	18	64.3	593	8	CN220637	CN220637 RA067B05
C 535	18	64.3	399	11	AQ580525	AQ580525	RPCL-11-4	608	18	64.3	593	14	FR0039902	FR0039902
C 536	18	64.3	401	5	CF034372	CF034372	QCF4d12.Y	609	18	64.3	594	10	DV718070	DV718070 RVL8652 W
C 537	18	64.3	401	7	BB799914	BB799914	BB799914	610	18	64.3	595	1	AJ392478	AJ392478
C 538	18	64.3	402	4	BY477482	BY477482	BY477482	611	18	64.3	597	10	DM591820	DM591820 smu81-012
C 539	18	64.3	402	5	CF034665	CF034665	QCF8b06.Y	612	18	64.3	597	13	CZ249297	CZ249297 A1A-aac9
C 540	18	64.3	402	10	DM591227	DM591227	smu81-008	613	18	64.3	598	3	BU485792	BU485792 603847534
C 541	18	64.3	404	1	AV541388	AV541388	AV541388	614	18	64.3	599	1	AL674692	AL674692 AL674692
C 542	18	64.3	412	1	AA724860	AA724860	ah97c11.B	615	18	64.3	599	8	CK072447	CK072447 UCRCS08_2
C 543	18	64.3	417	10	DM591802	DM591802	smu81-012	616	18	64.3	599	8	CK072448	CK072448 UCRCS08_2
C 544	18	64.3	420	8	BO568148	BO568148	k425f05.Y	617	18	64.3	600	14	BX975708	BX975708 Reverse B
C 545	18	64.3	427	8	BO555903	BO555903	HA036H07	618	18	64.3	600	14	CR099116	CR099116 Forward B
C 546	18	64.3	433	1	AI447266	AI447266	mt01a11.X	619	18	64.3	601	3	BU373737	BU373737
C 547	18	64.3	433	1	DM091829	DM091829	CLPY3117.	620	18	64.3	601	8	CN938769	CN938769 010615AVB
C 548	18	64.3	444	5	CD240213	CD240213	ARELSP1G5	621	18	64.3	602	8	CV852768	CV852768 gomod_EST
C 549	18	64.3	448	10	HA0780	HA0780	Y008b12.r1	622	18	64.3	603	4	CA054628	CA054628 aa11g5b52
C 550	18	64.3	454	2	BI804344	BI804344	H134C07 E	623	18	64.3	603	14	CITD10	AJ227432 C1oma int
C 551	18	64.3	455	7	BP149049	BP149049	uv58b03.X	624	18	64.3	604	4	CA039615	CA039615 aa11mh01
C 552	18	64.3	459	1	AJ397662	AJ397662	GAN006C12	625	18	64.3	605	3	BU398755	BU398755 603534057
C 553	18	64.3	463	9	CK625817	CK625817	GAN006C12	626	18	64.3	606	3	BU338275	BU338275 603514405
C 554	18	64.3	465	14	AC959426	AC959426	DY080ph11	627	18	64.3	606	3	BU352725	BU352725 603528626
C 555	18	64.3	471	4	CB130717	CB130717	K-EST0180	628	18	64.3	607	3	BU422137	BU422137 603232664
C 556	18	64.3	471	7	BF585741	BF585741	FM1_24_A0	629	18	64.3	607	9	DN855987	DN855987 4152699 B
C 557	18	64.3	476	5	CJ228478	CJ228478	CJ228478	630	18	64.3	611	3	BU463330	BU463330 603773864
C 558	18	64.3	477	4	BX554025	BX554025	BX554025	631	18	64.3	611	3	BU476643	BU476643 603840665
C 559	18	64.3	477	10	DT670077	DT670077	g13dLT19A	632	18	64.3	611	9	CK909043	CK909043 JG1-CAN1
C 560	18	64.3	491	4	CB637931	CB637931	OSJNEA05H	633	18	64.3	611	13	CZ429845	CZ429845 JG1-BBA010
C 561	18	64.3	494	4	CA347944	CA347944	679150 NC	634	18	64.3	612	3	BU398133	BU398133 603535384
C 562	18	64.3	497	7	BB772364	BB772364	BB772364	635	18	64.3	612	3	BU477540	BU477540 603845676
C 563	18	64.3	498	11	AZ366281	AZ366281	IM0115M14	636	18	64.3	613	13	CM880040	CM880040 Bhe2h57-2
C 564	18	64.3	505	2	BM509744	BM509744	1593d12.Y	637	18	64.3	614	3	BU339323	BU339323 603515635
C 565	18	64.3	508	4	BM890089	BM890089	L0847D06-	638	18	64.3	614	9	BU410489	BU410489 603158768
C 566	18	64.3	510	11	AQ328189	AQ328189	nbxb0042J	639	18	64.3	614	9	CK734109	CK734109 ja08d09.Y
C 567	18	64.3	512	7	BE627511	BE627511	uu52e04.Y	640	18	64.3	615	3	BU466476	BU466476 603373291
C 568	18	64.3	513	2	BG051759	BG051759	FM1_58_A0	641	18	64.3	615	4	CA382694	CA382694 662544 NC
C 569	18	64.3	513	2	BG051759	BG051759	SGP154579	642	18	64.3	616	3	BU473834	BU473834 603365557
C 570	18	64.3	525	12	CG183504	CG183504	PJUFPL86TD	643	18	64.3	616	11	BH270376	BH270376 CM230-139
C 571	18	64.3	525	12	CG183501	CG183501	PJUFPL86TD	644	18	64.3	617	3	BU421669	BU421669 603231785
C 572	18	64.3	532	14	AG951437	AG951437	DY080ph11	645	18	64.3	617	7	AM173933	AM173933 f137d08.Y
C 573	18	64.3	536	4	BM845887	BM845887	BM845887	646	18	64.3	621	7	AM173933	AM173933 603373751
C 574	18	64.3	537	2	BU654969	BU654969	BU654969	647	18	64.3	623	3	BU466995	BU466995 603373751
C 575	18	64.3	537	2	BU654969	BU654969	BU654969	648	18	64.3	624	3	BU475866	BU475866 603472339
C 576	18	64.3	537	4	BY477927	BY477927	BY477927	649	18	64.3	625	3	BU479441	BU479441 603847631
C 577	18	64.3	542	8	CN511028	CN511028	AGENCOURT	650	18	64.3	626	4	CA098635	CA098635 SCWCCU606
C 578	18	64.3	542	4	BY475492	BY475492	BY475492	651	18	64.3	627	3	BU350442	BU350442 603528992
C 579	18	64.3	543	7	BB762562	BB762562	BB762562	652	18	64.3	627	3	BU419033	BU419033 603955678
C 580	18	64.3	546	3	BU475536	BU475536	603777566	653	18	64.3	628	4	CB270838	CB270838 Pgm1C.PK0
C 581	18	64.3	547	11	AQ611675	AQ611675	HS_5087_B	654	18	64.3	628	4	CB270838	CB270838 Pgm1C.PK0
C 582	18	64.3	548	5	CK330463	CK330463	H8219C10-	655	18	64.3	630	13	CL539356	CL539356 OB_BA005
C 583	18	64.3	552	11	AQ426841	AQ426841	CITB1-EI-	656	18	64.3	631	8	CV872926	CV872926 PDUT8A1108
C 584	18	64.3	553	10	DR909004	DR909004	USDB-FP_1	657	18	64.3	631	8	CA038691	CA038691 aa11mh00
C 585	18	64.3	556	3	BO558672	BO558672	HA053F05-	658	18	64.3	634	11	A0783407	A0783407 HS_5563_A
C 586	18	64.3	559	2	BM527247	BM527247	sa151E09.	659	18	64.3	641	2	BI763897	BI763897 603049663
C 587	18	64.3	559	4	BX265504	BX265504	BX265504	660	18	64.3	641	2	BM733064	BM733064 BM733064
C 588	18	64.3	563	7	BB906788	BB906788	BB906788	661	18	64.3	641	7	BE225590	BE225590 MD049 Me
C 589	18	64.3	564	7	BB909647	BB909647	BB909647	662	18	64.3	643	4	CB511309	CB511309 aa11mh5 Me
C 590	18	64.3	567	14	BX965570	BX965570	Forward B	663	18	64.3	646	3	BU309147	BU309147 603533038
C 591	18	64.3	567	14	DR371125	DR371125	AL965570	664	18	64.3	648	1	AI230750	AI230750 EST227445
C 592	18	64.3	568	9	DN508079	DN508079	Danto rer	665	18	64.3	649	1	AV304964	AV304964 AV304964
C 593	18	64.3	568	11	BH087067	BH087067	RPCI-24-3	666	18	64.3	649	13	CZ041895	CZ041895 OM_BA002
C 594	18	64.3	568	11	BH087067	BH087067	RPCI-24-3	667	18	64.3	650	3	BU308795	BU308795 60358430
C 595	18	64.3	571	12	CE602308	CE602308	clgr-g88-	668	18	64.3	651	4	CA053862	CA053862 aa11g5b3
C 596	18	64.3	572	3	BU345640	BU345640	604173089	669	18	64.3	651	14	DE002403	DE002403 Branch108
C 597	18	64.3	574	8	CK258231	CK258231	1311396 X	670	18	64.3	652	4	BX087234	BX087234 BX087234
C 598	18	64.3	575	7	BB905012	BB905012	BB905012	671	18	64.3	658	1	AJ455332	AJ455332 AJ455332
C 599	18	64.3	576	3	BU766095	BU766095	STEARA01	672	18	64.3	658	13	BF693439	BF693439 602081085
C 600	18	64.3	585	11	AQ836855	AQ836855	HS_3463_A	673	18	64.3	660	13	CZ048622	CZ048622 OM_BA003
C 601	18	64.3	585	13	DU336589	DU336589	109842121	674	18	64.3	662	8	CV719843	CV719843 UCRCS08_0
C 602	18	64.3	586	3	BP125395	BP125395	BP125395	675	18	64.3	663	11	AZ941346	AZ941346 2M0201105
C 603	18	64.3	586	12	BZ868329	BZ868329	CH240_237	676	18	64.3	664	12	CG114957	CG114957 PUFOB42TB

677	18	64.3	666	3	BU478335	BU478335	603470342	750	18	64.3	780	7	BF239645	BF239645	601906892
678	18	64.3	666	11	BH505127	BH505127	BOHNP38TF	751	18	64.3	781	11	BZ471312	BZ471312	BONOO70TF
679	18	64.3	667	9	CX845727	CX845727	JGI_CAAK1	752	18	64.3	781	11	CG834123	CG834123	ZMMBC014
680	18	64.3	668	13	CZ173806	CZ173806	MIAA-2001	753	18	64.3	782	10	DV725494	DV725494	RYL147674
681	18	64.3	668	14	CNS05GMO	CNS05GMO	AL336885	754	18	64.3	782	10	BU118416	BU118416	603142667
682	18	64.3	672	4	CAS06869	CAS06869	UI-R-FUO-	755	18	64.3	784	13	CZ568449	CZ568449	C021AL-L-F
683	18	64.3	676	3	BU360503	BU360503	603788769	756	18	64.3	785	9	CX913086	CX913086	JGI_CANA3
684	18	64.3	676	14	AG175996	AG175996	Pan tCrog1	757	18	64.3	785	12	CG397273	CG397273	ZMMBC001
685	18	64.3	678	14	CB511412	CB511412	sealinh50	758	18	64.3	786	3	BU773192	BU773192	SJBFIC05
686	18	64.3	678	14	CT246510	CT246510	Sus scroF	759	18	64.3	787	9	CX399045	CX399045	JGI_XZT35
687	18	64.3	679	3	BU403409	BU403409	604140489	760	18	64.3	792	12	CC004433	CC004433	PUD0227TD
688	18	64.3	680	3	BM576558	BM576558	170006871	761	18	64.3	793	3	BU389636	BU389636	603511550
689	18	64.3	680	7	BB326822	BB326822	BB326822	762	18	64.3	794	13	DU031157	DU031157	12408 Tom
690	18	64.3	680	9	CX360499	CX360499	JGI_XZT13	763	18	64.3	796	12	BZ990181	BZ990181	PUGGW72TB
691	18	64.3	681	4	CA048121	CA048121	sealKhC00	764	18	64.3	797	13	CZ349316	CZ349316	ZMMBC014
692	18	64.3	681	11	BZ465576	BZ465576	BONFT82TF	765	18	64.3	803	3	BU237755	BU237755	603410114
693	18	64.3	682	9	DN959160	DN959160	USDA-PP/A	766	18	64.3	803	8	CR413724	CR413724	CA413724
694	18	64.3	684	14	AG218826	AG218826	DroboPh11	767	18	64.3	803	12	CC697423	CC697423	OGVAL95TF
695	18	64.3	685	5	CF837284	CF837284	UCRC803_0	768	18	64.3	806	11	BZ194850	BZ194850	CH230-370
696	18	64.3	685	8	CV719844	CV719844	UCRC808_0	769	18	64.3	809	10	DV614902	DV614902	EST121789
697	18	64.3	687	8	CO140355	CO140355	EST835026	770	18	64.3	813	9	CX399046	CX399046	JGI_XZT35
698	18	64.3	689	13	CM378730	CM378730	fbdb00160	771	18	64.3	813	12	CG458197	CG458197	PUGFW73TD
699	18	64.3	691	3	BM977444	BM977444	UI-CF-EN1	772	18	64.3	814	14	CT476371	CT476371	Sus scroF
700	18	64.3	694	1	AJ455323	AJ455323	AJ455323	773	18	64.3	818	9	CX961282	CX961282	JGI_CAA01
701	18	64.3	694	13	CZ197729	CZ197729	AIAA-aeg1	774	18	64.3	820	9	CX961291	CX961291	JGI_CAA01
702	18	64.3	695	13	DU591467	DU591467	UI-M-CD0-	775	18	64.3	821	10	DT347307	DT347307	JGI_CAA11
703	18	64.3	696	7	BF468449	BF468449	UI-M-CD0-	776	18	64.3	822	8	CX333400	CX333400	JGI_XZT69
704	18	64.3	699	12	BZ748780	BZ748780	EX00681_D	777	18	64.3	827	3	BU110689	BU110689	603126603
705	18	64.3	700	14	AG148120	AG148120	Pan tCrog1	778	18	64.3	827	10	DT451076	DT451076	JGI_CABR9
706	18	64.3	702	8	CN383191	CN383191	4117379_B	779	18	64.3	827	12	CG255521	CG255521	OG0BR36TV
707	18	64.3	704	11	AQ530921	AQ530921	RPCI-11-3	780	18	64.3	830	11	BH432496	BH432496	BOGFQ40TR
708	18	64.3	716	11	AZ562166	AZ562166	RPCI-23-2	781	18	64.3	831	14	CT259175	CT259175	Sus scroF
709	18	64.3	716	8	CB509606	CB509606	sealinh50	782	18	64.3	832	14	BX223370	BX223370	Danto rer
710	18	64.3	717	8	CX031704	CX031704	1343848_N	783	18	64.3	834	14	BX135201	BX135201	Danto rer
711	18	64.3	717	8	CX258232	CX258232	1311397_N	784	18	64.3	835	12	CG455202	CG455202	PUGFW73TB
712	18	64.3	721	5	CK935576	CK935576	CGF100455	785	18	64.3	838	14	CT434010	CT434010	Sus scroF
713	18	64.3	722	12	CG903456	CG903456	ZMMBC050	786	18	64.3	841	2	BM049606	BM049606	603624678
714	18	64.3	723	12	BZ90184	BZ90184	PUGGW72TD	787	18	64.3	844	2	BF863842	BF863842	963047A12
715	18	64.3	723	13	CZ660450	CZ660450	OM_BA021	788	18	64.3	848	14	DM018775	DM018775	EST122773
716	18	64.3	728	3	BU465521	BU465521	60377258	789	18	64.3	852	10	CT428450	CT428450	Sus scroF
717	18	64.3	733	5	CF833677	CF833677	UCRC802_0	790	18	64.3	857	14	DR876755	DR876755	JGI_CAB17
718	18	64.3	733	11	BH897937	BH897937	Gm_UHD001	791	18	64.3	859	10	DT407137	DT407137	JGI_CAB18
719	18	64.3	733	14	DX289424	DX289424	OR_Aba019	792	18	64.3	860	8	CR439116	CR439116	603439116
720	18	64.3	734	3	BU437725	BU437725	603019146	793	18	64.3	862	10	DT407137	DT407137	603439116
721	18	64.3	735	9	CX890781	CX890781	JGI_CAA03	794	18	64.3	863	11	BH136343	BH136343	ENTOR70TF
722	18	64.3	739	13	CL598493	CL598493	OR_BA006	795	18	64.3	866	14	CT134853	CT134853	Sus scroF
723	18	64.3	740	12	CC085680	CC085680	CSU-K33T-	796	18	64.3	867	12	CT198458	CT198458	ZMMBC025
724	18	64.3	741	5	CF837283	CF837283	UCRC803_0	797	18	64.3	867	14	DU599746	DU599746	CO_BA009
725	18	64.3	742	9	CF833676	CF833676	UCRC802_0	798	18	64.3	867	14	CR053018	CR053018	Forward B
726	18	64.3	743	3	CX668747	CX668747	UCRC801_0	799	18	64.3	870	9	DN910105	DN910105	Cu4_2 CO
727	18	64.3	744	3	BO850013	BO850013	OCB11G20_0	800	18	64.3	873	8	CV504104	CV504104	70620_1 M
728	18	64.3	744	14	DN061462	DN061462	JGI_CAB11	801	18	64.3	874	14	DU629500	DU629500	CO_BA013
729	18	64.3	744	14	AGS52560	AGS52560	Mus_muscu	802	18	64.3	876	12	CG322462	CG322462	PUGFW73TB
730	18	64.3	745	2	BU015509	BU015509	603471984	803	18	64.3	877	9	DN935437	DN935437	AGBNCOURT
731	18	64.3	745	3	BU482146	BU482146	603471984	804	18	64.3	878	3	BU119751	BU119751	603142358
732	18	64.3	745	14	SBC561077	SBC561077	Sus scroF	805	18	64.3	879	7	BF679455	BF679455	602153258
733	18	64.3	746	9	CX668748	CX668748	UCRC801_0	806	18	64.3	885	12	CC985642	CC985642	CUZAB91TV
734	18	64.3	747	14	DX300262	DX300262	OR_Aba010	807	18	64.3	886	10	DM171047	DM171047	603439116
735	18	64.3	748	3	BM968609	BM968609	UI-CF-DU1	808	18	64.3	889	4	CB096250	CB096250	AF53-RPF
736	18	64.3	752	5	CF731569	CF731569	UI-M-HA0-	809	18	64.3	889	14	CNS01763	CNS01763	AL166116
737	18	64.3	753	3	BU382903	BU382903	603857726	810	18	64.3	891	14	CR018070	CR018070	Forward B
738	18	64.3	757	11	AQ210780	AQ210780	HS_2229_A	811	18	64.3	894	13	BU398249	BU398249	603534238
739	18	64.3	760	5	CK937042	CK937042	CGF100451	812	18	64.3	894	12	CG097102	CG097102	PUGFW73TD
740	18	64.3	763	13	CZ464506	CZ464506	MCF755115	813	18	64.3	894	13	CZ216526	CZ216526	AIAA-aef2
741	18	64.3	765	9	CX783951	CX783951	HSC3_28	814	18	64.3	896	8	CO933136	CO933136	AGBNCOURT
742	18	64.3	768	2	BU604677	BU604677	603471984	815	18	64.3	897	14	AG170095	AG170095	Pan tCrog1
743	18	64.3	768	12	CG422244	CG422244	ZMMBC003	816	18	64.3	897	14	CR174287	CR174287	Forward B
744	18	64.3	770	11	AZ611475	AZ611475	IM0437N18	817	18	64.3	901	14	AG834289	AG834289	Olya rat
745	18	64.3	771	5	CF342419	CF342419	AGBNCOURT	818	18	64.3	903	2	BF964790	BF964790	602268038
746	18	64.3	774	4	CA918136	CA918136	EST642283	819	18	64.3	908	12	BZ786559	BZ786559	PUGFW40TD
747	18	64.3	775	5	CX358592	CX358592	AGBNCOURT	820	18	64.3	910	10	DV619521	DV619521	EST122251
748	18	64.3	778	12	CG114958	CG114958	PUP0842TD	821	18	64.3	912	12	CG255510	CG255510	BZ786554
749	18	64.3						822	18	64.3	912	12	CG255510	CG255510	OG0BR36TH

823	18	64.3	916	8	CO761123	brain	EST	896	17.8	63.6	634	13	CZ159101	OO	Ba000
824	18	64.3	921	3	BU119102			897	17.8	63.6	635	4	BX677900		
825	18	64.3	921	10	DT803481			898	17.8	63.6	637	13	CZ079135		
826	18	64.3	924	4	BX759355			899	17.8	63.6	639	11	AQ447489		
827	18	64.3	930	10	DT799123			900	17.8	63.6	640	13	CZ041507	OM	Ba002
828	18	64.3	931	12	CC187727	Ch261-145		901	17.8	63.6	649	8	CNS86235	USDA-FP	1
829	18	64.3	936	12	CG103302	PUBJ61TB		902	17.8	63.6	649	14	DUS68542	OO	Ba005
830	18	64.3	943	12	CG276996	CG3AM26TV		903	17.8	63.6	652	14	DUS98976	OO	Ba009
831	18	64.3	944	2	BI464720			904	17.8	63.6	653	14	DUS51688	OO	Ba002
832	18	64.3	945	3	BU136737	603125395		905	17.8	63.6	663	10	DM010486	w10n10_M1	
833	18	64.3	948	10	DM597236	CGX129-G0		906	17.8	63.6	680	11	BZ012237	oe16b010.	
834	18	64.3	954	10	DT804783	127377730		907	17.8	63.6	686	14	DUS87527	OO	Ba008
835	18	64.3	958	2	BG104489	602311126		908	17.8	63.6	690	13	CZ610987	OM	Ba013
836	18	64.3	983	13	CG920306	CGW920306		909	17.8	63.6	692	13	CZ669460	OM	Ba022
837	18	64.3	986	12	CC294866	CH261-89D		910	17.8	63.6	693	14	CT360232	Sus scrofa	
838	18	64.3	1045	10	DM037992	CFW275-E0		911	17.8	63.6	697	14	DUS65679	OO	Ba010
839	18	64.3	1058	9	DN791375	90936526		912	17.8	63.6	711	14	DUS48774	OO	Ba002
840	18	64.3	1062	9	DN654554	CEC11-G12		913	17.8	63.6	712	14	BX136427	Danlo rer	
841	18	64.3	1074	12	CC222198	CH261-71C		914	17.8	63.6	716	4	CB454422	711191 MA	
842	18	64.3	1296	8	CV861758	gonad	BST	915	17.8	63.6	719	12	CB326126	ligf-g88-	
843	18	64.3	1319	9	DN700141	CLJ27-G08		916	17.8	63.6	720	5	CK962095	4076530 B	
844	18	64.3	1384	6	AY812526	Sch1BFC080		917	17.8	63.6	727	14	DUS628804	OO	Ba013
845	18	64.3	1411	14	AJ854675	Bras61Ca		918	17.8	63.6	731	13	CZ060890	OO	Ba005
846	18	64.3	1422	3	BM911789	AGENCOURT		919	17.8	63.6	735	14	DUS66629	OO	Ba005
847	18	64.3	1433	9	DN720167	CMB132-C0		920	17.8	63.6	735	14	DUS74890	OO	Ba006
848	18	64.3	1552	12	BZ566603	CH261-164		921	17.8	63.6	737	14	DUS61538	OO	Ba011
849	18	64.3	1560	12	CC211685	CC211685	CH261-186	922	17.8	63.6	756	14	DUS40537	OO	Ba001
850	18	64.3	2217	14	AG278863	Mus muscu		923	17.8	63.6	758	14	DX261153	OK	ABa015
851	18	64.3	2325	6	AK046630	Mus muscu		924	17.8	63.6	759	5	CK459828	930051 MA	
852	18	64.3	2325	6	BC052999	Mus muscu		925	17.8	63.6	763	14	DUS48772	OO	Ba002
853	18	64.3	3255	6	AAK077691	Mus muscu		926	17.8	63.6	764	14	DUS48461	OO	Ba002
854	17.8	63.6	252	3	BP561315	BP561315		927	17.8	63.6	767	14	DUS48469	OO	Ba002
855	17.8	63.6	261	14	DUS48246	DUS48246	OO_Ba002	928	17.8	63.6	770	13	CZ881509	OC	Ba008
856	17.8	63.6	261	14	DUS48246	CL632137	XY03425-5	929	17.8	63.6	773	14	DUS70999	OC	Ba005
857	17.8	63.6	286	13	CL632137	DY127558	001106BEM	930	17.8	63.6	776	7	BF244931	601864331	
858	17.8	63.6	300	10	DY127558	CZ211797	OM_Ba015	931	17.8	63.6	785	8	CO724139	00180041-C	
859	17.8	63.6	317	10	DY127558	CZ211797	OM_Ba015	932	17.8	63.6	801	10	DT835590	LB004311.C	
860	17.8	63.6	320	14	DUS86279	OM_Ba007		933	17.8	63.6	818	14	DUS621056	OO	Ba012
861	17.8	63.6	333	13	CZ625803	OM_Ba016		934	17.8	63.6	824	14	DUS99884	OO	Ba009
862	17.8	63.6	346	13	CZ210313	OM_Ba012		935	17.8	63.6	832	10	DT840391	LB00454.C	
863	17.8	63.6	394	13	CZ649764	OM_Ba019		936	17.8	63.6	834	14	DUS61363	OO	Ba004
864	17.8	63.6	399	13	CZ090952	OM_Ba009		937	17.8	63.6	842	4	BX838246	BX838246	
865	17.8	63.6	402	14	DUS45877	OO_Ba002		938	17.8	63.6	885	10	DV908135	LB028101.C	
866	17.8	63.6	408	11	AQ0581856	CZ491883	OM_BB013	939	17.8	63.6	893	10	DV927878		
867	17.8	63.6	433	13	CZ491883	AA313711	EST185579	940	17.8	63.6	902	8	CO880504	BoYegen_08	
868	17.8	63.6	439	13	AA313711	CZ601288	OM_Ba012	941	17.8	63.6	902	14	DUS99934	OO	Ba009
869	17.8	63.6	449	13	CZ601288	AJ667832	AJ667832	942	17.8	63.6	902	14	DUS99934	OO	Ba009
870	17.8	63.6	452	13	CZ047632	CC798041	UGT_CAAJ1	943	17.8	63.6	912	12	CC262538	CH261-167	
871	17.8	63.6	459	13	AJ667832	CC798041	UGT_CAAJ1	944	17.8	63.6	1067	10	DM032270	CFW216-DO	
872	17.8	63.6	462	9	CX798041	CC286676	12_P8_abd	945	17.8	63.6	1069	12	CC284139	CC284139	
873	17.8	63.6	497	5	CD286676	CZ643334	OM_Ba018	946	17.8	63.6	1094	12	CC268770	CH261-72P	
874	17.8	63.6	505	13	CZ622708	OM_Ba016		947	17.8	63.6	1112	12	CC268770	CH261-72P	
875	17.8	63.6	514	13	CZ643334	OM_Ba018		948	17.8	63.6	1189	9	DN660749	CFW12-810	
876	17.8	63.6	526	13	CZ057765	OM_Ba005		949	17.8	63.6	1191	9	DN663210	CEC29-B06	
877	17.8	63.6	535	13	CZ613791	OM_Ba014		950	17.8	63.6	1195	9	DN657552	CEC29-B04	
878	17.8	63.6	536	14	DUS70392	OM_Ba005		951	17.8	63.6	1211	9	DN702449	CLJ41-G01	
879	17.8	63.6	542	14	CR822673	GR0AA52C		952	17.8	63.6	1230	9	DN659521	CEC41-B04	
880	17.8	63.6	548	13	CZ671177	OM_Ba022		953	17.8	63.6	1271	5	CD503083	CD503083	
881	17.8	63.6	550	13	CZ086633	OM_Ba008		954	17.6	62.9	92	1	AA253980	va09h12.r	
882	17.8	63.6	550	14	DUS603020	OM_Ba010		955	17.6	62.9	100	7	BF478272	nae45G04.	
883	17.8	63.6	554	14	DUS603020	OM_Ba010		956	17.6	62.9	110	11	AZ950433	2M0214F01	
884	17.8	63.6	559	13	CF792511	885454	MA	957	17.6	62.9	126	7	AM238566	x	
885	17.8	63.6	562	5	CF792511	885454	MA	958	17.6	62.9	134	11	BH772214	h989e05.g	
886	17.8	63.6	562	8	CV869399	PDUtB1066		959	17.6	62.9	149	5	CF623083	mu44f04.y	
887	17.8	63.6	563	13	CZ624289	OM_Ba016		960	17.6	62.9	166	1	A1197428	w113604.x	
888	17.8	63.6	568	13	CZ099676	OM_Ba010		961	17.6	62.9	169	7	BF286942	E5T451533	
889	17.8	63.6	579	13	CZ598385	OM_Ba005		962	17.6	62.9	169	7	AM238351	xp21d08.x	
890	17.8	63.6	587	14	LBAR093D09	BX540144	Leishmani	963	17.6	62.9	178	10	W14610	mb28d08.r1	
891	17.8	63.6	588	8	CV870158	PDUtB1075		964	17.6	62.9	183	8	CV794885	EST207-F3	
892	17.8	63.6	601	3	BP700624	BP700624		965	17.6	62.9	187	7	AM238686	xp30c05.x	
893	17.8	63.6	602	7	BF045997	BF045997		966	17.6	62.9	199	7	AM919414	EST350718	
894	17.8	63.6	613	14	DUS52880	DUS52880	OO_Ba003	967	17.6	62.9	201	2	BG020487	dc74e07.x	
895	17.8	63.6	626	14	DUS37792	DUS37792	OO_Ba000	968	17.6	62.9	212	1	A1115395	uh85b02.r	

c 969	17.6	62.9	220	7	BF420392	BF420392 UI-R-BJ2-
c 970	17.6	62.9	230	7	AM919342	AM919342 EST50646
c 971	17.6	62.9	231	7	AM238390	AM238390 XD24F08.X
c 972	17.6	62.9	235	1	AV150166	AV150166 AV150166
c 973	17.6	62.9	231	7	BE678370	BE678370 dF54N03.X
c 974	17.6	62.9	234	5	CF609345	CF609345 INF1001.0
c 975	17.6	62.9	229	13	CZ668582	CZ668582 OM_Ba022
c 976	17.6	62.9	272	5	CK401544	CK401544 PBUI6 Mou
c 977	17.6	62.9	273	2	BJ743794	BJ743794 BJ743794
c 978	17.6	62.9	275	1	AL838713	AL838713 AL838713
c 979	17.6	62.9	277	7	BB244244	BB244244 BB244244
c 980	17.6	62.9	278	7	AW919651	AW919651 EST350955
c 981	17.6	62.9	286	1	AI104033	AI104033 EST213322
c 982	17.6	62.9	287	10	DM319669	DM319669 LRAGE0447
c 983	17.6	62.9	291	10	DM311174	DM311174 LRAGE0460
c 984	17.6	62.9	292	1	AV025034	AV025034 AV025034
c 985	17.6	62.9	294	7	BB659810	BB659810 GM700010B
c 986	17.6	62.9	303	7	BF287189	BF287189 EST451780
c 987	17.6	62.9	309	7	BB928602	BB928602 BB928602
c 988	17.6	62.9	311	13	CZ079176	CZ079176 OM_Ba007
c 989	17.6	62.9	314	3	BQ146350	BQ146350 NF047E03F
c 990	17.6	62.9	316	10	DM294675	DM294675 LRAGE0575
c 991	17.6	62.9	322	10	DM297618	DM297618 LRAGE0604
c 992	17.6	62.9	322	12	CC178214	CC178214 KC289 Bay
c 993	17.6	62.9	326	10	DM300401	DM300401 LRAGE0622
c 994	17.6	62.9	326	13	CZ078596	CZ078596 OM_Ba007
c 995	17.6	62.9	328	1	AA958500	AA958500 ua13604.X
c 996	17.6	62.9	330	2	BI395675	BI395675 EST51546
c 997	17.6	62.9	333	8	CV676083	CV676083 mu44f04.K
c 998	17.6	62.9	343	1	AI703827	AI703827 UI-R-AC1-
c 999	17.6	62.9	346	1	AA899801	AA899801 UI-R-BO-d
1000	17.6	62.9	360	4	CB377556	CB377556 CMaE1_38

ALIGNMENTS

RESULT 1
LOCUS BQ106475 244 bp mRNA linear EST 16-APR-2002
DEFINITION fc2102.e Rose Petals (Fragrant Cloud) Lambda Zap Express Library
ACCESSION BQ106475
VERSION BQ106475.1 GI:20156137
KEYWORDS RST.
SOURCE Rosa hybrid cultivar
ORGANISM Rosa hybrid cultivar

REFERENCE
AUTHORS Guterman, I., Shalit, M., Menda, N., Plestun, D., Dafny-Yelin, M., Shalev, G., Bar, E., Davydov, O., Ovadis, M., Emanuel, M., Wang, J., Adam, Z., Pichersky, E., Lewinsohn, E., Zamir, D., Vainstein, A. and Weiser, D.
Rosa hybrid cultivar
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Rosales; Rosaceae; Rosoideae; Rosa.

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Rosa hybrid cultivar
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Rosales; Rosaceae; Rosoideae; Rosa.

ORIGIN
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Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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/dev_stage="Young open flower at stage four"
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.19; Mismatches 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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ORIGIN
Query Match 100.0%; Score 28; DB 3; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.19; Mismatches 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/clone="fc2102.e"
/cissue_type="Petals"
/dev_stage="Young open flower at stage four"
/clone_lib="Rose Petals (Fragrant Cloud) Lambda Zap Express Library"
/note="Vector: pBKCMV; Site_1: EcoRI; Site_2: XhoI"

ORIGIN
Query Match 100.0%; Score 28; DB 3; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.19; Mismatches 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/clone="fc2102.e"
/cissue_type="Petals"
/dev_stage="Young open flower at stage four"
/clone_lib="Rose Petals (Fragrant Cloud) Lambda Zap Express Library"
/note="Vector: pBKCMV; Site_1: EcoRI; Site_2: XhoI"

ORIGIN
Query Match 100.0%; Score 28; DB 3; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.19; Mismatches 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/clone="fc2102.e"
/cissue_type="Petals"
/dev_stage="Young open flower at stage four"
/clone_lib="Rose Petals (Fragrant Cloud) Lambda Zap Express Library"
/note="Vector: pBKCMV; Site_1: EcoRI; Site_2: XhoI"

ORIGIN
Query Match 100.0%; Score 28; DB 3; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.19; Mismatches 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/clone="fc2102.e"
/cissue_type="Petals"
/dev_stage="Young open flower at stage four"
/clone_lib="Rose Petals (Fragrant Cloud) Lambda Zap Express Library"
/note="Vector: pBKCMV; Site_1: EcoRI; Site_2: XhoI"

ORIGIN
Query Match 100.0%; Score 28; DB 3; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.19; Mismatches 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/clone="fc2102.e"
/cissue_type="Petals"
/dev_stage="Young open flower at stage four"
/clone_lib="Rose Petals (Fragrant Cloud) Lambda Zap Express Library"
/note="Vector: pBKCMV; Site_1: EcoRI; Site_2: XhoI"

SOURCE Branchiostoma floridae (Florida lancelet)
ORGANISM Branchiostoma floridae
Bukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
Branchiostoma.

REFERENCE 1
AUTHORS Fujiiyama, A., Toyoda, A., Kuroki, Y. and Sakaki, Y.
TITLE BAC end sequences of CHOR1-302 Amphioxus library
JOURNAL Published Only in Database (2005)
REFERENCE 2 (bases 1 to 677)
AUTHORS Fujiiyama, A.
TITLE Direct Submission
JOURNAL Submitted (12-AUG-2005) Aseo Fujiiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
(E-mail:afujiiyama@gsc.riken.jp, URL: http://stc.gsc.riken.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
PRIMERS

COMMENT Sequencing : TV
LIBRARY

FEATURES
source
Vector : PTARBAC2.1
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
Location/Qualifiers
1. .677
/organism="Branchiostoma floridae"
/mol_type="genomic DNA"
/db_xref="taxon:7739"
/clone="CH302-100_A12_TV"
/sex="male"
/rissue_type="sperm"
/clone_lib="CHOR10302 Amphioxus genomic BAC library"
/note="Common name: amphioxus"

ORIGIN
Query Match 75.7%; Score 21.2; DB 14; Length 677;
Best Local Similarity 88.5%; Pred. No. 2e+02;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AACGCAATACAAACCGTTGTGT 27
Db 170 AATAGCAATCAACAAACCGTTGTGT 145

RESULT 4
CNS03AIR 953 bp DNA linear GSS 01-SEP-2000
LOCUS Tetradon nigroviridis genome survey sequence T7 end of clone
DEFINITION 010C15 of library G from Tetradon nigroviridis, genomic survey
sequence.
ACCESSION AL235260
VERSION AL235260.1 GI:7894395
KEYWORDS GSS; genome survey sequence.
SOURCE Tetradon nigroviridis
ORGANISM Tetradon nigroviridis
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetradon.

REFERENCE 1
AUTHORS Roest Crolius, H., Jallion, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fitzner, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
TITLE Estimate of human gene number provided by genome-wide analysis
JOURNAL Nat. Genet. 25 (2), 235-238 (2000)
REFERENCE 2
AUTHORS Roest Crolius, H., Jallion, O., Dasilva, C., Ozouf-Costaz, C.,
Fitzner, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F.,
Saurin, W., Bernot, A. and Weissenbach, J.
TITLE Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetradon nigroviridis
JOURNAL Genome Res. 10 (7), 939-949 (2000)

PUBMED 10899143
REFERENCE 3 (bases 1 to 953)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetradon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/tetradon.

FEATURES
source
Location/Qualifiers
1. .953
/organism="Tetradon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="010C15"
/clone_lib="G"
/note="Genoscope sequence ID : COBG010AB08LP1
end : T7"

ORIGIN
Query Match 75.7%; Score 21.2; DB 14; Length 953;
Best Local Similarity 88.5%; Pred. No. 2.1e+02;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AACGCAATACAAACCGTTGTGT 27
Db 18 AATAGCAATCAACAAACCGTTGTGT 43

RESULT 5
BZ321278 527 bp DNA linear GSS 06-NOV-2002
LOCUS hz21g05.g1 WGS-2may9f (JM107 adapted methyl filtered) Zea mays
DEFINITION Genomic clone hz21g05 5', genomic survey sequence.
ACCESSION BZ321278
VERSION BZ321278.1 GI:24697359
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 527)
Rabinowitz, P.D., O'Shaughnessy, A.L., Balija, V., Dedhia, N.,
Katzemburger, F., King, L., Miller, B., Muller, S., Nascento, L.,
Zutavern, T., McCombie, W.R. and Martienssen, R.A.
Genomic shotgun sequences from Zea mays (methyl-filtered)
Unpublished (2002)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Plate: hz21 row: 9 column: 05
Seq primer: -21M13UnivRev
Class: shotgun
High quality sequence atp: 527.
Location/Qualifiers
1. .527
/organism="Zea mays"
/mol_type="genomic DNA"
/culivar="B73"
/db_xref="taxon:4577"
/clone="hz21g05"
/lab_host="JM107 or DH5a"
/clone_lib="WGS-2may9f (JM107 adapted methyl filtered)"
/note="Organ: Immature ears; Site 1: Xba I; Site 2: Xba I;
The vector was digested with XbaI and one nucleotide was
added by fill in in the recessive 3' end. The genomic DNA

was nebulized, end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments were between 0.8 and 3 kb and were cloned into the vector (x/y reads in M13mp19, b/g reads in pUC19). The same ligation was transformed in either JM107 or DH5a."

ligation was transformed in either JM107 or DH5a."

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E.coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 73.6%; Score 20.6; DB 11; Length 527;
Best Local Similarity 85.2%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GAACAGCATACAAACCGTTGTGT 27
|||||
Db 215 GAACACCATTAACAAATCGTGTGT 241

ORIGIN

Query Match 73.6%; Score 20.6; DB 11; Length 532;
Best Local Similarity 85.2%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AACAGCAATACAAACCGTTGTGTG 28
|||||
Db 515 AACAGCAATACACACCGTGTGTG 489

RESULT 6
AZ412297/c 532 bp DNA linear GSS 03-OCT-2000
LOCUS 1M0185M08R Mouse 10kb plasmid UGCM library Mus musculus genomic
DEFINITION clone UGCM10185M08 R, genomic survey sequence.
ACCESSION AZ412297
VERSION AZ412297.1 GI:10536310
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 532)
Dunn,D., Aoyagi,A., Barber,M., Beacom,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0185 row: M column: 08
Seq primer: CACACAGAAACAGCTATGAC
Class: plasmid ends
High quality sequence stop: 532.
Location/Qualifiers
1. 532
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCM10185M08"
/sex="Male"
/lab_host="R. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCM library"
/note="Vector: PWD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi14732114|gb|AF129072.1), a copy-number

RESULT 7
BZ314774/c 600 bp DNA linear GSS 06-NOV-2002
LOCUS h221g05.b1 MGS-ZmayrF (JM107 adapted methyl filtered) Zea mays
DEFINITION genomic clone h221g05 5', genomic survey sequence.
ACCESSION BZ314774
VERSION BZ314774.1 GI:24683701
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 600)
Rabinowicz,P.D., O'Shaughnessy,A.L., Bailly,V., Dedhia,N.,
Katzemburger,F., King,L., Miller,B., Muller,S., Nascimben,L.,
Zutavern,T., McCombie,W.R. and Martienssen,R.A.
Genomic shotgun sequences from Zea mays (methyl-filtered)
Unpublished (2002)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org
Plate: h221 row: g column: 05
Seq primer: -21M13univFwd
Class: shotgun
High quality sequence stop: 600.
Location/Qualifiers
1. 600
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="h221g05"
/lab_host="JM107 or DH5a"
/clone_lib="MGS-ZmayrF (JM107 adapted methyl filtered)"
/note="Organ: immature ears; Site 1: Xba I, Site 2: Xba I,
The vector was digested with XbaI and one nucleotide was
added by fill in in the recessive 3' end. The genomic DNA
was nebulized, end repaired, adaptor ligated and size
fractionated using sephadex. The resulting fragments were
between 0.8 and 3 kb and were cloned into the vector
(x/y reads in M13mp19, b/g reads in pUC19). The same
ligation was transformed in either JM107 or DH5a."

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0185 row: M column: 08
Seq primer: CACACAGAAACAGCTATGAC
Class: plasmid ends
High quality sequence stop: 532.
Location/Qualifiers
1. 532
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCM10185M08"
/sex="Male"
/lab_host="R. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCM library"
/note="Vector: PWD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi14732114|gb|AF129072.1), a copy-number

Unpublished (2002)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org
Plate: h221 row: g column: 05
Seq primer: -21M13univFwd
Class: shotgun
High quality sequence stop: 600.
Location/Qualifiers
1. 600
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="h221g05"
/lab_host="JM107 or DH5a"
/clone_lib="MGS-ZmayrF (JM107 adapted methyl filtered)"
/note="Organ: immature ears; Site 1: Xba I, Site 2: Xba I,
The vector was digested with XbaI and one nucleotide was
added by fill in in the recessive 3' end. The genomic DNA
was nebulized, end repaired, adaptor ligated and size
fractionated using sephadex. The resulting fragments were
between 0.8 and 3 kb and were cloned into the vector
(x/y reads in M13mp19, b/g reads in pUC19). The same
ligation was transformed in either JM107 or DH5a."

FEATURES

source

FEATURES
source

ORIGIN

Query Match 73.6%; Score 20.6; DB 11; Length 600;
Best Local Similarity 85.2%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GAACAGCATACAAACCGTTGTGT 27
|||||
Db 381 GAACACCATTAACAAATCGTGTGT 355

RESULT 8
CC274364/c 1058 bp DNA 1linear GSS 13-MAY-2003
LOCUS CH261-20G8.SP6.1 CH261 Gallus gallus genomic clone CH261-20G8,
DEFINITION genomic survey sequence.
ACCESSION CC274364
VERSION CC274364.1 GI:30631425
KEYWORDS GSS.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Phasiantidae; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 1058)
AUTHORS Krentitzki,C., Higgsinbotham,J., Wylie,K., Carter,J., McPherson,J.,
Warren,W., Graves,T., Mardis,E. and Wilson,R.
Gallus gallus BAC End Reads
JOURNAL Unpublished (2003)
COMMENT Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submis@wustl.edu
Insert Length: 182000 Std Error: 0.00
Seq primer: SP6 ATTAGTGACACTATAG
Class: BAC ends
High quality sequence start: 26
High quality sequence stop: 571.
Location/Qualifiers
1..1058
/organism="Gallus gallus"
/mol_type="genomic DNA"
/strain="Red Jungle Fowl"
/db_xref="taxon:9031"
/clone="CH261-20G8"
/sex="female"
/cell_line="UCD001, inbred 256"
/clone_1fb="CH261"
/note="Vector: PTARBAC2.1; Site_1: SCORI; Site_2: SCORI;
CH261 Female Chicken library - for library and clone
ordering information: <http://www.chori.org/bacpac>"

ORIGIN
Query Match 73.6%; Score 20.6; DB 12; Length 1058;
Best Local Similarity 85.2%; Pred. No. 3.8e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACAGCAATACCAACCGCTGTCTG 27
Db 422 GAACAGCAATACCAACCGCTGTCTAT 396

RESULT 9
AA075030/c 207 bp DNA 1linear GSS 20-AUG-1998
LOCUS CIT-HSP-2364011.TR CIT-HSP Homo sapiens genomic clone 2364011,
DEFINITION genomic survey sequence.
ACCESSION AA075030
VERSION AA075030.1 GI:3435601
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.
REFERENCE 1 (bases 1 to 207)
AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Baas,S., Linher,K., Golden,K.,
Berry,K., Granger,D., Sun,E., Wible,C., Shizuya,H., Simon,M. and
Venter,J.C.
Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building
JOURNAL Unpublished (1998)

TITLE
JOURNAL
COMMENT
Other_GSSs: CIT-HSP-2364011.TF
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.
Location/Qualifiers
1..207
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="2364011"
/sex="Male"
/cell_type="Sperm"
/clone_1fb="CIT-HSP"
/note="Vector: pBelOBAC11; Site_1: HindIII; Site_2:
HindIII"

FEATURES
source

COMMENT Other GSSs: CIT-HSP-2364011.TF
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.
Location/Qualifiers
1..207
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="2364011"
/sex="Male"
/cell_type="Sperm"
/clone_1fb="CIT-HSP"
/note="Vector: pBelOBAC11; Site_1: HindIII; Site_2:
HindIII"

FEATURES
source

ORIGIN
Query Match 71.4%; Score 20; DB 11; Length 207;
Best Local Similarity 82.1%; Pred. No. 6.1e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GAACAGCAATACCAACCGCTGTGTG 28
Db 127 GAACAGCAATACCAACCGCTGTGTG 100

RESULT 10
AA065336 593 bp DNA 1linear GSS 27-OCT-1998
LOCUS CITBI-E1-2506L6.TF CITBI-E1 Homo sapiens genomic clone 2506L6,
DEFINITION genomic survey sequence.
ACCESSION AA065336
VERSION AA065336.1 GI:3793536
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.
REFERENCE 1 (bases 1 to 593)
AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Baas,S., Linher,K., Golden,K.,
Berry,K., Granger,D., Sun,E., Wible,C., Shizuya,H., Simon,M. and
Venter,J.C.
Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building
JOURNAL Unpublished (1998)
COMMENT Other_GSSs: CITBI-E1-2506L6.TF
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.
Location/Qualifiers
1..593
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

REFERENCE 1 (bases 1 to 846)
AUTHORS Humphray,S.J., Plumb,R.W. and Durham,J.L.
TITLE Direct Submission
JOURNAL Submitted (01-NOV-2005) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humphrey@sanger.ac.uk Unpublished

COMMENT This sequence was generated from the T7 end of BAC 181F11. 181F11 is part of the CHOBI-742 BAC library created by P. de Jong. Further details: http://www.sanger.ac.uk/Projects/S_scrofa/. Location/Qualifiers

FEATURES
Source 1..846
/mol_type="Sus scrofa"
/db_xref="taxon:9823"
/clone="CH242-181F11"
/tissue_type="White blood cells"
/notes="vector pTARBAC1.3_BamHI sex female"

ORIGIN
Query Match 71.4%; Score 20; DB 14; Length 846;
Best Local Similarity 82.1%; Pred. No. 6.9e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 1 GAACAGCAATACAAACCGTTGTGTG 28
Db 48 GAACGCAATACAAACCGTTGTGTG 75

RESULT 14
LOCUS BG776822 897 bp mRNA linear EST 15-MAY-2001
DEFINITION 602664002F1 NIH_MGC_59 Homo sapiens CDNA clone IMAGE:4809169 5', mRNA sequence.
ACCESSION BG776822
VERSION BG776822.1 GI:14047139
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 897)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Plate: LNCM1663 row: d column: 02
High quality sequence stop: 459.
Location/Qualifiers

FEATURES
Source 1..897
/mol_type="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4809169"
/tissue_type="mucoepidermoid carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_1lb="NIH MGC 59"
/notes="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggcgccctcgcc); Site_2: SfiI (ggcgccatcgcc); Double-stranded CDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAAGCGCAATTAGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGCCGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average

insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN
Query Match 71.4%; Score 20; DB 2; Length 897;
Best Local Similarity 82.1%; Pred. No. 6.9e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 1 GAACAGCAATACAAACCGTTGTGTG 28
Db 527 GACCAACCAACCAACCGATTGTGTG 554

RESULT 15
LOCUS BE306182/c 1531 bp mRNA linear EST 26-OCT-2000
DEFINITION 601101310F1 NCI_CGAP_Lu29 Mus musculus CDNA clone IMAGE:3493587 5', mRNA sequence.
ACCESSION BE306182
VERSION BE306182.1 GI:9159012
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 1531)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Plate: LLM6541 row: d column: 04
High quality sequence stop: 101.
Location/Qualifiers

FEATURES
Source 1..1531
/mol_type="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:3493587"
/tissue_type="spontaneous tumor, metastatic to mammary. Stem cell origin."
/lab_host="DH10B"
/clone_1lb="NCI CGAP Lu29"
/notes="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

ORIGIN
Query Match 71.4%; Score 20; DB 7; Length 1531;
Best Local Similarity 82.1%; Pred. No. 7.2e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 1 GAACAGCAATACAAACCGTTGTGTG 28
Db 157 GAGCAGCAGCAGCAGCAGCGTTGTGTG 130

RESULT 16
LOCUS BG512658 502 bp mRNA linear EST 28-MAR-2001

DEFINITION dad31b04.x1 wellcome CRC PCS107 tropicalis Sc10-12 Xenopus tropicalis cDNA clone IMAGE:4440919 3' similar to SW:SET_HUMAN 001105 SET PROTEIN ;, mRNA sequence.

ACCESSION BG512658

VERSION BG512658.1 GI:13483315

KEYWORDS EST.

SOURCE Xenopus tropicalis (western clawed frog)

ORGANISM Xenopus tropicalis

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae; Xenopus; Silurana.

AUTHORS 1 (bases 1 to 502)
Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D., Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R., Waterston,R. and Wilson,R.

Washu Xenopus EST project, 1999

Unpublished (1999)

Other ESTs: dad31b04.y1

Contact: Sandy Clifton, Ph.D.
Washu Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

Library constructed by A. Zorn and J. Mason (Wellcome/CRC Institute). DNA sequencing by: Washington University Genome Sequencing Center

Clone distribution: Xenopus clones from this library are available through the I.M.A.G.E. Consortium/BLNI at: infoimage.llnl.gov

Possible reversed clone: similarity on wrong strand

Seq primer: -40UP from Gibco

High quality sequence stop: 486.

Location/Qualifiers

1..502

/organism="Xenopus tropicalis"

/mol_type="mRNA"

/db_xref="taxon:8354"

/clone="IMAGE:4440919"

/issue_type="whole embryo, stages 10-12"

/lab_host="DHI0B (pHage-resistant)"

/clone_lib="Wellcome CRC PCS107 tropicalis Sc10-12"

/notes="Vector: PCS107; Site 1: NotI; Site 2: EcoRI; CDNAs were oligo-dT primed and directionally cloned. Average insert size 1.5 kb. range 0.5-4 kb. Library constructed by A. Zorn and J. Mason (Wellcome/CRC Institute)."

ORIGIN

Query Match 70.7%; Score 19.8; DB 2; Length 502;
Best Local Similarity 91.3%; Pred. No. 8.1e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGCAATACAAACCGCTT 23
||||| ||||||| |||||
250 GAACGAAATACAAACGCGTT 272

Db

RESULT 17

LOCUS BP707553 631 bp mRNA linear EST 19-JUL-2004

DEFINITION BP707553 Osada Taira anterior neuroectoderm (ANE) PCS105 cDNA library Xenopus laevis cDNA clone XL491g22ex 5', mRNA sequence.

ACCESSION BP707553

VERSION BP707553.1 GI:46055952

KEYWORDS EST.

SOURCE Xenopus laevis (African clawed frog)

ORGANISM Xenopus laevis

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae; Xenopus; Xenopus.

AUTHORS 1 (bases 1 to 631)
Osada,S., Kitayama,A., Ueno,N. and Taira,M.

TITLE Expression analysis of genes which are expressed in the anterior neuroectoderm of Xenopus embryos

JOURNAL Unpublished (2004)

COMMENT Contact: Masanori Taira
Department of Biological Sciences
Graduate School of Science, University of Tokyo, Japan
Science and Technology Corporation, Japan
7-3-1 Hongo, Bunkyo-Ku, Tokyo 113-0033, Japan
Tel: 81-03-5841-4434
Fax: 81-03-5841-4434
Email: m_taira@biol.s.u-tokyo.ac.jp,
URL: <http://www.shigen.nig.ac.jp/ndbp/xenopus/est/>.

Location/Qualifiers

1..631

/organism="Xenopus laevis"

/mol_type="mRNA"

/db_xref="taxon:8355"

/clone="XL491g22ex"

/issue_type="anterior neuroectoderm"

/dev_stage="late gastrula (stage 12.5)"

/clone_lib="Osada Taira anterior neuroectoderm (ANE) PCS105 cDNA library"

ORIGIN

Query Match 70.7%; Score 19.8; DB 3; Length 631;
Best Local Similarity 91.3%; Pred. No. 8.2e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ACACGCAATACAAACCGCTG 25
||||| ||||||| |||||
215 ACACGCAATACAAACCGCTG 237

Db

RESULT 18

LOCUS BP700663 637 bp mRNA linear EST 19-JUL-2004

DEFINITION BP700663 Osada Taira anterior neuroectoderm (ANE) PCS105 cDNA library Xenopus laevis cDNA clone XL490g22ex 5', mRNA sequence.

ACCESSION BP700663

VERSION BP700663.1 GI:46049019

KEYWORDS EST.

SOURCE Xenopus laevis (African clawed frog)

ORGANISM Xenopus laevis

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae; Xenopus; Xenopus.

AUTHORS 1 (bases 1 to 637)
Osada,S., Kitayama,A., Ueno,N. and Taira,M.

Expression analysis of genes which are expressed in the anterior neuroectoderm of Xenopus embryos

Unpublished (2004)

Contact: Masanori Taira
Department of Biological Sciences
Graduate School of Science, University of Tokyo, Japan
Science and Technology Corporation, Japan
7-3-1 Hongo, Bunkyo-Ku, Tokyo 113-0033, Japan
Tel: 81-03-5841-4434
Fax: 81-03-5841-4434
Email: m_taira@biol.s.u-tokyo.ac.jp,
URL: <http://www.shigen.nig.ac.jp/ndbp/xenopus/est/>.

Location/Qualifiers

1..637

/organism="Xenopus laevis"

/mol_type="mRNA"

/db_xref="taxon:8355"

/clone="XL490g22ex"

/issue_type="anterior neuroectoderm"

/dev_stage="late gastrula (stage 12.5)"

/clone_lib="Osada Taira anterior neuroectoderm (ANE) PCS105 cDNA library"

Best Local Similarity 91.3%; Pred. No. 8.2e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 ACAGCAATACAAACCGTTGT 25
Db 215 ACAACAAATACAAACCGTTGT 237

RESULT 19

LOCUS

CO382721/c 811 bp mRNA linear EST 30-JUN-2004
DEFINITION Agencourt 26189827 Blumberg Cho dorsal blastopore 11p Xenopus laevis cDNA clone IMAGE:7295911 5', mRNA sequence.

ACCESSION

CO382721
VERSION CO382721.1 GI:49490823

KEYWORDS

SOURCE

ORGANISM

Xenopus laevis (African clawed frog)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Xenopus; Xenopus.

1 (bases 1 to 811)
NIH-MGC http://mgs.nci.nih.gov/.

REFERENCE

Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgsaps-r@mail.nih.gov
Tissue Procurement: Bruce Blumberg

JOURNAL

COMMENT

CDNA Library Preparation: B. Blumberg
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM1538 row: n column: 05
High quality sequence spot: 639.
Location/Qualifiers

FEATURES

SOURCE

1. 811
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8155"
/clone="IMAGE:7295911"
/sex="both"
/tissue_type="dorsal blastopore 11p"
/lab_host="TOP10"
/clone_lib="Blumberg_Cho dorsal blastopore 11p"
/notes="Organ: embryo; Vector: pBluescript SK-; Site_1:
ECORI; Site_2: XhoI; Library: prepared from 50 ug of
total RNA by oligo-dT priming and AMV reverse
transcriptase. After addition of EcoRI linkers and
EcoRI-XhoI digestion, the cDNA was size selected by
chromatography on Sepharose CL-4B columns and fractions
containing cDNAs larger than 500 bp were ligated into
EcoRI-XhoI-digested lambda ZAPIT (Unizap-XR) and packaged
in vitro. Average insert size is 1.4 kb. The original
library contained 6 x 10⁶ recombinants, of which 3 x 10⁶
were amplified and stored at -70 C in 5M buffer containing
7% DMSO. 3 x 10⁶ pfu were mass excised and the resulting
phagemids used to infect TOP10P. References: Science 253,
196-196 and Methods in Molecular Biology 97, 555-574.
Additional sequences from this library have been deposited
under the name Xenopus laevis dorsal blastopore 11p.
Library constructed by Bruce Blumberg (University of
California, Irvine, Department of Developmental and Cell
Biology)."

ORIGIN

Query Match 70.7%; Score 19.8; DB 8; Length 811;
Best Local Similarity 91.3%; Pred. No. 8.4e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 ACAGCAATACAAACCGTTGT 25
Db 146 ACAACAAATACAAACCGTTGT 124

RESULT 20

LOCUS

CN471390 311 bp mRNA linear EST 22-APR-2004
DEFINITION hh AB Brain2000_000005240 A. burtoni Cichlid Brain cDNA library
2000, Russell Fernald Astacotilapia burtoni cDNA clone
hh AB Brain2000_000005240 5', mRNA sequence.

ACCESSION

CN471390
VERSION CN471390.1 GI:46491834

KEYWORDS

SOURCE

ORGANISM

Astacotilapia burtoni
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes;
Labroidae; Cichlidae; African cichlids; Pseudocrenilabrinae;
Haplochromini; Astacotilapia.
1 (bases 1 to 311)
Renn, S.C., Aubin-Horth, N. and Hofmann, H.A.
Biologically meaningful expression profiling across species using
heterologous hybridization to a cDNA microarray
BMC Genomics 5 (1), 42 (2004)
15238158

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

Contact: Hans A. Hofmann
Bauer Center for Genomics Research
Harvard University
7 Divinity Avenue, Cambridge, MA 02138, USA
Tel: 617-384-8058
Fax: 617-495 2196
Email: hane@gr.harvard.edu
PCR Primers
FORWARD: C5VP3: AAGCGGCAATTAACCTCACTA
BACKWARD: C5VP2: TTCCAGTCACGACGTTGTAATA
Plate: 054 row: E column: 05
Seq primer: C5VP3: AAGCGGCAATTAACCTCACTA.
Location/Qualifiers

FEATURES

SOURCE

1. 311
/organism="Astacotilapia burtoni"
/mol_type="mRNA"
/db_xref="taxon:8153"
/clone="hh AB Brain2000_000005240"
/sex="mixed"
/tissue_type="brain"
/dev_stage="mixed"
/lab_host="X11-Blue MRF" E.coli"
/clone_lib="A. burtoni Cichlid Brain cDNA library 2000,
Russell Fernald"
/notes="Vector: DBS11sk-; Site 1: EcoRI; Site 2: XhoI; mRNA
was isolated from the brains of A. burtoni for both sexes
at all stages of development and reproductive status."

ORIGIN

Query Match 70.0%; Score 19.6; DB 8; Length 311;
Best Local Similarity 84.6%; Pred. No. 9.5e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GAACAGCAATACAAACCGTTGTG 26
Db 89 GAACAGCAATACAAACCGTTGTG 114

RESULT 21

LOCUS

CB500937/c 355 bp mRNA linear EST 16-MAY-2003
DEFINITION bsalpbth003037 head Salmo salar cDNA, mRNA sequence.

ACCESSION

CB500937
VERSION CB500937.1 GI:29312163

KEYWORDS

EST.

SOURCE Salmo salar (Atlantic salmon)

ORGANISM Salmo salar

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Salmo. 1 (bases 1 to 355)

AUTHORS Rise, M.L., von Schalburg, K.R., Brown, G.D., Mawer, M.A., Devlin, R.H., Kuipers, N., Busby, M., Beetz-Sargent, M., Alberto, R., Gibbs, A.R., Hunt, P., Shuklin, R., Zelnik, J.A., Nelson, C., Jones, S.R., Smalnu, D.E., Jones, S.J., Schein, J.E., Marra, M.A., Butterfield, Y.S., Stott, J.M., Ng, S.H., Davidson, W.S. and Koop, B.F. Development and application of a salmonid EST database and cDNA microarray: data mining and interspecific hybridization characteristics

TITLE Genome Res. 14 (3), 478-490 (2004)

JOURNAL 14962987

COMMENT Contact: Koop, B.F.
Centre for Biomedical Research
University of Victoria
PO Box 3020 STN CSC, Victoria BC, V8W 3N5, Canada
Tel: 250 472 4067
Fax: 250 472 4075
Email: dkoop@uvic.ca
Centre for Biomedical Research, University of Victoria cDNA preparation and sequencing: Roberto Alberto, Marianne Beetz-Sargent, Maura Busby, Peter Hunt, Linda McKinnel, B.F. Koop.
bioinformatics: Gordon D Brown.

FEATURES Location/Qualifiers

source 1..355

/organism="Salmo salar"

/mol_type="mRNA"

/strain="McConnell"

/db_xref="taxon:8030"

/clone_lib="head"

/note="Vector: pBluescriptISK+, Library Creator: Kristian R von Schalburg ; Atlantic salmon tissue contributors: Carlo Biagi, Mitch Un and Robert Devlin (DFO, Vancouver, B.C.), Simon Jones (PBS, Nanaimo, B.C.), Seaspriing Hatchery (Crofton, B.C.), Rachel Roper (University of Victoria)"

ORIGIN

Query Match 70.0%; Score 19.6; DB 4; Length 355;
Best Local Similarity 84.6%; Pred. No. 9.6e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 ACAGCAATACACAAACCGTTGTG 28
|||||
283 ACATCATACACAAACCGTTATGTG 258
|||||

RESULT 22 DV085458 487 bp mRNA linear EST 01-DEC-2005

LOCUS 327-384-16 L07 T7 Nematostella vectensis normalized cDNA library

DEFINITION 327 Nematostella vectensis cDNA clone 327-384-16_L07_T7, mRNA sequence.

ACCESSION DV085458

VERSION DV085458.1 GI:82866851

KEYWORDS EST.

SOURCE Nematostella vectensis

ORGANISM Eukaryota; Metazoa; Chordata; Anthozoa; Hexacoralia; Actiniaria; Edwardsiidae; Nematostella.

REFERENCE 1 (bases 1 to 487)

AUTHORS Technau, U., Rudd, S., Maxwell, P., Gordon, P.M.K., Saina, M., Grasso, L.C., Hayward, D.C., Senses, C.W., Saint, R., Holstein, T.W., Ball, E.B. and Miller, D.J.

TITLE Maintenance of ancestral complexity and non-metazoan genes in two basal cnidarians

JOURNAL Trends Genet. (2005) In press

COMMENT Contact: Ulrich Technau
Sars Centre for Marine Molecular Biology

FEATURES Location/Qualifiers

source 1..487

/organism="Nematostella vectensis"

/mol_type="mRNA"

/db_xref="taxon:45351"

/clone="327-384-16_L07_T7"

/sex="thermaphrodite"

/issue_type="whole embryos"

/dev_stage="mixed stages from unfertilized eggs to primary polyps"

/clone_lib="Nematostella vectensis normalized cDNA library 327"

/note="Vector: pBluescript II SK(+); Site 1: NotI; Site 2: EcoRI; Normalized oligo dT primed cDNA library using poly A+ RNA from mixed embryonic stages of Nematostella vectensis. Cloned directionally into pBluescript II SK(+). Ligated in NotI, EcoRI"

ORIGIN

Query Match 70.0%; Score 19.6; DB 10; Length 487;
Best Local Similarity 84.6%; Pred. No. 9.9e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACAGCAATACACAAACCGTTGTG 26
|||||
220 GAACAGCAATACACAAACCGAAGTG 195
|||||

RESULT 23 BE111725 496 bp mRNA linear EST 13-JUN-2000

LOCUS BE111725

DEFINITION UI-R-BJ1-avx-a-12-0-UI.s1 UI-R-BJ1 Rattus norvegicus cDNA clone

ACCESSION BE111725

VERSION BE111725.1 GI:8503830

KEYWORDS EST.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Rattus.

TITLE 1 (bases 1 to 496)

AUTHORS Bonaldo, M.P., Lemmon, G. and Soares, M.B.

JOURNAL Normalization and subtraction: two approaches to facilitate gene discovery

COMMENT Genome Res. 6 (9), 791-806 (1996)

CONTACT Soares, MB

COORDINATED Laboratory for Computational Genomics

UNIVERSITY of Iowa

375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA

TEL: 319 335 8250

FAX: 319 335 9565

EMAIL: Bento-soares@iowa.edu

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized ventricle at 16.5 dpc library cDNA library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.reagen.com)

SEQ PRIMER: M13 Forward

POLYA=Yes.

FEATURES Location/Qualifiers

source 1..496

/organism="Rattus norvegicus"

/mol_type="mRNA"

/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UT-R-BJ1-ava-a-12-0-UT"
/lab_host="DH10B (Life Technologies)"
/clone_lib="UT-R-BJ1"
/note="Vector: pTR73D-Pac1; Site 1: Not I; Site 2: Eco RI;
The UT-R-BJ1 library is a subtracted library derived from
the following tissues: atrium at 16.5 dpc, ventricle at
16.5 dpc, AV canal at 16.5 dpc, atrium at 15 dpc,
ventricle at 15 dpc, AV canal at 15 dpc, ventricle at 13
dpc, and adult heart. For a detailed description of the
library from which this clone was derived, please visit
our web site at ratest.eng.ualowa.edu. The subtraction has
been previously described in (Bonaldo, Lennon and Soares,
Genome Research 6:791-806, 1996)
TAG TISSUE=ventricle at 16.5 dpc
TAG LIB=UT-R-BJ1
TAG_SEQ=GTTCC"

ORIGIN

Query Match 70.0%; Score 19.6; DB 7; Length 496;
Best Local Similarity 84.6%; Pred. No. 9.9e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AACAGCAATACAAACCGTTGTGT 27
Db 58 AACGCAATACAAACCAATTAGT 83

RESULT 24
LOCUS A0325004 579 bp DNA linear GSS 08-JAN-1995
DEFINITION mgxb0020B07r CUGI Rice Blast BAC Library Magnaporthe grisea genomic
clone mgxb0020B07r, genomic survey sequence.
ACCESSION A0325004
VERSION A0325004.1 GI:4116856
KEYWORDS GSS.
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM Magnaporthe grisea

REFERENCE Bukaryota; Fung1; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
1 (bases 1 to 579)
AUTHORS Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
Genome

TITLE Unpublished (1998)
JOURNAL Contact: Dean RA
COMMENT Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdeane@clemson.edu
Seq primer: GGAACACGCTATGACCATG
Classes: BAC ends
High quality sequence stop: 343.
Location/Qualifiers

FEATURES
source
1..579
/organism="Magnaporthe grisea"
/mol_type="genomic DNA"
/strain="70-15"
/db_xref="taxon:148305"
/clone="mgxb0020B07r"
/issue_type="Protolaests"
/lab_host="E. coli DH10B"
/clone_lib="CUGI Rice Blast BAC library"
/note="Vector: pBACWCH; Site 1: HindIII; Site 2: HindIII;
Rice Blast is one of the most devastating fungal diseases
of rice world wide. It is a filamentous ascomycete with
a haploid genome (n=7) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
numerous aspects of the fungal-host interaction. In

order to facilitate genome wide analysis, a BAC library
containing 9216 clones with an average insert size of 130
kbp was constructed. This library represents greater
than 25X genome coverage. High density colony filters
are available upon request."

ORIGIN

Query Match 70.0%; Score 19.6; DB 11; Length 579;
Best Local Similarity 84.6%; Pred. No. 1e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AACAGCAATACAAACCGTTGTGT 27
Db 466 AACAGCAATACAAATCAGTTCTGT 441

RESULT 25
LOCUS CV232583 658 bp mRNA linear EST 21-SEP-2004
DEFINITION WS0198.B21.A22 PT-DX-N-A-10 Populus trichocarpa cDNA clone
WS0198.A22.3', mRNA sequence.
ACCESSION CV232583
VERSION CV232583.1 GI:52388271
KEYWORDS EST.
SOURCE Populus trichocarpa (Populus balsamifera subsp. trichocarpa)
ORGANISM Populus trichocarpa

REFERENCE Populus trichocarpa; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Malpighiales; Salicaceae; Salicaceae; Populus.
1 (bases 1 to 658)
AUTHORS Ralph, S., Cooper, D., Kolosova, N., Oddy, C., Butterfield, Y.,
Kirpatrick, R., Liu, J., Palmquist, D., Scott, J., Barber, S., Yang, G.,
Babakoff, R., Brown-John, M., Chand, S., Featherstone, R., Mason, A.,
Mayo, M., Moran, J., Olson, T., Wong, D., Rittland, C.E., Siddiqui, A.,
Holt, R., Jones, S., Marra, M., Ellis, B.E., Douglas, C., Rittland, K. and
Bohlmann, J.

TITLE The poplar transcriptome: Analysis of expressed sequence tags from
multiple cDNA libraries
JOURNAL Unpublished (2004)
COMMENT Contact: Joerg Bohlmann
Genome BC forest genomics program
University of British Columbia
Michael Smith Laboratories, 6174 University Boulevard, Rm. 237,
Vancouver, British Columbia, Canada, V6T 1Z3
Tel: 1-604-822-0282
Fax: 1-604-822-2114
Email: bohlmann@msl.ubc.ca
Plate: WS0198 row: A column: 22
High quality sequence stop: 658.
Location/Qualifiers

FEATURES
source
1..658
/organism="Populus trichocarpa"
/mol_type="mRNA"
/cultiware="VF-125"
/db_xref="taxon:3694"
/clone="WS0198.A22"
/sex="Not determined"
/lab_host="E. coli DH10B T1 phage resistant cells"
/clone_lib="PT-DX-N-A-10"
/note="Vector: pBluescript II SK (+) XR; Site 1: EcoRI (5'
end of cDNA); Site 2: XhoI (3' end of cDNA); Outer xylem
from 5 year old trees harvested every two weeks between
April and October of 2002 at the University of British
Columbia south campus farm in Vancouver, British Columbia.
mRNA was isolated from each tissue source independently
and equal quantities of mRNA from each tissue were then
pooled. cDNA was prepared from 5 micrograms of mRNA and
directionally ligated into the pBluescript II SK (+) XR
vector using the pBluescript II XR cDNA library
Construction Kit according to manufacturer's instructions
with modifications (Stratagene). Plasmid DNA was then
transformed by electroporation into DH10B cells
(Invitrogen) for propagation. Normalization was applied

ORIGIN according to published methods [Bonaldo M.F. et al. (1996) Genome Research 6(9):791] in order to reduce the abundance of highly expressed transcripts."

Query Match 70.0%; Score 19.6; DB 8; Length 656;
Best Local Similarity 84.6%; Pred. No. 1e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AACAGCAATACAAACCGTGTGT 27
DB 123 AACACCAAAACAAACCCCTGTGT 98

RESULT 26
LOCUS CL544775 677 bp DNA linear GSS 14-JUN-2004
DEFINITION OB_BA0073112.f OB_Ba Oryza brachyantha genomic clone
OB_BA0073112 5', genomic survey sequence.
CL544775
CL544775.1 GI:47615377
GSS.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza brachyantha
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 677)
Klm.H., Yu.Y., Stum.D., Yost.D., Rao.K., Luo.M., Jetty.R.,
Kudrna.D., Muller.C., Hatfield.J., Soderlund.C. and Wing.R.
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: rwing@genome.arizona.edu

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Insert Length: 145000 Std Error: 0.00
Plate: 0073 row: 1 column: 12
Seq primer: TAA TAC GAC TCA CTA TAG GG
Class: BAC ends.

FEATURES
source location/Qualifiers

1..677
/organism="Oryza brachyantha"
/mol_type="genomic DNA"
/db_xref="taxon:4533"
/clone="OB_BA0073112"
/cissue_type="leaves"
/dev_stage="mature"
/lab_host="DH10B"
/clone_lib="OB_Ba"
/note="Vector: PACIBAC1, Site_1: HindIII, Site_2: HindIII"

ORIGIN

Query Match 70.0%; Score 19.6; DB 13; Length 677;
Best Local Similarity 84.6%; Pred. No. 1e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AACAGCAATACAAACCGTGTGT 27
DB 52 AACACCAATTTACAAAGGTACTGT 77

RESULT 27
LOCUS CF234787/c 682 bp mRNA linear EST 05-AUG-2003
DEFINITION PcaUT0015B4B04.04 Poplar cDNA library from young tension xylem
Populus alba x Populus tremula cDNA 5', mRNA sequence.

ACCESSION CF234787 GI:33454216
VERSION
KEYWORDS
SOURCE
ORGANISM

Populus alba x Populus tremula
Populus alba x Populus tremula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eucosids I; Malpighiales; Salicaceae; Salicaceae; Populus.
1 (bases 1 to 682)
Dejardin,A., Leple,J.-C., Lesage-Descauses,M.-C., Costa,G. and
Pilate,G.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Expressed sequence tags from poplar wood tissues - A comparative
analysis from multiple libraries
Plant Biol. 6 (1), 55-64 (2004)
15095135
Contact: Leple JC
Unit of Forest Improvement, Genetics and Physiology
National Institute for Agricultural Research (INRA)
Domaine de l'Imere, BP20619 ARDON, 45166 OLIVET CEDEX, FRANCE
Tel: 33 02 38 41 78 00
Tel: 33 02 38 41 78 00
Fax: 33 02 38 41 78 79
Email: Jean-Charles.Lepie@ Orleans.inra.fr
PCR Primers
FORWARD: Triplexa 5' CTCGGAAAGCGCCATTGTG 3'
BACKWARD: Triplexa 5' ATACGACTCTACTATAGCGCA 3'
Plate: PcaUT0015 row: B column: 4
Seq primer: Triplexa 5' CTCGGAAAGCGCCATTGTG 3'.
Location/Qualifiers

FEATURES
source

1..682
/organism="Populus alba x Populus tremula"
/mol_type="mRNA"
/strain="clone 717-1-B4"
/db_xref="taxon:80863"
/sex="female"
/cissue_type="Young differentiating xylem harvested on the
tension wood side of tilted trees"
/dev_stage="3-years-old poplar trees grown in the nursery"
/clone_lib="Poplar cDNA library from young tension xylem"
/note="A cDNA library was made with mRNA isolated from
tension wood tissues corresponding to the differentiating
xylem collected with a scalpel after debarking the stem.
The sampling was done on 3 different tilted trees grown in
the nursery. cDNAs were cloned in an oriented way into
SfiI (A and B) restriction sites. A one-step conversion of
Lambda Triplex2 to the corresponding triplex2 plasmid was
done via site-specific recombination at loxp sites
(Clontech; SMART cDNA library construction kit). cDNA
inserts were PCR amplified using flanking primers and then
sequenced on a ABI3100 Genetic Analyzer (Applied
Biosystem)"

ORIGIN

Query Match 70.0%; Score 19.6; DB 5; Length 682;
Best Local Similarity 84.6%; Pred. No. 1e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AACAGCAATACAAACCGTGTGT 27
DB 89 AACACCAAAACAAACCCCTTGTGT 64

RESULT 28
LOCUS CZ749731 689 bp DNA linear GSS 26-JUL-2005
DEFINITION OC_BA0099B06.r OC_Ba Oryza coarctata genomic clone OC_BA0099B06
3', genomic survey sequence.
CZ749731
CZ749731.1 GI:71185246
GSS.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza coarctata (Porteresia coarctata)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep

```
REFERENCE
AUTHORS      1 (bases 1 to 689)
              clade: Ehrhartoideae; Oryzeae; Oryza.
              Kim,H., Collura,K., Wasotski,M., Byrne,M., Stum,D., Smart,D.,
              Rao,K., Luo,M., Jettly,R., Kudrna,D., Miller,C., Soderlund,C. and
              Wang,R.
              OMAF (Oryza Map Alignment Project) - Arizona Genomics Institute
              Unpublished (2005)
JOURNAL
COMMENT       Contact: Rod A. Wang
              Arizona Genomics Institute
              University of Arizona
              Forbes Building Room 303, Tucson, AZ 85721-0036, USA
              Tel: 520 626 9595
              Fax: 520 621 1259
              Email: rtwing@genome.arizona.edu
              PCR Primers
              FORWARD: TAA TAC GAC TCA CTA TAG GG
              BACKWARD: CAC TCA TTA GGC ACC CCA
              Plate: 0099 row: B column: 06
              Seq primer: CAC TCA TTA GGC ACC CCA
              Class: BAC ends.

FEATURES
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    /mol_type="genomic DNA"
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    /clone="OC_Ba0099B06"
    /cissue_type="leaves"
    /dev_stage="mature"
    /lab_host="DH10B"
    /clone_1lb="OC_Ba"
    /note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN
Query Match      70.0%; Score 19.6; DB 13; Length 689;
Best Local Similarity 84.6%; Pred. No. 1e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY
  2 AACAGCAATACAAACCGTTGTGT 27
  61 AACAGCAATACAAACCGTTGTGT 86

RESULT 29
LOCUS      BM085832      691 bp      mRNA      linear      EST 27-MAY-2005
DEFINITION BM085832 Nori Satoh unpublished cDNA library, larva Clona
ACCESSION   BM085832
VERSION     BM085832.1 GI:24261112
KEYWORDS    EST.
SOURCE      Clona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Plebobranchia; Clonidae; Clona.
REFERENCE   1 (bases 1 to 691)
AUTHORS     Satou,Y., Shin-I,T., Kohara,Y. and Satoh,N.
TITLE       Expressed genes in Clona intestinalis (2002c)
JOURNAL     Unpublished (2002)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
            Location/Qualifiers
              1..691
              /organism="Clona intestinalis"
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              /clone="rcilv043e07"
              /cissue_type="whole animal"
              /dev_stage="larva"

FEATURES
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    1..689
    /organism="Oryza coarctata"
    /mol_type="genomic DNA"
    /db_xref="taxon:77588"
    /clone="OC_Ba0099B06"
    /cissue_type="leaves"
    /dev_stage="mature"
    /lab_host="DH10B"
    /clone_1lb="OC_Ba"
    /note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN
Query Match      70.0%; Score 19.6; DB 13; Length 689;
Best Local Similarity 84.6%; Pred. No. 1e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY
  2 AACAGCAATACAAACCGTTGTGT 27
  61 AACAGCAATACAAACCGTTGTGT 86

RESULT 29
LOCUS      BM085832      691 bp      mRNA      linear      EST 27-MAY-2005
DEFINITION BM085832 Nori Satoh unpublished cDNA library, larva Clona
ACCESSION   BM085832
VERSION     BM085832.1 GI:24261112
KEYWORDS    EST.
SOURCE      Clona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Plebobranchia; Clonidae; Clona.
REFERENCE   1 (bases 1 to 691)
AUTHORS     Satou,Y., Shin-I,T., Kohara,Y. and Satoh,N.
TITLE       Expressed genes in Clona intestinalis (2002c)
JOURNAL     Unpublished (2002)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
            Location/Qualifiers
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              /organism="Clona intestinalis"
              /mol_type="mRNA"
              /db_xref="taxon:7719"
              /clone="rcilv058d20"
              /cissue_type="whole animal"
              /dev_stage="larva"
              /clone_1lb="Nori Satoh unpublished cDNA library, larva"

FEATURES
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    1..735
    /organism="Clona intestinalis"
    /mol_type="mRNA"
    /db_xref="taxon:7719"
    /clone="rcilv058d20"
    /cissue_type="whole animal"
    /dev_stage="larva"
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ORIGIN
Query Match      70.0%; Score 19.6; DB 3; Length 735;
Best Local Similarity 84.6%; Pred. No. 1e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY
  2 AACAGCAATACAAACCGTTGTGT 27
  87 AACAGCAATACAAACCGTTGTGT 112

RESULT 31
LOCUS      DM577165      737 bp      mRNA      linear      EST 17-JAN-2006
DEFINITION DM577165 EST ssal rpb2_41584 rpb2 Salmo salar cDNA clone
ACCESSION   DM577165
VERSION     DM577165.1 GI:85048987
KEYWORDS    EST.
SOURCE      Salmo salar (Atlantic salmon)
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei;
            Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
REFERENCE   1 (bases 1 to 737)
AUTHORS     Koop,B.P., Davidson,W.S. and cGRASP Consortium.
TITLE       Expressed Sequence Tags from Atlantic Salmon Unpublished (2006)
JOURNAL     Unpublished (2006)
COMMENT     Contact: Koop BP

FEATURES
  source
    1..735
    /organism="Clona intestinalis"
    /mol_type="mRNA"
    /db_xref="taxon:7719"
    /clone="rcilv058d20"
    /cissue_type="whole animal"
    /dev_stage="larva"
    /clone_1lb="Nori Satoh unpublished cDNA library, larva"

ORIGIN
Query Match      70.0%; Score 19.6; DB 3; Length 735;
Best Local Similarity 84.6%; Pred. No. 1e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY
  2 AACAGCAATACAAACCGTTGTGT 27
  87 AACAGCAATACAAACCGTTGTGT 112

RESULT 31
LOCUS      DM577165      737 bp      mRNA      linear      EST 17-JAN-2006
DEFINITION DM577165 EST ssal rpb2_41584 rpb2 Salmo salar cDNA clone
ACCESSION   DM577165
VERSION     DM577165.1 GI:85048987
KEYWORDS    EST.
SOURCE      Salmo salar (Atlantic salmon)
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei;
            Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
REFERENCE   1 (bases 1 to 737)
AUTHORS     Koop,B.P., Davidson,W.S. and cGRASP Consortium.
TITLE       Expressed Sequence Tags from Atlantic Salmon Unpublished (2006)
JOURNAL     Unpublished (2006)
COMMENT     Contact: Koop BP
```

Centre for Biomedical Research
University of Victoria
PO Box 3020 STN CSC, Victoria BC, V8W 3N5, Canada
Tel: 250 472 4067
Fax: 250 472 4075
Email: bkoop@vic.ca

Sequenced by: Genome Sciences Centre, BC Cancer Agency Rob Holt, M. Marra. Bioinformatics: Centre for Biomedical Research, University of Victoria Jong Leong, BF Koop.
Insert Length: 737 Std Error: 0.00
Plate: 567
Seq primer: M13 Forward
High quality sequence stop: 737.
Location/Qualifiers
1. 737
/organism="Salmo salar"
/mol_type="mRNA"
/strain="McConnell"
/db_xref="taxon:8030"
/clone="asal_rgd2_567_161.fwd"
/issue_type="mixed tissue"
/clone_lib="rgd2"
/note="Organ: brain, kidney, spleen; Vector: pCMVSPORT6; asalrgb2 mixed tissue Salmo salar cDNA, mRNA sequence."
Contributors: Robert Devlin (DFO, Vancouver, B.C.)"

ORIGIN
Query Match 70.0%; Score 19.6; DB 10; Length 737;
Best Local Similarity 84.6%; Pred. No. 1e+03; Mismatches 22; Conservative 0; Indels 0; Gaps 0;

QY 3 ACAGCAATACACAAACCGTTGTG 28
|||||
692 ACATCAATACACACCCCTTATGTG 717
|||||

RESULT 32
CA064299 753 bp mRNA linear EST 04-MAR-2003
LOCUS asalrgb530194 mixed_tissue Salmo salar cDNA, mRNA sequence.
DEFINITION CA064299
ACCESSION CA064299.1 GI:24394542
VERSION
KEYWORDS
SOURCE EST.
ORGANISM Salmo salar (Atlantic salmon)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
1 (bases 1 to 753)
Rise,M.L., von Schallburg,K.R., Brown,G.D., Mawer,M.A., Devlin,R.H., Kuipers,N., Busby,M., Beetz-Sargent,M., Alberto,R., Gibbs,A.R., Hunt,P., Shukin,R., Zelnik,J.A., Nelson,C., Jones,S.R., Smalhus,D.E., Jones,S.J., Schein,J.E., Marra,M.A., Butterfield,Y.S., Stott,J.M., Ng,S.H., Davidson,W.S. and Koop,B.F. Development and application of a salmonid EST database and cDNA microarray: data mining and interspecific hybridization characteristics
Genome Res. 14 (3), 478-490 (2004)
14962987
Contact: Koop BF
Centre for Biomedical Research
University of Victoria
PO Box 3020 STN CSC, Victoria BC, V8W 3N5, Canada
Tel: 250 472 4067
Fax: 250 472 4075
Email: bkoop@vic.ca
Genome Sciences Centre, BC Cancer Agency
cDNA preparation, sequencing and bioinformatics:
Y Butterfield, R Kirkpatrick, J Asano, N Gilm, R Guin, D Lee, S Lee, T Olson, P Pandoh, A Prabhu, D Smalhus, L Spence, J Stott, S Taylor, G Yang, J Schein, S Jones and M Marra.
POLYA=Yes.
Location/Qualifiers

FEATURES
JOURNAL PUBMED
COMMENT

source 1. 753
/organism="Salmo salar"
/mol_type="mRNA"
/strain="McConnell"
/db_xref="taxon:8030"
/clone_lib="mixed tissue"
/note="Vector: pCMVSPORT6; Library Creator: Research Genetics; Atlantic salmon tissue contributors: Carlo Biagi, Mitch Un and Robert Devlin (DFO, Vancouver, B.C.), Simon Jones (PBS, Nanaimo, B.C.), Seaspriing Hatchery (Crofton, B.C.), Rachel Roper (University of Victoria)"

ORIGIN
Query Match 70.0%; Score 19.6; DB 4; Length 753;
Best Local Similarity 84.6%; Pred. No. 1e+03; Mismatches 22; Conservative 0; Indels 0; Gaps 0;

QY 3 ACAGCAATACACAAACCGTTGTG 28
|||||
670 ACATCAATACACACCCCTTATGTG 695
|||||

RESULT 33
CA056575 764 bp mRNA linear EST 04-MAR-2003
LOCUS asalrgb536212 mixed_tissue Salmo salar cDNA, mRNA sequence.
DEFINITION CA056575
ACCESSION CA056575.1 GI:24386818
VERSION
KEYWORDS
SOURCE EST.
ORGANISM Salmo salar (Atlantic salmon)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
1 (bases 1 to 764)
Rise,M.L., von Schallburg,K.R., Brown,G.D., Mawer,M.A., Devlin,R.H., Kuipers,N., Busby,M., Beetz-Sargent,M., Alberto,R., Gibbs,A.R., Hunt,P., Shukin,R., Zelnik,J.A., Nelson,C., Jones,S.R., Smalhus,D.E., Jones,S.J., Schein,J.E., Marra,M.A., Butterfield,Y.S., Stott,J.M., Ng,S.H., Davidson,W.S. and Koop,B.F. Development and application of a salmonid EST database and cDNA microarray: data mining and interspecific hybridization characteristics
Genome Res. 14 (3), 478-490 (2004)
14962987
Contact: Koop BF
Centre for Biomedical Research
University of Victoria
PO Box 3020 STN CSC, Victoria BC, V8W 3N5, Canada
Tel: 250 472 4067
Fax: 250 472 4075
Email: bkoop@vic.ca
Genome Sciences Centre, BC Cancer Agency
cDNA preparation, sequencing and bioinformatics:
Y Butterfield, R Kirkpatrick, J Asano, N Gilm, R Guin, D Lee, S Lee, T Olson, P Pandoh, A Prabhu, D Smalhus, L Spence, J Stott, S Taylor, G Yang, J Schein, S Jones and M Marra.
Location/Qualifiers
1. 764
/organism="Salmo salar"
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/strain="McConnell"
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/clone_lib="mixed tissue"
/note="Vector: pCMVSPORT6; Library Creator: Research Genetics; Atlantic salmon tissue contributors: Carlo Biagi, Mitch Un and Robert Devlin (DFO, Vancouver, B.C.), Simon Jones (PBS, Nanaimo, B.C.), Seaspriing Hatchery (Crofton, B.C.), Rachel Roper (University of Victoria)"

ORIGIN
Query Match 70.0%; Score 19.6; DB 4; Length 764;
Best Local Similarity 84.6%; Pred. No. 1e+03;

Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 ACAGCATACACAAACCGTTGTG 28
 |||||
 DB 686 ACATCATACACACCCCTTATGTG 711
 |||||

RESULT 34
 CB643162/c
 LOCUS
 DEFINITION OSJNB03108. r OSJNB Oryza sativa (japonica cultivar-group) cDNA
 ACCESSION CB643162
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 PUBMED
 COMMENT

1 (bases 1 to 782)
 Jantsuriyarat C., Gowda, M., Haller, K., Hatfield, J., Lu, G.,
 Stahlberg, E., Zhou, B., Li, H., Kim, H., Yu, Y., Dean, R. A., Wing, R. A.,
 Soderlund, C. and Wang, G. L.
 Large-scale identification of expressed sequence tags involved in
 rice and rice blast fungus interaction
 Plant Physiol. 138 (1), 105-115 (2005)
 15886863
 Contact: Rod Wing
 Arizona Genomics Institute
 University of Arizona
 Biological Sciences West, 440A, P.O. Box 210088, Tucson, AZ
 85721-0088, USA
 Tel: 520 626 3967
 Fax: 520 621 9288
 Email: twing@genome.arizona.edu
 PCR Primers
 FORWARD: gta aac cga cgg cca gtc
 BACKWARD: gga aac agc tac gac cat g
 Plate: 03 row: L column: 08
 Seq primer: gga aac agc tac gac cat g.
 Location/Qualifiers
 1. 782
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nipponbare"
 /db_xref="taxon:39947"
 /clone="OSJNB03108"
 /issue_type="Leaf"
 /dev_stage="3 week"
 /lab_host="DH10B"
 /clone_lib="OSJNB"
 /note="Vector: Bluescript II KS +; Site 1: EcoRI; Site 2:
 XhoI; 24 hrs after inoculation with Rice Blast (Che
 86061)"

ORIGIN

Query Match 70.0%; Score 19.6; DB 4; Length 782;
 Best Local Similarity 84.6%; Pred. No. 1e+03;
 Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AACGCAATACACAAACCGTTGTG 27
 |||||
 DB 29 AAAGCAATGACAAACCACTGTGT 4
 |||||

RESULT 35
 BU255194
 LOCUS
 DEFINITION BU255194. 792 bp mRNA linear EST 26-NOV-2002
 60374612cF1 CSBQCHN38 Gallus gallus cDNA clone CHEST651c8 5', mRNA
 sequence.
 ACCESSION BU255194
 VERSION BU255194.1 GI:25511921

KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.

REFERENCE
 AUTHORS Boardman, P. E., Sanz-Ezquerro, J., Overton, I. M., Burt, D. W., Bosch, E.,
 Pong, W. T., Tickle, C., Brown, W. R. A., Wilson, S. A. and Hubbard, S. J.
 A Comprehensive Collection of Chicken CDNA
 Curr. Biol. 12 (22), 1965-1969 (2002)
 12445392

TITLE
 JOURNAL
 PUBMED
 COMMENT

Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology
 (UMIST)
 PO Box 88, Manchester, M60 10D, UK
 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.

FEATURES
 source
 1. 792
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="White Leghorn, Hixex"
 /db_xref="taxon:9031"
 /clone="CHEST651c8"
 /dev_stage="36"
 /lab_host="DH10B"
 /clone_lib="CSBQCHN38"
 /note="Organ: limbs; Vector: pbluescript II KS(+); Site 1:
 EcoRI; Site 2: NotI. This normalized library was
 constructed from 1 million independent clones. cDNA
 synthesis was initiated using an oligo(dT) primer, using
 methylated C in the first strand synthesis reaction.
 Following this first strand reaction, double-stranded cDNA
 was blunt-ended, ligated to NotI adapters, digested with
 EcoRI, size-selected, and cloned into the NotI and EcoRI
 compatible sites of a custom modified MCS of the
 pbluescript (KS+) vector. The library was normalized in 2
 rounds using conditions adapted from Soares et al., PNAS
 (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
 (1996): 791, except that a significantly longer
 reannealing hybridization was used."

ORIGIN

Query Match 70.0%; Score 19.6; DB 3; Length 792;
 Best Local Similarity 84.6%; Pred. No. 1e+03;
 Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 ACAGCATACACAAACCGTTGTG 28
 |||||
 DB 652 ACAGCATACAAACCAACCGTTGTG 627
 |||||

RESULT 36
 BU087205
 LOCUS
 DEFINITION BU087205. 793 bp mRNA linear EST 27-MAY-2005
 BU087205 Nori Satoh unpublished cDNA library, larva Clona
 intestinalis cDNA clone rcily048h03 3', mRNA sequence.
 ACCESSION BU087205
 VERSION BU087205.1 GI:24262485
 KEYWORDS
 SOURCE
 ORGANISM

Clona intestinalis
 Clona intestinalis
 Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
 Phlebobranchia; Cloniidae; Clona.

REFERENCE
 AUTHORS Satou, Y., Shin-I, T., Kohara, Y. and Satoh, N.
 TITILE Expressed genes in Clona intestinalis (2002c)
 JOURNAL Unpublished (2002)
 COMMENT Contact: Nori Satoh
 Department of Zoology

Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@acidian.zool.kyoto-u.ac.jp.

FEATURES

source

Location/Qualifiers
1. .793
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="rc11048h03"
/tissue_type="whole animal"
/dev_stage="larva"
/clone_lib="Norl Satoh unpublished cDNA library, larva"

ORIGIN

Query Match 70.0%; Score 19.6; DB 3; Length 793;
Best Local Similarity 84.6%; Pred. No. 1e+03; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 4;

Qy 2 AACAGCATACAAACCGTTGTG 27
Db 99 AACGCAATACAAACCGTTGTTT 124

RESULT 37
DM577166 822 bp mRNA linear EST 17-JAN-2006
LOCUS
DEFINITION
EST_ssal_rpb2_41585_rpb2_Salmo salar clone
DM577166
VERSION
KEYWORDS
SOURCE
ORGANISM
Salmo salar (Atlantic salmon)
EST.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
1 (bases 1 to 822)
Koep.B.F. Davidson, M.S. and cGRASP Consortium.
Expressed Sequence Tags from Atlantic Salmon Unpublished (2006)
Unpublished (2006)
Contact: Koep BF
Centre for Biomedical Research
University of Victoria
PO Box 3020 STN CSC, Victoria BC, V8W 3N5, Canada
Tel: 250 472 4067
Fax: 250 472 4075
Email: bkoop@vic.ca

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Koep.B.F. Davidson, M.S. and cGRASP Consortium.
Expressed Sequence Tags from Atlantic Salmon Unpublished (2006)
Unpublished (2006)
Contact: Koep BF
Centre for Biomedical Research
University of Victoria
PO Box 3020 STN CSC, Victoria BC, V8W 3N5, Canada
Tel: 250 472 4067
Fax: 250 472 4075
Email: bkoop@vic.ca

Sequenced by: Genome Sciences Centre, BC Cancer Agency Rob Holt, M.
Marra. Bioinformatics; Centre for Biomedical Research, University
of Victoria Jong Leong, BF Koep.
Insert Length: 822 Std Error: 0.00
Plate: 567

Seg primer: M13 Reverse
High quality sequence stop: 822.

FEATURES

source

Location/Qualifiers
1. 822
/organism="Salmo salar"
/mol_type="mRNA"
/strain="McConnell"
/db_xref="taxon:8030"
/clone="asal_rpb2_567_161_rev"
/tissue_type="mixed tissue"
/clone_lib="rpb2"
/note="Organ: brain, kidney, spleen; Vector: pCMVSPORT6;
asalrpb2 mixed tissue Salmo salar cDNA; Tissue
contributors: Robert Devlin (DFO, Vancouver, B.C.)"

ORIGIN

Query Match 70.0%; Score 19.6; DB 10; Length 822;
Best Local Similarity 84.6%; Pred. No. 1e+03; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 4;

Qy 3 ACAGCATACAAACCGTTGTG 28
Db 712 ACATCAATACAAACCGCTTATGTG 687

RESULT 38
CG219751 832 bp DNA linear GSS 22-AUG-2003
LOCUS
DEFINITION
CG219751 832 bp DNA linear GSS 22-AUG-2003
genomic survey sequence.
CG219751
VERSION
KEYWORDS
SOURCE
ORGANISM
Zea mays
Zea mays
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 832)
Resnick A., Fraser, C.M., Budiman M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: OGM1Q26TV
Contact: Cathy Whitelaw
TTR

REFERENCE

AUTHORS

9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seg primer: TR
Class: methylation filtered.
Location/Qualifiers
1. 832
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMBM0612P03"
/clone_lib="ZM_0.7-1.5_KB"
/note="Vector: pBCK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

FEATURES

source

Location/Qualifiers
1. 832
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMBM0612P03"
/clone_lib="ZM_0.7-1.5_KB"
/note="Vector: pBCK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN

Query Match 70.0%; Score 19.6; DB 12; Length 832;
Best Local Similarity 84.6%; Pred. No. 1e+03; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 4;

Qy 1 GAACAGCATACAAACCGTTGTG 26
Db 676 GAACAGCAAAACATACAGTTTG 651

RESULT 39
CG452337 839 bp DNA linear GSS 17-SEP-2003
LOCUS
DEFINITION
CG452337 839 bp DNA linear GSS 17-SEP-2003
genomic survey sequence.
CG452337
VERSION
KEYWORDS
SOURCE
ORGANISM
Zea mays
Zea mays
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

AUTHORS

White, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics

JOURNAL Unpublished (2002)
 COMMENT Other GSSs: OGVH026TH
 TIGR Contact: Cathy Whitelaw
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whitelaw@cigr.org
 Seq primer: TP
 Class: methylation filtered.
 Location/Qualifiers
 1. 839
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone_1db="ZMMBMA0485F03"
 /clone_1lb="ZM 0.7 1.5 KB"
 /note="Vector: pBCK-; Site 1: HindIII; 0.7-1.5 kb
 methylation filtered genomic DNA library"

ORIGIN
 Query Match 70.0%; Score 19.6; DB 12; Length 839;
 Best Local Similarity 84.6%; Pred. No. 1e+03;
 Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACAGCAATACAAACCGTTGTG 26
 |||||
 Db 720 GAACAGCAAAACATTAACAGTTTGG 745

RESULT 40
 CG219765 959 bp DNA linear GSS 22-AUG-2003
 LOCUS OGMLO26TV ZM 0.7 1.5 KB Zea mays genomic clone ZMMBMA0612F03,
 DEFINITION genomic survey sequence.
 ACCESSION CG219765
 VERSION CG219765.1 GI:34119653
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoidae; Andropogoneae; Zea.
 1 (bases 1 to 959)
 WhiteJaw,C.A., Quackenbush,J., Van Aken,S., Utecherback,T.,
 Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
 Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
 Consortium for Maize Genomics
 Unpublished (2002)
 Other GSSs: OGMLO26TH
 Contact: Cathy Whitelaw
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whitelaw@cigr.org
 Seq primer: TP
 Class: methylation filtered.
 Location/Qualifiers
 1. 959
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone_1db="ZMMBMA0612F03"
 /clone_1lb="ZM 0.7 1.5 KB"
 /note="Vector: pBCK-; Site 1: HindIII; 0.7-1.5 kb
 methylation filtered genomic DNA library"

ORIGIN
 Query Match 70.0%; Score 19.6; DB 12; Length 959;
 Best Local Similarity 84.6%; Pred. No. 1e+03;
 Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACAGCAATACAAACCGTTGTG 26
 |||||
 Db 737 GAACAGCAAAACATTAACAGTTTGG 762

RESULT 41
 CZ104695 595 bp DNA linear GSS 13-JAN-2005
 LOCUS OM_Ba0113L07.r OM_Ba Oryza minuta genomic clone OM_Ba0113L07 3',
 DEFINITION genomic survey sequence.
 ACCESSION CZ104695
 VERSION CZ104695.1 GI:57680996
 KEYWORDS GSS.
 SOURCE Oryza minuta
 ORGANISM Oryza minuta
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BCP
 clade; Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 595)
 Kim,H., Collura,K., Wisotscki,M., Byrne,M., Stum,D., Smart,D.,
 Rao,K., Luo,M., Jetly,R., Kudrna,D., Muller,C., Soderlund,C. and
 Wing,R.
 OMAP (Oryza Map Alignment Project) - Arizona Genomics Institute
 Unpublished (2005)
 Contact: Rod A. Wing
 Arizona Genomics Institute
 University of Arizona
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA
 Tel: 520 626 9595
 Fax: 520 621 1259
 Email: rwing@genome.arizona.edu
 Plate: 0113 row: L column: 07
 Class: BAC ends.
 Location/Qualifiers
 1. 595
 /organism="Oryza minuta"
 /mol_type="genomic DNA"
 /db_xref="taxon:63629"
 /clone_1db="OM_Ba0113L07"
 /issue_type="leaves"
 /lab_host="DH10B"
 /clone_1lb="OM_Ba"
 /note="Vector: pCUGIBAC1; Site 1: HindIII; Site 2:
 HindIII"

ORIGIN
 Query Match 69.3%; Score 19.4; DB 13; Length 595;
 Best Local Similarity 95.2%; Pred. No. 1.2e+03;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CAATACACAAACCGTTGTG 27
 |||||
 Db 203 CAATACACAAACCGTTGTG 223

RESULT 42
 DE039251 522 bp DNA linear GSS 16-AUG-2005
 LOCUS Branchiostoma floridae DNA, clone: CH302-061024.F, genomic survey
 DEFINITION sequence.
 ACCESSION DE039251
 VERSION DE039251.1 GI:62283060
 KEYWORDS GSS.
 SOURCE Branchiostoma floridae (Florida lancelet)
 ORGANISM Branchiostoma floridae
 Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
 Branchiostoma.
 1
 Fujiyama,A., Toyoda,A., Kuroki,Y. and Sakaki,Y.
 BAC end sequences of CHORI-302 Amphioxus library
 Published Only in Database (2005)

```

REFERENCE      2 (bases 1 to 522)
AUTHORS        Fujiyama, A.
TITLE          Direct Submmission
JOURNAL        Submitted (31-MAR-2005) Aaso Fujiyama, The Institute of Physical
               and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
               1-7-22 Suenhiro-Chou, Tsurumi-Ku, Yokohama, Kanagawa, 230-0045, Japan
               (E-mail:afujiyam@gsc.riken.jp, URL:http://hsp.gsc.riken.jp/,
               Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT        PRIMERS
               Sequencing : T7
LIBRARY        Vector : pTARBAC2.1
               R.site 1 : EcoRI
               R.site 2 : EcoRI.
FEATURES       Location/Qualifiers
               1..522
               /organism="Branchiostoma floridae"
               /mol_type="genomic DNA"
               /db_xref="taxon:7739"
               /clone="CH302-061024.F"
               /sex="male"
               /issue_type="sperm"
               /clone_lib="CHOR10302 Amphioxus genomic BAC library"
               /note="common name:amphioxus"

ORIGIN
Query Match      68.6%; Score 19.2; DB 14; Length 522;
Best Local Similarity 87.5%; Pred. No. 1.5e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY              3 ACAGCATATACAAACCGTTGTG 26
                |||||
Db              270 ACAGCATATCATCATTCATTGTG 293

RESULT 43
B0626720      524 bp mRNA linear EST 01-JUL-2002
LOCUS         p226b03.y1 Pratylenchus penetrans mixed stage SL1 TOPO v1
DEFINITION    Pratylenchus penetrans cDNA 5' similar to SW:RS15_HUMAN P11174 40S
               RIBOSOMAL PROTEIN S15 ;, mRNA sequence.
ACCESSION     B0626720
VERSION       B0626720.1 GI:21653898
KEYWORDS      EST.
SOURCE        Pratylenchus penetrans
ORGANISM      Pratylenchus penetrans
               Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
               Tylenchoidea; Pratylenchidae; Pratylenchinae; Pratylenchus.
REFERENCE     1 (bases 1 to 524)
AUTHORS       McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,
               Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,
               Bowers, Y., Gibbons, M., Rittler, E., Bennett, J., Franklin, C.,
               Tsagarishevili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,
               Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,
               Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
               McCann, R., Waterson, R. and Wilson, R.
JOURNAL       The Washington Univ. Nematode EST Project, 1999
COMMENT       Unpublished (1999)
               Contact: McCarter JP
               The Washington Univ. Nematode EST Project, 1999
               Washington University School of Medicine
               4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
               Tel: 314 286 1800
               Fax: 314 286 1810
               Email: est@wustl.edu
               The library was constructed by Claire Murphy and Dr. James McCarter
               at Washington University, St. Louis. RNA was provided by Andrew
               Kloek of Divergence Inc., St. Louis, MO.
               Putative full length read
               The vector to vector length is 567
               Seq primer: SL1 primer.
FEATURES       Location/Qualifiers
               1..524
               /organism="Pratylenchus penetrans"
               /mol_type="mRNA"
               /db_xref="taxon:45929"
               /dev_stage="mixed stage"
               /lab_host="DH10B (Invitrogen)"
               /clone_lib="Pratylenchus penetrans mixed stage SL1 TOPO
               v1"
               /note="Vector: PCR11-TOPO (Invitrogen); Site 1: EcoRI;
               Site 2: EcoRI; The library was constructed by Claire
               Murphy and Dr. James McCarter at Washington University,
               St. Louis. Oligo (dT)-SL1 PCR based library. cDNA PCR
               products of size >400 nucleotides containing SL1 on the 5'
               end and oligo (dT) on the 3' end were non-directionally
               cloned into PCR11-TOPO (Invitrogen) following the TOPO TA
               cloning protocol. RNA was provided by Andrew Kloek of
               Divergence, Inc., St. Louis, MO."

```

```

ORIGIN
Query Match      68.6%; Score 19.2; DB 3; Length 524;
Best Local Similarity 87.5%; Pred. No. 1.5e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY              1 GAACAGCATATCAACAAACCGTTG 24
                |||||
Db              114 GAGCAGCAATTCACAAACCGTTG 137

RESULT 44
B0627018      524 bp mRNA linear EST 01-JUL-2002
LOCUS         p230b06.y1 Pratylenchus penetrans mixed stage SL1 TOPO v1
DEFINITION    Pratylenchus penetrans cDNA 5' similar to SW:RS15_HUMAN P11174 40S
               RIBOSOMAL PROTEIN S15 ;, mRNA sequence.
ACCESSION     B0627018
VERSION       B0627018.1 GI:21654196
KEYWORDS      EST.
SOURCE        Pratylenchus penetrans
ORGANISM      Pratylenchus penetrans
               Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
               Tylenchoidea; Pratylenchidae; Pratylenchinae; Pratylenchus.
REFERENCE     1 (bases 1 to 524)
AUTHORS       McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,
               Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,
               Bowers, Y., Gibbons, M., Rittler, E., Bennett, J., Franklin, C.,
               Tsagarishevili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,
               Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,
               Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
               McCann, R., Waterson, R. and Wilson, R.
JOURNAL       The Washington Univ. Nematode EST Project, 1999
COMMENT       Unpublished (1999)
               Contact: McCarter JP
               The Washington Univ. Nematode EST Project, 1999
               Washington University School of Medicine
               4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
               Tel: 314 286 1800
               Fax: 314 286 1810
               Email: est@wustl.edu
               The library was constructed by Claire Murphy and Dr. James McCarter
               at Washington University, St. Louis. RNA was provided by Andrew
               Kloek of Divergence Inc., St. Louis, MO.
               Putative full length read
               The vector to vector length is 576
               Seq primer: SL1 primer.
FEATURES       Location/Qualifiers
               1..524
               /organism="Pratylenchus penetrans"
               /mol_type="mRNA"
               /db_xref="taxon:45929"
               /dev_stage="mixed stage"
               /lab_host="DH10B (Invitrogen)"
               /clone_lib="Pratylenchus penetrans mixed stage SL1 TOPO
               v1"
               /note="Vector: PCR11-TOPO (Invitrogen); Site 1: EcoRI;
               Site 2: EcoRI; The library was constructed by Claire
               Murphy and Dr. James McCarter at Washington University,
               St. Louis. Oligo (dT)-SL1 PCR based library. cDNA PCR
               products of size >400 nucleotides containing SL1 on the 5'
               end and oligo (dT) on the 3' end were non-directionally
               cloned into PCR11-TOPO (Invitrogen) following the TOPO TA
               cloning protocol. RNA was provided by Andrew Kloek of
               Divergence, Inc., St. Louis, MO."

```

Site 2: EcorI; The library was constructed by Claire Murphy and Dr. James McCarter at Washington University, St. Louis. Oligo(dT)-SLI PCR based library. cDNA PCR products of size >400 nucleotides containing SLI on the 5' end and oligo(dT) on the 3' end were non-directionally cloned into pCRII-TOPO(Invitrogen) following the TOPO TA cloning protocol. RNA was provided by Andrew Kloek of Divergence, Inc., St. Louis, MO."

ORIGIN

Query Match 68.6%; Score 19.2; DB 3; Length 524;
Best Local Similarity 87.5%; Pred. No. 1.5e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAACAGCAATTCACAAACGCTTG 24
Db 123 GAGCAGCAATTCACAAACGCTTG 146

RESULT 45

LOCUS B0627107 524 bp mRNA linear EST 01-JUL-2002

DEFINITION p31d03.y1 Pratylenchus penetrans mixed stage SLI TOPO v1

Pratylenchus penetrans cDNA 5' similar to SW:RS15_HUMAN P11174 40S

ACCESSION B0627107.1 GI:21654285

VERSION B0627107.1

KEYWORDS Pratylenchus penetrans

SOURCE Eukaryote; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;

ORGANISM Tylenchoidea; Pratylenchidae; Pratylenchinae; Pratylenchus.

REFERENCE 1 (bases 1 to 524)

McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,

Wyle, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,

Bowers, Y., Gibbons, M., Rilter, E., Bennett, J., Franklin, C.,

Tagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,

Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,

Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,

McCann, R., Waterston, R. and Wilson, R.

The Washington Univ. Nematode EST Project, 1999

Unpublished (1999)

Contact: McCarter JP

The Washington Univ. Nematode EST Project, 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.wustl.edu

The library was constructed by Claire Murphy and Dr. James McCarter at Washington University, St. Louis. RNA was provided by Andrew Kloek of Divergence, Inc., St. Louis, MO."

ORIGIN

Query Match 68.6%; Score 19.2; DB 3; Length 524;
Best Local Similarity 87.5%; Pred. No. 1.5e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAACAGCAATTCACAAACGCTTG 24
Db 102 GAGCAGCAATTCACAAACGCTTG 125

RESULT 46 B0626527 573 bp mRNA linear EST 01-JUL-2002

LOCUS B0626527

DEFINITION p31d01.y1 Pratylenchus penetrans mixed stage SLI TOPO v1

Pratylenchus penetrans cDNA 5' similar to SW:RS15_HUMAN P11174 40S

RIBOSOMAL PROTEIN S15 ; , mRNA sequence.

ACCESSION B0626527.1 GI:21653705

VERSION B0626527

KEYWORDS Pratylenchus penetrans

SOURCE Eukaryote; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;

ORGANISM Tylenchoidea; Pratylenchidae; Pratylenchinae; Pratylenchus.

REFERENCE 1 (bases 1 to 573)

McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,

Wyle, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,

Bowers, Y., Gibbons, M., Rilter, E., Bennett, J., Franklin, C.,

Tagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,

Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,

Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,

McCann, R., Waterston, R. and Wilson, R.

The Washington Univ. Nematode EST Project, 1999

Unpublished (1999)

Contact: McCarter JP

The Washington Univ. Nematode EST Project, 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.wustl.edu

The library was constructed by Claire Murphy and Dr. James McCarter at Washington University, St. Louis. RNA was provided by Andrew Kloek of Divergence, Inc., St. Louis, MO."

ORIGIN

Query Match 68.6%; Score 19.2; DB 3; Length 573;
Best Local Similarity 87.5%; Pred. No. 1.5e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAACAGCAATTCACAAACGCTTG 24

FEATURES

source 1..573
/organism="Pratylenchus penetrans"
/mol_type="mRNA"
/db_xref="taxon:45929"
/dev_stage="mixed stage"
/lab_host="DH10B (Invitrogen)"
/clone_lib="Pratylenchus penetrans mixed stage SLI TOPO v1"
/note="Vector: pCRII-TOPO (Invitrogen); Site_1: EcorI; Site_2: EcorI; The library was constructed by Claire Murphy and Dr. James McCarter at Washington University, St. Louis. Oligo(dT)-SLI PCR based library. cDNA PCR products of size >400 nucleotides containing SLI on the 5' end and oligo(dT) on the 3' end were non-directionally cloned into pCRII-TOPO(Invitrogen) following the TOPO TA cloning protocol. RNA was provided by Andrew Kloek of Divergence, Inc., St. Louis, MO."

Db 121 GAGCAGCAATTCACAAACGTTG 144

RESULT 47
LOCUS BU220286
DEFINITION BU220286 707 bp mRNA linear EST 25-NOV-2002
sequence. 603107182F1 CSEBCHN04 Gallus gallus cDNA clone CHEST48C21 5', mRNA
ACCESSION BU220286
VERSION BU220286
KEYWORDS GI:25405987
SOURCE EST.
ORGANISM Gallus gallus (chicken)
Gallus gallus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianidae; Gallus.
1 (bases 1 to 707)
Boatman, P.B., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken CDNAS
Curr. Biol. 12 (22), 1965-1969 (2002)
12445392
JOURNAL
PUBMED
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers

FEATURES
source
1..707
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hisex"
/db_xref="taxon:9031"
/clone="CHEST48C21"
/issue_type="whole embryo"
/dev_stage="20-21"
/lab_host="DH10B"
/clone_lib="CSEBCHN04"
/note="Organ: whole embryo; Vector: pBluescript II KS(+);
Site 1: EcoRI; Site 2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunt-ended, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

ORIGIN
Query Match 68.6%; Score 19.2; DB 3; Length 707;
Best Local Similarity 87.5%; Pred. No. 1.5e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAACAGCAATTCACAAACGTTG 24
|||||
Db 329 GAACAGCATATACAAACGTTG 352
|||||

RESULT 48
LOCUS DR154444/c
DEFINITION DR154444 783 bp mRNA linear EST 16-JUN-2005
pseudoboscurea cDNA clone K19 3', mRNA sequence.
ACCESSION DR154444

VERSION DR154444.1 GI:67899534
KEYWORDS EST.
SOURCE Drosophila pseudoboscurea
ORGANISM Drosophila pseudoboscurea
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 783)
Richard, S., Liu, Y., Bettencourt, B.R., Hradecky, P., Letovsky, S.,
Nielsen, R., Thornton, K., Hubisz, M.J., Chen, R., Meisel, R.P.,
Courtois, O., Hua, S., Smith, M.A., Zhang, P., Liu, Y., Bussemaker, H.J.,
van Batenburg, M.F., Howells, S.L., Scherer, S.B., Sodergren, E.,
Matthews, B.B., Crosby, M.A., Schroeder, A.J., Ortiz-Barrientos, D.,
Wheeler, C.M., Metzker, M.L., Muzny, D.M., Scott, G., Steffen, D.,
Rieser, D.A., Worley, K.C., Havlak, P., Dublin, K.J., Egan, A.,
Gill, R., Hume, J., Morgan, M.B., Miner, G., Hamilton, C., Huang, Y.,
Waldron, L., Verdugo, D., Clerc, Blankenburg, K.P., Dubchak, I.,
Noor, M.A., Anderson, W., White, K.P., Clark, A.G., Schaeffer, S.W.,
Gelbart, W., Weinstein, G.M. and Gibbs, R.A.
Comparative genome sequencing of Drosophila pseudoboscurea:
chromosomal, gene, and cis-element evolution
Genome Res. 15 (1), 1-18 (2005)
15632085
JOURNAL
PUBMED
COMMENT Contact: Stephen Richards
Human Genome Sequencing Center
Baylor College of Medicine
One Baylor Plaza, Houston, TX 77030, USA
Tel: 713-798-6667
Email: stephen@bcm.tmc.edu
NCBI Trace Archive: 22669758
Insert Length: 1750 Std Error: 0.25.
Location/Qualifiers

FEATURES
source
1..783
/organism="Drosophila pseudoboscurea"
/mol_type="mRNA"
/db_xref="taxon:7237"
/clone="K19"
/dev_stage="0-18h embryos"
/clone_lib="Drosophila pseudoboscurea embryonic cDNA
library"
/note="Vector: pOTB7; Site 1: EcoRI; Site 2: XhoI; oligo
dt priming from poly A+ RNA, directionally cloned"

ORIGIN
Query Match 68.6%; Score 19.2; DB 9; Length 783;
Best Local Similarity 87.5%; Pred. No. 1.5e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAACAGCAATTCACAAACGTTG 24
|||||
Db 764 GAACAGCAATTCACAAACGTTG 741
|||||

RESULT 49
LOCUS BI153495
DEFINITION 602915583F1 NC1_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5066108 5',
mRNA sequence.
ACCESSION BI153495
VERSION BI153495
KEYWORDS GI:14613496
SOURCE EST.
ORGANISM Mus musculus (house mouse)
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
REFERENCE NIH-MGC http://mgs.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
plate: L1AM1178 row: e column: 21
High quality sequence start: 29
High quality sequence stop: 815.
Location/Qualifiers

FEATURES

source
1..817
/organism="Mus musculus"
/mol_type="mRNA"
/strain="Czech II"
/db_xref="taxon:10090"
/clone="IMAGE:5066108"
/tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DH10B"
/clone_lib="NCI CGAP Lu29"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Salt;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

ORIGIN

Query Match 68.6%; Score 19.2; DB 2; Length 817;
Best Local Similarity 87.5%; Pred. No. 1.5e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AACAGCAATACAAACCGTTGT 25
|||||
Db 664 AACAGCAATACAAACCGTTGT 687

RESULT 50
CT474369 818 bp DNA linear GSS 03-NOV-2005
LOCUS
DEFINITION
Sus scrofa genomic clone CH242-469H10, genomic survey sequence.
CT474369
CT474369.1 GI:80214467
GSS.

KEYWORDS
Sus scrofa (pig)
Sus scrofa
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae;
Suidae;
Sus.

REFERENCE
AUTHORS
TITLE
JOURNAL
1 (bases 1 to 818)
Humphray, S.J., Plumb, R.W. and Durham, J.L.
Direct Submission
Submitted (01-NOV-2005) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humphrey@sanger.ac.uk Unpublished

COMMENT
This sequence was generated from the T7 end of BAC 469H10. 469H10
is part of the CHOBI-242 BAC library created by P. de Jong. Further
details: http://www.sanger.ac.uk/Projects/S_scrofa/.
Location/Qualifiers

FEATURES

source
1..818
/organism="Sus scrofa"
/mol_type="genomic DNA"
/db_xref="taxon:9823"
/clone="CH242-469H10"
/tissue_type="white blood cells"
/note="vector pTARBAC1.3_BamHI
sex female"

ORIGIN

Query Match 68.6%; Score 19.2; DB 14; Length 818;
Best Local Similarity 87.5%; Pred. No. 1.5e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 AGCAATACAAACCGTTGTGTG 28
|||||

Db 511 AGCAATACAAACCGTTGTATG 534

Search completed: May 24, 2006, 07:54:55
Job time: 1999.02 secs

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